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Search information blook:
Ouery: Us-09-471-276-831
Ouery length: 126
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CCTGCTCCCTGGCTCTCGATGGCGCCAGT 404
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/sex~"male"
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Align seg 1/1 to: W25099 from: 1
                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDITINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w25099 457 bp mRNA EST zb68b07.rl Soares_fetal_lung_NbHL19W Homo sapiel IMAGE:308725 5' similar to SW:ALBG_HUMAN P04217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cst@watson.wustl.edu
This clone is available royalty-free through LLNL: contact the
IMAGE Consortium (info@image.linl.gov) for further information.
Insert Length: 1951 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Netazoa: Chordata; Craniata; Vertebreta; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 457)
                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 267
Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                        Ratio:
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//note-*Organ: lung 'wester: pT779 (Phirmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI: late strand cDM, was primed with a Not I: oligo(dT) primer: [5'-rograpocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacorgosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosacocaArcrosac
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89.844
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/dev_stage="19 weeks"
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/db_xref."GDB:1252138"
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1 MCtScrmctLcuValValPheLcuLcuTcuTrpGlyValThrTrpGlyPr 17

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COMMENT
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                                                                                                                                                                                                                    MGI:418554
Seq primer:
                                                                                                                                                                                                                                                                                                                         WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L/
Tcl: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA250460 495 bp mRNA mw99e06.rl Soares mouse NML Mus similar to SW:AlBG_HUMAN P04217 sequence.
                                                                                                                                                                                                                                                       This clone is available royalty-free through LLNL ; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellanberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
AA250460
AA250460.1 GI:1882326
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                    primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                       quality sequence stop: 493.
Location/Qualifiers
                    /clone_lib="Soares mouse NML"
/tissue_type="Liver"
/lab_host="DH10B"
                                                                                   /db_xref="taxon:10090"
/clone="IMAGE:678850"
  /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus cDNA clone IMAGE:678850 ALPHA-1B-GLYCOPROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bowles, M., Dietrich, N., Dubuque, T
                                                                                                                                                                                                                                                                                                                                                                      St. Louis,
                                                                                                                                                                                                                                                          further information
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                                                                                                                                                                                                                                                                                  contact the
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REFERENCE
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LOCUS AA700860
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                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AA250460 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                 412 GGCT 415
                                                                                                                                                                                                                                                                                                                                                                                           120 uAla 121
                                                                                                                                                     115 bp mRNA EST 19-DEC-1997 zj36b07.sl Soares_fetbl_liver_spleen_lNFLS_Sl Homo sapiens cDNA clone TMGE:452341 3' similar to SN:AlBG_HUMAN P04217 AA700860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 115)
                                                                                                           EST
                                                                                                                                AA700860.1
                                                                                      human.
                                                                                                                                                  AA700860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
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1.543
59.559
                                                                                                                             GI:2704025
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362 CTAAGCAATGCTGTGGAGGTGACAGGGAAAGAGCCCCTTGCCTCGGCCCTT
                             104 LeuSerLysLeuLeuGluLeuThrGlyProLysValLeuAlaCysSerLe
                                                                                        312 TGGAACCCCCTGTTGACATTCACCTGCCAGCACTGAACAAGTGGACCATG
                                                                                                                                                                                        262 GGGGGCCATTACAAGTAACAACAGTGGCATCTACCGCTGCAGATGTGGCG
                                                                                                                                                                                                                                                                                    212 CTGAGTCAAGTCCGACTTGAGACACAGGTGCTGTCATACCGCTTTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                162 CAGTTGATTTGCCGACTAAGGTCTTCGAGCTGATCCAGAACGGGTGGTTC
                                                                                                                                                                                                                               83 u.....ThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyL
                                                                                                                                                                                                                                                                                                                                                                                                          50 oGlyProProGlyAspSerArgLeuProAla.ValGlnGluTrpGlyAla 66
                                                                                                                                      97 euSer.....ThrGlyTrp***Gln
                                                                                                                                                                                                                                                                                                                              67 GlnGluProValHisLeuAspSerProAlaIleLysHisGlnPheLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 lu.SerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AGGARATACTCTAATGCTCGATTCTGGCAGTGAACCTAAACTATGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 ATGTCTCTGCTGGCTACTGTACTGCTGTGGGGGGTTCACTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCTCAGTCCCTGCT...GGAACCCTGGGCAAACCTGACCCTGGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed and normalized by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st
was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O
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5
34.559
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seq_name: gb_est2:BG397331
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ORIGIN
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                                                                                 DEFINITION
                                                                                                                                  seq_documentation_block:
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          VERSION
                               ACCESSION
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 GCCATATTTTGTGAGACGCAGCGCGGCGTGTGGGCAGAGTCCGAATCACT
                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                          55
                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                    38 *LeuLySThrLeuGlyGlnCysAspAlaAspValProGlyProProGlyA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 AlaIlePheTyrGluThrGln***SerLeuTrpAlaGluSerGluHis**
                                                                                                                                                                                                                                                                                      spSerArgLeuPro 59
                                                                                                                                                                                                                                                                                                                                        GCTGAA.ACCCTTGGCCAATGTGACGCTGACGTGCAGTGCCCGCGTGGAG
                                                                                                                                                                                                                                     ACTCCAGAGTTCCA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BG397331
BG397331.1 GI:13290779
                                                                          BG397331 916 bp mRNA EST 12-MAR-2001 602439123F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4565549 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMAGE Consortium (info@image.lini.gov) for further information. Trace considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK, School of Medicine Washington University School of Medicine A444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Possible reversed clone: similarity on wrong strand Seq primer: -40m13 fwd. ET from Amersham
                                                                                                         BG39733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dbv_stage.*20 week-post conception fetus*
//tbb_host DH108 (ampicillin resistant)**T7730 (Pharmacia)
//note**Organ: Liver and Spleen: Vector: pT7730 (Pharmacia)
with a modified polylinker: Site_i: Pac I: Site_2: Ecc R:
This is a subtracted version of the original Soares fetal
liver spleen INFLS ilbrary. Ist strand cDNA was primed
with a Pac I - oligo(dT) primer [5'
AACTGCANGANTWANGTANGCTTWTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Ecc RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Ecc RI sites of the modified pT73 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaido.*
23 a 37 c 32 g 23 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114.00
3.677
81.579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism'"Homo sapiens"
/db_xref:"GDB:1388697"
/db_xref:"taxon:9606"
/clone:"IMAGE:452341"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib. "Soares_fetal_liver_spleen_infLS_S1"
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Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.684
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                                                                                    555 AGCACTCTGGATTACACGGATCCCACAGGAGCTT.
                                                                                                                                                                                   505 CAGGGGGGCCAGGAGACCCAGGAGTACCGTCTATATAGAGAAAAAGAAAAC
                                                                                                                                                                                                                                                                                      458 AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT 504
                                                                                                                                                                                                                                                                                                                                                                                         408 CAGGACCCACGTGCAGGCAGGCCACCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
       78 ysHisGinPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr
                                                                                                                                                                                                                                                                                                                                    34 luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP
                                                                                                                                                                                                                                                                                                                                                                                                                                              17 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                 50 roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                               .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://image.llnl.gov
Plate: LLCM1282 row: m column: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Nealth, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Tncyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Directionally cloned into EcoRL/Xhol sites using the following 5' adaptor: GECARCAGG(9. Size-selected >900bp for average insert size 1.8kb. Library constructed by Lir liong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies). Note: this is a NIH_MCC_library."
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1.493
56.693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type."primary B-cells from tonsils (cell line)"
/lab_host_bulb8 (phage-resistant)"
/note."Organ: B-cells, Vector: p0%B7; Site_1: Xho1;
/note."Organ: B-cells, Vector: p0%B7; Site_1: Xho1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib~"NIH_MGC_48"
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/db_xref~"taxon:9606"
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JOURNAL
COMMENT
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AUTHORS
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VERSION
                                                                                                    US-09-471-276-831 x AA530090
                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina
1 (bases 1 to 506)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dut
Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Ten, F., Underwood, K., Moore, B
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28m13 rev1 ET from Amersham
High quality sequence stop: 287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST project
WashIngton University School of Medicinep
WashIngton University School of Medicinep
4444 Porest Park Parkway, Box 8501, St. L
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/tisse_type='diaphragm"
/dey_stage="adult"
/dey_stage=
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                          quality sequence stop: 521.
Location/Qualifiers
/note="Organ: brain; Vector; pBluescriptR (modified pBluescript KS+); Site_1: BamHI: Site_2: Sail-Yaho! (gtogag ); Oligo-dp primed using primer 5'-TYTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and
                                                                                                                                                                                          /clone="IMAGE:4795550"
/clone_lib="NIH_MGC_96"
                                                                                                                           /tissue_type-"hypothalamus"
/lab_host-"DH10B"
                                                                                                                                                                                                                                                               /db_xref="taxon:
                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                 Unpublished (2000)
                                                                                                                                                                                                                                                     Edwaryota, Metazoa: Chordata: Craniata: Vortebrata: Euteleostomi;
Mammalia: Eutheria: Cetartiodbctyla: Suina; Suidae; Sus.
1 (bases 1 to 268)
Fahrenkrug.S.C., Freking.B.A., Rohrer.G.A., Smith, T.P.L., Casas, E.,
                                                                                                                                                                                                                                                                                                                                                                                                            AW359511
AW359511.1 GI:6864161
                                                                                                                                                                                                                                                                                                                                                                                                                                                   46143 MARC 2PIG Sus scrofa cDNA
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  Single
                                                                                                                               Contact: Smith TPL
                                                                                                                                                                                          and Keele, J. W.

Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                  stone,R.T., Heaton,M.P.,
and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                              pig.
Sus scrofa
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pass sequencing. Bases called and trimmed with phred
                    smith@email.marc.usda.gov
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                                                                                                                                                                                                                                   Grosse, W.M., Bennett, G.A., Laegreid, W.W.
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ACCESSION
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ORGANISM
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US-09-471-276-831 x AW359511
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                                                                 JOURNAL
                                                                                                             TITLE
                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 alProGlyPro.....ProGlyAspSerArgLeuProAlaVal 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACGCCCTCCTCATGGATGGGGGACTCAGATCCAGGGACAGA 254
                                        EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                       Mammalia: Eutheria: Cetartiodactyla; Suina: Suidae: I (basea 1 to 273)
Fairenkrug.S.C., Frekling,B.A., Rohrer,G.A., Smith,T. Fatnenkrug.S.C., Frekling,B.A., Rohrer,G.A., Smith,T. Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., and Keele,J.M.
Design and use of two pooled tissue normalized cDNA
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                       pig.
Sus scrofa
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Plate: 28 row: H column: 24
Seq primer: ATTTAGGTGACACTATAG
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PCR PRimers
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1.968
58.025
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/lab_host.."DH10B"
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/db_xref·"taxon:9823"
/clone_lib-"MARC 2PIG"
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Gaps: 4
Identity: 32.099
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                                                                                                                                                                               Smith, T.P.L., Casas, E.
                                                                                                             cDNA libraries for
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                                                                                                                                                      Laegreid, W.W.
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seq_name: gb_est2:BI337778
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                                                                                                                                                                                                                                                                                                                                       pig.
Sus scrofa
                             and Keele,J.W.

Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                       Bukaryota, Metazoa; Chordata; Craniata, Pertebrata; Buteleostomi; Nammalia; Butheria; Cetartiodactyla; Sulna; Suldae; Sus. 1 (bases 1 to 514)
1 (bases 1 to 514)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361317 MARC 1PIG Sus scrofa cDNA
BI337778
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Seq primer: ATTTAGGTGACACTATAG.
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Fax: 402 762 4390
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discovery in swine
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/tissue_type="pooled"
/tab_bast="bBiDe"
/hab_bast="bBiDe"
/habe="Vector: pCWV SPORT6; Site_1: XbaI; Site_2: XhoI;
/habe="Vector: pCWV SPORT6; Site_be: XbaI; Site_be: XbaI
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/clone_lib="MARC 2PIG"
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SOURCE

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COMMENT
                     REFERENCE
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LOCUS BE012583
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   AUTHORS
                                                                                                                                                                                                                                                                                                                               316 ACACGCCCTCCTCATGGATGGGGGACTCAGATCCAGGGACAGA 358
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         Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
1 (bases 1 to 544)
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Single pass sequencing Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the .minscore
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PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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Contact: Smith TPL
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A.,
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Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
a 179 c 125 g 98 t
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/db_xref="taxon:9823"
/clone_lib="MARC IPIG"
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Identity: 32.099
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   Smith, T.P.L., Casas, E.
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SOURCE
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VERSION
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LOCUS BC733169
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US-09-471-276-831 x BE012583
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                              BG733169.1
BG733169.1
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Ratio:
                                                                                        BG733169 548 bp mRNA EST 1346903 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
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Plate: 48 row: D column: 21
Seq primer: ATTTAGGTGACACTATAG
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Dasign and use of two pooled tissue normalized cDNN libraries for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
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scrofa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Vector: pCMV SPORTS; Site_1: XhaI; Site_2: XhaI;
Library made from pooled tissue from day 11, 13, 15, 20
and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organismo"Sus scrofa"
/db_xrefo"taxon:9823"
/clone_libo"MARC 1PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type…"pooled"
/lab_host…"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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1.968
                                                          GI:14019453
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Gaps:
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ORIGIN
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AUTHORS
seq_name: gb_est2:T68210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: BG733169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-471-276-831 x BG733169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                                                                           216 AGGAGCTGGGGATCCCCCTCCCCCCATGCACTGTGAAGGACCCTCGTTTAC 265
                                                                                                                                                                                                                                      172 TCCCCAGCCCGGAGACATACTTGAAGGGCCAGAGCCGG.....GAGGTG 215
                                                                                                                                                                                                                                                                                                                                    131 GGCGCTTCCTGAA.
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                                                                                              78
                                                                                                                                                                                            62
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GlyProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTr 32
                                                                                                                                                                                     GinGluTrpGlyAlaGinGluProValHisLeuAspSerProAlaTlcLy 78
                                                                                       sHisGlnPheLeuLeuThrGlyAspThrGlnGlyArgTyrArg 92
                                                                                                                                                                                                                                                                                alProGlyPro.....ProGlyAspSerArgLeuProAlaVal 61
                                                                                                                                                                                                                                                                                                                                                                           pAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspV 49
                                                                                                                                                                                                                                                                                                                                                                                                                        GGCCCAGTCCCCCCACCCTCAGTCTAC....TGACAGGGAGGAGGCTG 130
                                                ACACGCCCTCCTCATGGATGGGGGACTCAGATCCAGGGACAGA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 108 row: H column: 14
Seg primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Smith Ppt.
USDA, ARS US Meat Animal Research Center
PO Box 166, Clay Conter, NE 68933-0166, U
Tel: 402 762 436
Fax: 402 762 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swinc upon tissue (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and -minmatch 12 options.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stone, R.T., He and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalla; Eutheria; Getartiodactyla; Suina; Suidae;
1 (bases 1 to 548)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib."MARC IPTG"
//Lisus_type_'ppooled*
//lab_lost."DBLD9"
//lost."CBLDD PCHV SPORTG: Site_1: xbal; Site_2: xhol;
Library made from pooled tissue from dby 11, 13, 15, 20,
and 30 cmbryos."
a 187 c 149 g 93 t
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1.968
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/db_xref··"taxon:9823"
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                                                                                                                                                                                                                                                                                                                                 .....GGTGCTGAGGGCCAGGGAGAAGCTCCTC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 32.099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Casas, E.
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seq_documentation_block: LOCUS T68210

97 bp

mRNA

22-FEB-1995

DEFINITION

yc40b03.rl Stratagene liver (#937224) Homo sapiens cDNA clone IMAGE:83117 5' similar to SP:A1BG_HUMAN P04217 ;, mRNA sequence

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BASE COUNT
ORIGIN
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ORGANISM
seq_documentation_block
                                               seq_name: gb_est2:BG819104
                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-471-276-831 x T68210
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                                                                                                                                                                                                                                                                                            Align seg 1/1 to: T68210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                           39
                                                                                                                                                                                                                                          23 TlePheTyrGluThrGln***SerLeuTrpAlaGluSerGluHis***Le 39
                                                                                              uLysThrLeuGlyGlnCysAsgAlaAspValProGlyProProGly 54
                                                                                                                                                                                             ATATTTTATGAGACGCAGCCCAGCCTGTAGGAGGAGTCCNAATCACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High qality sequence starts: 1 High qality sequence stops: 15 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Possible reversed cloner similarity on wrong strand Insert Length: 87 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chissoe, S., Dietrich, M., Dubeque, T., Ravello, A., Cish, W., Hawkins, M., Hultman, M. Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohling, T., Ostes, M.B., Tan, F., Therry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags cenome, Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13RP1
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab.host="SoLR cells (kanamycin resistant)"
/note="Organ: liver; Vector: pBluescript SK, Site_1: EcoRI
/Site_2: Xho; Cloned unidirectionally Primer: Oligo
ff: Hepatectomy from normal male caucasian. Average insert
size: 1.1 kb, Uni-ZAP XR Vector; -5 dadptor sequence: 5'
GANTYCGCACGAG 3' -3' adaptor sequence: 5'
CTCGAGTTYTTTTTTTTTTTTTTTT" 3'"
a 26 c 23 g 19 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                92.00
3.538
81.250
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/db_xref="GDB:500174"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib-"Stratagene liver (#937224)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:83117"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
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Gaps: 0
Percent Identity: 75.000
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: BG819104 from: 1 to: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-471-276-831 x BG819104/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
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                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                                                                                                                                                        100 GlyTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValLe 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 ....CATCTGATACAGGTGACCACTCCATCTTTAAAATGGAGTTTTAACT 138
      49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 aGlnGluProValHisLeuAspSerProAlaTleLysHisGlnPheLeuL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 ProGlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGlyAl 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGCAGAGAGTCTGATAGGAGGCTTCCTTCGTTGGCCTCCTGGGGA.. 184
ARACGTTGGTGTGCCCCAGGATGGA 25
                                                                                                                                                                                                                                                                                                                                                     TGACTCCAGAAACACAGCATTCTTAT....
                                                                                                                                                                                                                                                                                                                                                                                                                                      euThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThr 99
                                                                                uAlaCysSerLeuAlaLeuAspGly 124
                                                                                                                                                                       TCACTGCCACTTCTCAGTGTCCTCTGACAGCTCTCCTCTTCCAAATCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryofa; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 80); 1 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG819104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10857 row: i column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Const
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-Porgan: brain: Vector: pCMV-SPORTG: Site_J
Site_J: Sail_Cloned unddirectionally primer: C
Nerrage insert size_J.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library.
180 c 180 g 19/t
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2.022
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/clone_11b="NCI_CGAP_Brn67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host-"DH10B (Tl phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="anaplastic oligodendroglioma with lp/19q/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.000
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Gaps: 2
Percent Identity: 34.667
                                                                                                                                                                                                                                                                                                                                                            . TTTCTTCCAACG
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seq_name: gb_est2:BG775650

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ACCESSION
VERSION
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                             us-09-471-276-831 x BG775650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: BG775650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                          502
                                                                                                                                                                           479 C.....TACAACCCCAAAACAAAACTT 501
                                                                                                                                                                                                                                                                      429 ATGTGGTTGGAGGAAGAGCATGGACTGAAGACTTTGAATACTGTAGAGTG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                      64
                                                                                                                                                                                                                                 47
GTACTGGAAGGTCCCATGTATGCCGTAGGAGGACATGATGGCTGGAGCTA 601
                                           ...LeuAspSerProAlaIleLys......HisGlnPh 81
                                                                                       GGAGTGTGATGCCACCTATGTCCACACATAGACATGGCCTTGGTGTGGCT 551
                                                                                                                                rpGlyAlaGlnGluProValHis.....
                                                                                                                                                                                                                          aAspValProGlyProProGlyAspSerArgLeuProAlaValGlnGluT
                                                                                                                                                                                                                                                                                                                  LeuTrpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAl 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 780.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM1613 row: h column: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Buteleoscomi; Mammalia; Eutheria; Primatea; Catarfrini; Hominidae; Homo.

1 (bases 1 to 943)

NIH-MGC http://mgc.nci.nih.gov/.

National_institutes of Health, Mammalian Gene Collection (MGC)
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BG775650.1 GI:14045967
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602650592F1 NIH_MGC_40 Homo sepiens cDNA clone IMAGE:4761286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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CDA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DMA Sequencing by: Incyte Genonics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note-"Organ: prostate; Vector: poTBJ; Site_1: XNDI; Site_2: ECORI; CDNA made by Oilgo-dy priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACCAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkoley) using AAP-CDNA synthosis kit (Stratagene) and Superscript II R (Life Technologies).

Note: this is a NHH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism "Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4761286"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type "carcinoma, cell line"
/lab_host "DH10B (phago-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib~"NIH_MGC_40"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.735
                                                                                                                                                                                                                                                                                                                                                                 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 25,641
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                                                                                                                                                                                                                                                                                                                                                                    943
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AUTHORS
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
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                  1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr 17
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alignment_block:
US-09-471-276-831 x BF525381/rev
                                                                                                                                                                                                        altgnment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
Align seg 1/1 to reverse of: BF525381
                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                702 AAGTGGAAAACTTTATGCAAGTTGGTGGTCGTGACTGGAAGTTCTTGTCT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 u 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 GlyTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValle 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eLeuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeu.
:||| ||| |||||:::||| ||| |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C 752
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                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov, plate: LLAM9783 row: e_column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata; Vertebrata;
Mammalla; Eutheria, Primates; Catarrhini; Hominidae
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5', mRNA sequence.
BF525381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 696.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                268
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                                                                                                                                                                                                                                                                                                             'cissue_type."giloblöstoma with BEFR amplification"
//ab.host-"byHDB (T1 phage resistant)"
//acte 'Organ: brain; vector: PCMV-SPORT6; Site_1: Noti;
Site_2: Sall: Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.57 kb. Constructed by Life
Technologies. Note: this is a NCL_CCAP Library."

3 38 c 291 g 214 t
                                                                                                                             90.00
1.364
49.624
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/db_xref⊷"taxon:9606"
/clone∵"IMAGE:4212470"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib "NCI_CGAP_Brn64"
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                                                                                                                             Percent Identity:
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   from: 1 to: 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens cDNA clone IMAGE:4212470
                                                                                                                                 27.820
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1052 GTGAGTACTGCTAGTGTGTTTTTTTTGTGTGTCTCTTTTCCTCGACTCC 1003

JOHNAL Unpublished (1998) COMMENT Clemson University Genomics Institute Clemson University Genomics Institute Clemson University Genomics Institute 100 Jordan Hall State Clemson University, Clemson, SC 29634 Tel: 864 655 973 Pax: 865 973 Pax: 864 655 973 Pax: 865 973	NISM NCE ORS	seq_documentation_block: 500 bp DNA GSS 06-MAR-1999 DEFINITION mgxb0006122f CUGI Rice Blast BAC Library Magnaporthe grisea genomic clone mgxb0006122f, DNA sequence. ACCESSION AQ400188 VERSION AQ400181. GI:4371215 KEYMODDS GSS. SOURCE Magnaporthe grisea.	811 CTCATATTCGCAGTTTTTCTGAGCGCAGGTCGAGGCACAGCG 765 89	45CysAspAlaAspValProGlyProProGly: .ArgLeuProA1 60 911 GTGTCTCGCTTGGATAGTCGGGGGGCCCCCGGGGCTCCATGGTGCAC 662 60 aValGLnGluTrpGlyAlaGlnGluProValHisLeuAspSerP 75 111:::	17 OVAIThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG 34 :::
seq_name: gb_estl:AM056411 seq_documentation_block: AM056411 DEFINITION	87 hrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGly 100	54 GlyAspSerArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProVa 70 111	GlyProValThrG1 ::: GCTGTCTGCCCCC pAlaGluSerGluH ::: ::: ACTAAATTCTGACT laaSpalProGly llaspalProGly TAAAAGTA	alignment_scores: Quality: 89.00 Length: 114 Percent Similarity: 50.877 Percent Identity: 33.33 alignment_block: US-09-471-776-831 x AQ400188/rev	order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 23X genome coverage. High density colony filters are available upon request. BASE COUNT 147 a 131 c 98 g 124 t

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order to facilitate genome wide analysis, a BAC library containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25X genome coverage. High density colony filters are available upon request."
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                                                                                                                            IleLysHisGlnPheLeuLeuThrGlyAspT 87
                                                                                                                                                                                               laValGlnGluTrpGlyAlaGlnGluProVa
                                                                                                                                                                                                                                                                                          yGlnCysAspAlaAspValProGlyProPro 53
                                                                                                                                                                                                                                                                                                                                                                            ***SerLeuTrpAlaGluSerGluHis***L 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyvalThrTrpGlyProvalThrGluAlaAl 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              f: AQ400188
GTGGGCTTGTAGGTCTGGGATG.....
                        .TyrArgCysArgSerGlyLeuSerThrGly 100
                                                                                     ATCAAGGGT....CTGTTGTCAGGGACAC 163
                                                                                                                                                                          CATGTCAAGAAATGCAAATAGAAAACCCGGT 207
                                                                                                                                                                                                                                                            TTGTCGGGAGTTAAAAGTA.......
                                                                                                                                                                                                                                                                                                                                                    TCTTCTTTGCAACTAAATTCTGACTCGCATC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                         CATATTCTTGGGCTGTCTGCTCCGCCGACGC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 114
Gaps: 5
Percent Identity: 33.333
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REFERENCE
AUTHORS
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ORGANISM
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US-09-471-276-831 x AW056411
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                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                    DEFINITION
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LOCUS AW656229
                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est1:AW656229
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                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                         VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 GluTrpGlyAlaGlu.ProValHisLeuAspSerProAlaTleLysH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                          T<sub>G</sub>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eu 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAAGTGGACAATGCTAAGCAATGCTTTGGAGGTGACAGGGAAAGAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCGATGTGGCGTGGAACCCCCCTGTTGACATTCAACTGCCAGCGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rGlyTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValL 116
Smith.T.P.L., Grosse, H.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegraid, H.W., Rohrer, G.A., Chitko-McKown, C.G., Portce, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peccora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                     AW656229 529 bp mRNA EST 108362 AWRC 1BOV Bos taurus cDNA 5', mRNA sequence. AW656229 AW656229.1 GI:7422055
                                                                                                                                                                                                                                                                                                                                                                                                                                          208
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Insert Length: 233 Std Error: 0.00
Seq primer: M13 Forward.
                                                                                                                                                                                                          COW
                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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Email: petra.tolle
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                                                                                             (bases 1 to 529)
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//tisue_type:"liver"
//dev_stage:"2 year old"
//note-"Hepetic cDNA obtained from vehicle or GH-treated
old male rats were used as driver (vehicle) and tester
(GH), or vice versa, to generate gene products that were
induced or repressed by GH. After two rounds of
subtraction and amplification, using hybridization
tester-driver ratios of 1:100 and 1:800, difference
products were cloned in the BamHl site of the pBluescript
II SK+ vector "
63 c 64 g 54 t
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2.011
64.706
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/strain·"Sprague-Dawley"
/db_xref·"taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex."male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib . Representational Difference Analysis Products
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                     seq_name:
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BASE COUNT
ORIGIN
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                                                     103 TCATTGAGCGGCTGAACCACATTTCCTTGTTCTCTGCAGCTAAGAGGG 56
                                                                                             109 GluLeuThrGlyProLysValLeuAlaCysSerLeuAlaLeuAspGly 124
                                                                                                                                                   150 AT...AGCCCAGGATGGAGTGAGGCCAGAGCAGGTGCGACCCTGCTGAGA 104
                                                                                                                                                                                                                                                    185 TCAG....
                                                                                                                                                                                                                                                                                                                                               229 GGGTGGATTCAGGAGGGACTCTGGCTCCTGGGGGGACCT.....GACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                            279 AGCAGGACAGCCCTGGACCACCAGGCAGGACAGGGCCTCCAGGGTCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 spAlaAspValProGlyProProGlyAspSerArgLeuProAlaValGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 aGluSer.....GluHis***LeuLysThrLeuGlyGlnCysA 46
                                                                                                                                                                                           96 lyLeuSerThrGlyTrp***Gln.....LeuSerLysLeuLeu
                                                                                                                                                                                                                                                                                            79 sGlnPheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ProValThrGluAlaAlaTlePheTyrGluThrGln***SerLeuTrpAl
gb_est2:BG178413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine CDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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Plate: 93 row: D column: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
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/db_xref~"taxon:9913"
/clone_lb~"MARC 1BOV"
/tissue_type~"pooled"
/lab_host~"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pCMV SPORTS; Site_1: XbaI; Site_2: Library made from pooled tissue from lymph node, c fat, hypothalamus, and pituitary."

171 c 145 g 126 t 1 others
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alignment_block:
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AUTHORS
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LOCUS BG178413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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  395
                                                                                                                                                                                                                                       248
                                                                                                                                                         295 CGTGACCCTCTGGTGTCAGGGGGATCCTGGAGACCCAGGAGTACCGTCTGT
                                                                                                                                                                                                                                                                                                                       198 GGGCTGAGTCTGGGCCCCAGGACCCACGTGCAGGCAGGGACCCTCCCCAA 247
                                                                                                               61 1.GlnGlu......TrpGlyAlaGlnGluProValHisLeu
                                                                                                                                                                                                  45
                                    73 AspSerProAlaIleLysHisGlnPhe.....LeuLeuThrGlyAs 86
                                                                                                                                                                                                                                                                           28 n***SerLeuTrpAlaGluSerGluHis***LeuLysThrLeuGly.Gln 44
                                                                                                                                                                                                                                                                                                                                                         12 GlyValThrTrpGlyProValThrGluAlaAlaIlePheTyrGluThrGl
                                                                                                                                                                                                CysAspAlaAspValProGlyProProGlyAspSerArgLeuProAlaVa
                                                                                                                                                                                                                                       GCCCACACTCTGGGCTGAGCCAGGCTCTGTGATC...ACCCAGGGAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
place: LLAM10166 row: b column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 892)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              602330201F1 NIH_MGC_91 Homo sapiens cDNA clone IMAGE:4431264 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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.GTGAAGAAGGGCCAGTTCCCCATCCCGTCCATCACCTGGGA 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type-"adenocarcinoma, cell line"
//lab.host="DBH108 (phage-resistant)"
/note="Organ: prostate; Vector: pCHV-SPORT6; Site_1: NotI;
Site_2: Sali; Cloned unidirectionally; oligo-df primed.
Average insert size 1.4 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NHH_MC_Library."
a 275 c 247 g 171 t
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1.509
52.727
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/clone_lib="NIH_MGC_91"
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/db_xref="taxon:9606"
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Consortium (LLNL)
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308 TGACCATCTGGTGTYAGGGGAGCCTGGAGGCCCAGGAGTACCAACTGGAT
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                                                  37 is***LeuLysThrLeuGlyGlnCysAspAla.....
                                                                                                                                                                             28 n***SerLeuTrpAlaGlu.....SerGluH 37
                                                                                                                                                                                                                                                                                                12 GlyValThrTrpGlyProValThrGluAlaAlaTlePheTyrGluThrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL532540 920 bp mRNA EST 13-FEB-2001 AL532540 LTI_NFL001_NBC4 Homo sapiens cDNA clone CS0DM006Y106 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 920)
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AL532540
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Technologies, a division of Invitrogen 9800 Medical Center 
Drive Rockville, Haryland 20850, USA Fax : (1) 301 610 
8371 Email : flangelifetech.com URL :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-Oilgo(dT) primer. Five prime end enrichted, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://fulllength.invitrogen.com"
a 297 c 261 g 156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DM006Y106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
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BF441074
                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: smitheemail.marc.usda.gov
Single pass sequencing. Bases called and all_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
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Fahrenkiug S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E
Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, M.W.
and Keele, J.W.
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BF441074
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Library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pitultary, and placenta."
156 c 132 g 80 t 1 others
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/lab_host..."DH10B"
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/clone_lib~"MARC 2PIG"
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/strain∵"TREU927"
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Missange ac.u.

Constructed at the Institute for Genomic Research (TIGR)

Constructed at the Institute for Genomic Research (TIGR)

Rockville. M. Genomic DMA Isolated from a cloned population of 
Rockville. M. Genomic DMA Isolated from a cloned population of 

Trypanosoma bruce! (TRED92774 GUTat 10.1) was mechanically sheared 
to give a tight size distribution to 

A kD). The v + 1 method used for the lutery construction is 
described in detail in Smith, H. and Venter J.C. (Making small 
Insert libraries for whole genome shough sequencing a Protical Approach, eds. M. Vaudin and B. 
Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing project, Sanger Centre, The Wellome Trust Genome Campus, Hinxton, Cambridge CBIO 18A, E-mail: barrell&sanger.ac.uk and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall.M., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TA319D090 555 pp DMA clone 319d09, reverse sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              at http://www.sanger.ac.uk/Projects/T_brucei/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NA SS 27-JAN-2000 Sheared DNA-43C17.FF Sheared DNA-Trypanosoma brucel genomic clone Sheared DNA-43C17, DNA sequence. AQ39939
                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from the Trypanosoma brucel GUT91 10.1 sheared DNA library constructed at TIGR. Clones will be available for distribution through ATCC. Sheared DNA end sequences search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Najib M. El-Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ939939.1 GI:6763293
GSS.
                                                                                                                                                                                                                                                                                                                                     Class: shotgun
                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/mdb/tbdb/.
Seg primer: M13-Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_GSSs: Sheared DNA-43C17.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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10.1 sheared DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerrard, C., Leech, V., de, Fraser, C. and Adams, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nelsayed@tigr.org
/note-*Vector: pUCl8: Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is
                                                                                                                                                          /clone_lib="Sheared DNA"
                                                                                                                                                                                  /db_xref="taxon:5691"
/clone="Sheared DNA-43C17"
                                                                                                                                                                                                                                  /organism="Trypanosoma brucei"
/strain="TREU927/4 GUTat 10.1"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suh, E., Malek, J., Fujii, C
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                                                      USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                               1 (bases 1 to 506)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297863 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG382087
   Single pass sequencing. Bases called and alt_trimmed with phred
                              Email: smlth@email.marc.usda.gov
                                                                                                                                                          Contact: Smith TPL
                                                                                                                                                                                                                                  Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                          and Keele, J.W.
                                                                                                                                                                                                                                                                              Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
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12-MAR-2001

Laegreid, W.W.

Casas

Euteleostomi;

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165 c
                                                                                                                                          described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach eds. M. Vaudin and B. Barell, Oxford University ress; 1999).
87.00
1.450
54.545
  Percent Identity: 30.000
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alignment_block:
US-09-471-276-831 x AQ939939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 CCCTCTCCCCAAAGTAAACATCCATCCTTGCGCCTTCTGCATGCGAATAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 GTGGAGCGGCTCAGCGGCAGGGAGCGAATACGCAAGAACCTTTGCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AspSerProAlaIleLysHisGlnPhe....LeuLeuThrGlyAspTh 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 euProAlaValGlnGluTrpGlyAla.....GlnGluProValHisLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 rLeuGlyGlnCysAspAlaAspValProGlyProProGlyAspSerArgL 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGCAACTCCAGCGACGCAGTCGCTTCTCCCCCGGGGGTGCGCAGCACGA 207
                                                                                                                                  ValLeuAlaCysSerLeuAlaLeuAspGly 124
                                                                                                                                                                                                 TAGGAGGGATTGTTAGTGTTTCGCCTCCTCACAGTCCTGCGAACGCGTCC
                                                                                                                                                                                                                                                                                                                                   TAAGGGGAAGTTACGTTGCACAAACCCCGTTGCATCTGAAGGGGGCTGTGC 357
                                                                                                                                                                                                                                                                                                                                                                                         rGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnL 104
                                                                       GTCGGCGCGTGTCCTCACGGCCGTGACGGG
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gb_est2:BG382087
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and minmatch 12 options.
PCR PRIMETS
PCHAND: AGGNANCAGUNTONCCAT
BACKWARD: GTTTTCCCAGTCAGGG
Place: 2 row: 1 column: 22
Seq primer: AGTTAGGTGAGACTATAG.
                                                                                                                                     Mammalle; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 548)
1 (bases 1 to 548)
Fabrenkrug.S.C., Frekling,B.A., Rohrer,G.A., Smith,T.P.L., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegry
                                                                                                                                                                                                                                      pig
Sus scrofa
                                                                                                                                                                                                                                                                                                                       323811 MARC 1PIG Sus scrofa cDNA
EG609827
                                      Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                  EST
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                             Design and use of two pooled tissue normalized cDNA librarics EST discovery in swine
                                                                                                                       and Keele, J.W.
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/lab_host:"billo"
/note-"Wector: pCMV SPORTG; Site_1: Xbal; Site_2: Xhol;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30_embryos_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism "Sus scrofa"
/db_xref taxon:9823"
/clone_lib MARC 1PIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGCTGGGGATCCCCCCCCCCATGCACTGTGAAGGACCCTCGTTTAC 520
NHH-WGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammallan Gene Collection (WGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602430265F1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4547992 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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PCR PRimers
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscorv
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence
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BACKWARD: GTTTTCCCAGTCAGGACG
Plate: 99 row: M column: 22
Seq primer: ATTTAGGTGACACTATAG.
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Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                 human.
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/db_xref-"taxon:9823"
/clone_lib-"MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  874 bp
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Gaps: 4
Percent Identity: 32.432
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11 13, 15, 20,
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alignment_block:
US-09-471-276-831 x BG330746/rev
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ORIGIN
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LOCUS BG365440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 ValProGlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGl 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCCCCAGCCTCCCAACTTCAGCACCACCATCTCTTCTCCACCAG....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yAlaGlnGluProValHisLeuAspSerProAlaIleLysHisGlnPheL 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est2:BG365440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (20 DAP) Hordeum vulgare
BG365440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: DCTD/DTP/Gazdar
                                                                       Wood
                                                                                                   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch, D., Y., Anderson, H., Dale, J., Henry,D., Kernodle,S., Palmer,M., R. T., Saskl,C., Schwartzbeck,J., Simmons,J., Choi,p.W., Main,b.
                                                                                                                                                                                                                                                                          Hordeum vulgare
Eukaryota; Vildiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                        EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVSME10002L07f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10002L07f, mRNA sequence.
Development of a genetically and physically anchored for barley genomics \dot{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG365440.1 GI:13254539
                                                                                                                                                                                                                                                                                                                                                                                       barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
                                                                                                                                                                                                                                             Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                            (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
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//clone_lib="MI_MCC_18"
//clone_lib="MI_MCC_18"
//clone_type="large cell carcinoma"
//las.bost="MBI010 (phage-resistunt)"
//las.bost="MBI010 (phage-resistunt)
//las.bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersocript II RT (Life Technologies). Note: this is a NHL MGC Library."

200 c 274 g 190 t
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/db_xref="taxon:9606"
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                                      EST resource
                                                                                                                                                                           Frisch, D.,
                                                                                                                                         SOURCE
ORGANISM
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US-09-471-276-831 x BG365440
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LOCUS BG337700
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VERSION

SOURCE

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Align seg 1/1 to: BG365440 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCACACCTGGCAGTGGAGGCCATGCGTTTGGATTGTCGCCGTTACTTCC 468
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 o 945) Viages.nci.nih.gov/.
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Seq_primer: AATTAACCCTCACTAAAGGG
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HYCDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="50LR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 gLeuProAlaValGlnGluTrpGlyAlaGlnGluPro.ValHis.....
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BG396925 886 bp mRNA EST 12-mar-2001 602433829F1 NTH_MGC_20 Homo sapiens cDNA clone IMAGE:4552014 5',
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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/db_xref·"taxon:9606"
/clone-"IMAGE:4553199"
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Gaps: 3
Percent Identity: 31.461
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                                     TCAAATTCATATGCTTGTCAAAAGCCTTAAAGGTGCCAAT 525
                                                                                                                                                                                                                                                                                                        LeuSerThrGlyTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyPr 113
                                                                                                                                                                                                                                                                                                                                                                                                      .....ACCCAGACCCGCTTTTCTTCACGCTCTGGTTTG 615
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Ratio:
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Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
http://image.llnl.gov
Plate: LLCM1247 row: 1 column: 07
High quality sequence stop: 702.
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Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammallan Gene Collection (MGC)
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/lab_host-type."melanoric melanoma"
/lab_host-type."melanoric melanoma"
/lab_host-type."melanoric melanoric mela
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/db_xref·"taxon:9606"
/clone·"IMAGE:4552014"
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REFERENCE
AUTHORS
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                                                                                                                                                                                                        547
                                                                                                                                                                                                                                                                                                                                                                                                              457 CTGTGGCATTTCGATTGGGGGGGGGATCTTCAAAAAAGGCTCTATTCAGAGA 506
645 TACTGTGATAAAGTTCGGGGGGGGGGAGAGTCCCTCCCACGCTGGGGAGGGGA 694
                                                                                                    595 TTTACAAACGCCCTGTGGCGGGTGCTTGCCCACAACTTTAGAAGAGAAAC 644
                                              59 oAlaValGlnGluTrpGlyAlaGlnGluProValHisLeu........... 73
                                                                                                                                                                                                                                                       43 lyGlnCysAspAlaAspValProGlyProPro......53
                                                                                                                                                                                                                                                                                                                                                           26 uThrGln***SerLeuTrpAlaGluSerGluHis***LeuLysThrLeuG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LeuTrpGlyValThrTrpGlyProValThrGluAlaAlaIlePheTyrGl 26
                                                                                                                                                                                                                                                                                                      ACGGGCGTCTTCCTTGTGGGCACAA.....ATATTAGAAACCCTA. 546
                                                                                                                                                                                                        ..AGGTGTGGGGCGTGTGTTGCTCCCCCCACAGTTGCTTGGGGGGTATTGT 594
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Plate: LLAW494 row: j column: 22
High quality sequence stop: 150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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1 (bases 1 to 1025)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
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CONA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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48.980
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Site_2: Sall; Cloned unidirectionally. Primer: Oilgo dT
Average insert size 1.5 kb. Library prepared by Life
Technologies: 9
a 219 c 294 g 217 t
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/cell_line="MGC36"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:3452661"
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87 CTCACGGGAAGACTGTGGTACCAGTGCGTGTTGGTCGGGTGGTTCATCAT 136
                                           36 ......GluHis 37
                                                                                                37 GCAAAATTTTACGAAAAGTCAGATTCACCCGTGGAGCCAGAACCTTCTTT 86
                                                                                                                                                   22 AlaIlePheTyrGlu.ThrGln***SerLeuTrpAlaGluSer.....
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 481)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /notia-"organ: colon: Vector: pyryib.Pec (Pharmacia) with a modified polylinker: Site_1: Not 1; Site_2: Eco RI: 1st strand cDNA was primed with a Mot I: Jibo(dT) Primer [5' TGTMACCAMTCRAACTGGGGGGGGCGCCCTTTTTTTTTTTTTTTTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Mot I and Eco RI sites of the modified pTT/3 vector. Library went through one round of normalization. Tissue samples provided by Dr. Brian Dieckraefe (Mashington University, dieckeim wusti.cdu); colonic mucosa represents a range of disease: samples include both perforating (fistulas) and non-perforating samples. Library constructed by Bento Soares and M. Ratina Bonaldo. "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2521060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
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                                                                                                                                                                                                                                                                                                                                  43.750
                                                                                                                                                                                                                                                                                                                                                               83.50
1.704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B (phage-resistant)"
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COMMENT
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BE753233.1 GT:10167225
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith PPL
USDA, ARS US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tal: (02 762 4366
Fax: (02 762 4390)
                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGACG
Plate: 47 row: B column: 22
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                 Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith, P. L., Grosse, M. M., Freking, B. A., Roberts, A. J., Stone, R. T., Casas, E., Wray, J. E., White, J., Cho, J., Fahrenkrug, S. C., Bennett, G. L., Heaton, M. P., Laegreid, M. M., Rohrer, G. A., Chitch, Checken, C. G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
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Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                      132
                                                                                                                                                                                                                                                                                                                                                                -minmatch 12 options
                                         /mote-"vector: pCMV SPORT6; Site_1: xba1; Site_2: xbo1; Library made from pooled tissue from testis, thymus, semitendonosus muscle, longissimus muscle, pancreas, arean1. and endometrium."
                                                                                                                 /clone_lib."MARC 2BOV"
/tissue_type."pooled"
/lab_hosto"DH10B"
                                                                                                                                                                              /organism·"Bos taurus"
/db_xref·"taxon:9913"
                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                       sequence.
AL239600
AL239600.1
                   Unpublished
2 (bases 1
                                                                                                                                                                                                                                                            Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                GSS; genome survey sequence. 
Tetraodon nigroviridis.
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                                                                                                 Weissenbach, J.
                                                                                                                                                        Tetraodontidae; Tetraodon.
1 (bases 1 to 844)
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2 (bases 1 to 844)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                             Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosteni; Retinopterygi; Nepteleosteni; Retinopterygi; Recata; Euteleosteta; Euteleosteni; Recanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378
                                                                                                                                                                                                                                                                              240 GTCTCTG 234
                                                                                                                                                                                                                                                                                                                  118 sSerLeu 120
                                                                                                                                                                                                                                                                                                                                                          278 AGCCAG..
                                                                                                                                                                                                                                                                                                                                                                                           102 ***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValLeuAlaCy 118
                                                                                                                                                                                                                                                                                                                                                                                                                                 328 ACCCAAAGGATTCCGTTCTGCTTTTGTCACCAGGCAGGAGCGTCTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 ..TGGACTCTCCAGGACCACCTGGACCAGGTCCCCCTGGACTCTCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466 CCTGGACTCTCCAGGTCCACCTGGACTCTCCAGGTCCCCC....... 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              504 TCCACCTGGACTCTCCAGGACCAC......CTGGACCAGGTCCC 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 lyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 ProValHisLeuAspSerProAlaIleLysHisGlnPheLeu.LeuThrG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 luTrpGlyAlaGlnGlu.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 pAlaAspValProGlyProProGlyAspSerArgLeuProAlaValGlnG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 SerLeuTrpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACCTGGACTCTCCAGGCCCCCCCTGGAGCCATCAGCTCATCCCTAGAAG
                                                                                                                                                                                                                                      gb_est2:BF606165
                                                                                              BF606165.1 GI:11706497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
                                                           Bos taurus
                                                                              COW.
                                                                                                                                                       BF606165 413 bp mRN/
273126 MARC 3BOV Bos taurus
  Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="019A07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.50
1.777
45.631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Genoscope sequence
222 c 266 g 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib+"G"
                                                                                                                                                                                                                                                                                                                                                          .CTGGACCCCCAGGACCAGACGCCCTGGGGGG 241
     Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity:
                                                                                                                                                                             mRNA
                                                                                                                                                          CDNA
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                                                                                                                                                       5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID : COBGO19AAO4LP1-end : T7*
t 1 others
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32.039
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                     Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
  seq_documentation_block:
LOCUS BE753245
                                                      seq_name: gb_est1:BE753245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: BF606165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-471-276-831 x BF606165/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                    98 erThrGlyTrp 101
                                                                                                 GCACCGGCTGG
                                                                                                                                                                                                                yArgTyrArgCysArg......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
Plate: 59 row: J column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 413)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
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                                                                                                 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.00
1.976
59.155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="MARC 3BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Bos taurus"
  535
bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 71
Gaps: 6
Percent Identity: 42.254
  mRNA
  EST
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233 .... CGGCGGTGCCGGCGAGCTGGAGCAGAGTGAGGGGGGCTGGAGGCG
                                                                                                                                                                    281 ATGATCCCGCTCAAAAGCCAGCAGTTTCTCCTGGAACGTCAGACACAG...
                                                                                                                                                                                                                                                                                                                                        325 GCCAGCTGCT.....TGGCCAGAGACACGTGAGCCCCTGGCACGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 CTGGGAACTTGTTCCGCAGATAGGCCTGTAGTTCCAGGGCAATGTCGCCC 326
                                                                                                                                                                                                                                          73 spSerProAlaIleLys.HisGlnPheLeuLeuThrGlyAspThrGlnGl 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 LeuGlyGlnCysAspAlaAspValProGlyProProGlyAspSerArgLe
                                                                                                                                                                                                                                                                                                                                                                                                                    58 uProAlaValGlnGluTrp...GlyAlaGlnGluProVal...HisLeuA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett (G.L., Heaton, M.P., Laegereid, W.M., Robrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18 and .minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /hote="vector: powv sporm6; Site_1: xbai; Site_2: xhoi; Library made from pooled Lissue from marrow, alveolar macrophage, ovary, fetal senitendonosus muscle, and fetal sonits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 413
                                                                                  SerGlyLeuS
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ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
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ORIGIN
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AUTHORS
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SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-471-276-831 x BE753245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: BE753245 from: 1
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                                                                                                 225 GGATTGAGTCCAACTAC
                                                                                                                                                                                        181 GGGT...GTGACACCAATGGCAGTGATG...CCATCTCAACCGGAGCTAT 224
                                                                                                                                                                                                                                                                                          131 ACCATGCTGCGGACGTTCACTCTTACTCTTTTGTGCTGCACTGACTCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                           49 ValProGlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGl
                                                                                                                                      32 rpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAsp 48
                                                                                                                                                                                                                                    15 pGlyProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuT 32
                                                                                                                                                                                                                                                                                                                                  2 SerMetLeuValValPheLeuLeuTrp.......GlyValThrTr 15
...CCCCAGGCCCCTTGGGAGAAC.....ATCACACTCTGG..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smithecmail.marc.usda.gov
Email: smithecmail.marc.usda.gov
v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 2118001; Smith TPL contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 535)
Smith.T. L., Grosse W. M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas E., Wry, J.E., White, J., Cho.J., Fahrenkrug, S.C., Bennett
Casas E., Hoston, M.P., Laegroid, M. M., Rohrer, G.A., Chitko-McKown, C.G.,
Pertea, G., Holt, L., Karamycheva, S., Liang, F., Ouackenbush, J. and
Keele, J. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BACKWARD: GTTTTCCCAGTCACGACG
Plate: 47 row: E column: 20
Seq primer: ATTTAGGTCACACTATAG
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BE753245
BE753245.1 GI:10167237
EST.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type."pooled*
//lab.host."billOM*
//lab.host."billOM*
//note-"wector: pCMV SPORTG; Site_1: Xbai; Site_2: Xhoi;
Library made from pooled tissue from testis, thymus,
semitendonosus muscle, longissimus muscle, pancreas,
addrenal, and endometrium."
a 139 c 133 g 118 t
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1.352
42.958
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/db_xrefo"taxon:9913"
/clone_libo"MARC 280V"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 142
Gaps: 9
Percent Identity: 28.873
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65	yAlaGinGluProValHisLeuAspSerProAlaIleLysHisGlnP 81
275	TGTAAAAGCCCCTCTCAGATTTCAAGCAAGT 305
81 306	heLeuLeuThrGlyAsp86 TUTTOTTCCTGAAGGATAAGACAGAGATGACCTGGATCCGGCCTTTCCCGA 355
87 356	AAGACCTTCCAAGTTCACTCACGTGGGTGACCTTACTCAGCGAAATAC 405
89 406	.GlyArgTyrArgCysArgSerGlyLeuScrThrClyTrp***GlnLeuS 105
105 456	ertysLewieuGluLeuThrGlyPro 113 ::: ::: GTAAAGTTTTAGAGTTGGAGGCACCA 481
eq_name:	gb_est2:BG442106
eq_docun OCUS DEFINITIO	eq_documentation_block: OCUS BG442106 792 bp mRNA DEFINITION GA_Ea0015M19f Gossyplium arboreum 7-10 dpa fiber library Gossyplium arboreum constant from GA_Ea0015M19f Gossyplium arboreum constant from GA_Ea015M19f mBNA_secretors
CCESSION ERSION EYWORDS	BG442106.1 GI:13351758
ORGANISM	
AUTHORS	
TITLE	An integrated analysis of the genetics, development, and evolution of the cotton (ther
JOURNAL COMMENT	_
	Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293
e de la composición dela composición de la composición de la composición dela composición dela composición dela composición de la composición de la composición de la composición dela composición de la composición dela c	Email: rwingGclemson.edu Seq primer: TARYACGACTCACTATAGG High quality sequence stop: 719.
sourc	ø
	/db_wref: taxon:29729" /clome_"GA_BA0015M19f" /clome_lb:"Gossyplum arboreum 7-10 dpa flber llbrary" /tlssue_type="flbers isolated from bolls harvested 7-10 dpa" dpa"
NASE COUNT	219
ılignment	_scores: Quality: 82.50 Length:
Percent	Ratio: 1.500 Gaps: 6 Similarity: 48.246 Percent Identity: 32.456

alignment_block: US-09-471-276-831 x BG442106

ORIGIN

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seq_name:
                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGGTCCTTTCATATGCCCCAAATTCCCTGGCTCAGTGCGCTTGTCATTG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATCCAGATGCAAAAGGAAGATACAATTGT.....TCTTCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValGlnGluTrpGlyAlaGlnGluPro.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nth.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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Plate: LLAM10157 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clone distribution: MGC clone distribution information can
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                      189
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Organism "Homo sapiens"

Adb_xref "taxon:9606"

/clone=lib="RIH_MCC_85"

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 **LeuLysThrLeuGlyGlnCysAspAlaAspValProGlyProProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 aAlaIlePheTyrGluThrGln***SerLeuTrpAlaGluSerGluHis*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         euGluLeuThrGlyProLysValLeuAlaCysSerLeuAlaLeuAspGly 124
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                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutoleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 591)
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                                                                                                                                                                                                                                      91006 EVRY cedex - France
segref@genoscope.cns.fr, i
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1.375
44.776
             /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                               /clone="CS0DI078YO11"
                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                      Web : www.genoscope.cns.fr
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alignment_block:
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                                                                                                                                                         VERSION
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                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                   seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
TITLE
JOURNAL
                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                          293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 GCCCAGCACCCTKGGACATACATKWSCCACTTTATCCCAAGAACAAGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 GTGTCAGGGGACCCTGGAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAA 222
                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SerMetLeuValValPhe....LeuLeuLeuTrpGlyValThrTrpGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpA 33
                                                                                                                                                                                                                                                                                                                                                       hrGlyTrp***Gln 103
                                                                                                                                                                                                                                                                                                                                                                                       CATGACAGAGGACTATGCAGGGAGATACCGCTGTTACTATCGCAGCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValProGlyProProGlyAspSerArgLeuProAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGCCAGGCTCTGTGATCAG....CTGGGGGAACTCTGTGACCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTGAGTCTGGG
                                                                                                                                                                                                                                                                                                                     TAGGCTGGTCACAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   laGluSerGluHis***LeuLysThrLeuGlyGln...CysAspAlaAsp
                                                                                                                                                                                                                                                                                   gb_est1:AL110419
                                                                                                                                                                                                                                                                                                                                                                                                                         .LeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laGlnGluProValHisLeuAspSerProAlaIleLysHisGlnPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....ValGInGluTrpGlyA 66
                                                                                                                                                                                         ALI10419 760 bp mRNA EST 29-FEB-2000
DKFZp434L1031 1 344 (syponym: htes3) Homo sapiens cDNA clone
DKFZp434L1031 5', mRNA sequence.
Unpublished (1999)
                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Cuturrhini; Hominidae; Homo.

1. (bases 1 to 766)
                                                                                                                                           EST.
                                  Blum, H., Bauersachs, S., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
                                                                                                      Homo sapiens
                                                                                                                                                         AL110419.1 GI:5866027
                                                                                                                                                                               AL110419
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1.491
45.082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 122
Gaps: 6
Percent Identity: 31.148
                                                                                                                                                                                                                                                                                                                                                                                                                                                           . CAGATTCTCCATCGCGCGATC
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DEFINITION ACCESSION VERSION

mRNA sequence. BI331839 BI331839.1 GI

602982517F1 NCI_CGAP_L19

919 bp

mRNA Mus

musculus cDNA clone

seq_documentation_block:

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COMMENT
seq_name: gb_est2:BI331839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-471-276-831 x AL110419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                         288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 CCAACTACCCCCA.GGCCCCTTGGGAGAACATCACGCTTTGGTGCCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 GGGTATGACATCGATAGTGATGGACCCTCAACCGGAGTTGTGGATAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 ACCATGCTGAAGACATTCACTGTTTTGCTCTTTTGCATTCGGATGAGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                     97
                                                                                                                                                                                                                                                                                                                                                                                                                                      52 ProProGlyAsp...SerArgLeuProAlaValGlnGluTrpGlyAlaGl 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 erGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 lThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaGluS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyProVa
                                                                                                                                                                                                                                                                            TGACCTGGATCCGCCCTTCCCACAAGACCTTCCAAGTTTCATTCCTTATA 387
                                                                                                                                                                                                                                                                                                                             nGlu.....ProValHisLeuAspSerProAlaIleLysHisGln. 80
                                                                                                                                                                                                                                                                                                                                                                                     CCCCTCTCGGATATCAAGCAAGTTCCTGCTGCTGAAGGATAAGACACAGA 337
                                                            GGAGACAGGCTGGTCAAAGCCCAGTAAAGTTCTAGAGTTGGAGGCACCA 486
                                                                                                             uSerThrGlyTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyPro 113
                                                                                                                                                                      GGTGCCCTTACTGAGTCCAATGCAGGTCTTTACCGGTGCTGCTACTGGAA 437
                                                                                                                                                                                                                       PheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLe 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Am Klopferspitz lab D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wlemann, Molecular Genome Analysis, German Cancer
Research Center (OKF2); Email s. Wlemannedkfz heidelberg.de;
sequenced by LMM (Indwig Maximilians University,
Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No s1 sequence available. This clone (DKT294341.031) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubherweg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Blum H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Organism."Homo sapiens"
/ab_xref: taxon:9606.
Colone "DKEpp434L1031"
/clone_1b:*d34 (synonym: htes3)"
/tissue_type:"tes5ls"
/dev_stage:"adult"
/lab_host: "Dilos"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.00
1.242
56.410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 c
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Percent Identity: 32.479
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171 t
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REFERENCE
AUTHORS
TITLE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
seq_documentation_block:
                                                seq_name: gb_est2:BF347835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0S-09-471-276-831 x BI331839/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: BI331839
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                                                                                                       685
                                                                                                                                                                                                               735
                                                                                                                                                                                                                                                                   101
                                                                                                                                                                                                                                                                                                                       785
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                                                                                                                                                                                                                                                                                                                                                                                                                           820 CGCCTTTACCATCCACAAGCCCTGGA.....ACCCTGGCG 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      867 GCCACCACGTTCTGCGCCGTGGCCTGGC...CGACAATGGCATGCGCAAC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              917 GGAAATTGCCCAAGGGACTGGCAAGGAGGTACCACTCCAGTGCTCCCGAG 868
                                                                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 luProValHisLeuAspSerProAlaIleLysHisGlnPheLeuLeuThr 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 yProProGlyAspSerArgLeuProAlaValGlnGluTrpGlyAlaGlnG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 GlyGlnCysAspAlaAsp......ValProGl
                                                                                                       CAGCATGC 678
                                                                                                                                                                                                                                                           ....Trp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValL 116
                                                                                                                                                                                                                                                                                                                                                                       GlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGly.. 100
                                                                                                                                                       euAlaCys 118
                                                                                                                                                                                                           AACCTGGCACAGGCACCGTGATCTTGCCAGCCTCAGTGTCCCACCGTGAA 686
                                                                                                                                                                                                                                                                                                                       GGACCCACTCGCTGCGCTTTCAGTCCCCGGGTTGGCCTCAATTCTGGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencian by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 686.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11332 row: b column: 06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MCI_CGAP_Li9"
//ab_host="DBIB_(Ti_phage-resistant)"
//ab_host="DBIB_(Ti_phage-resistant)"
//ont="Organ_liver; Vector; pcMv-s809f6; Site_l: Not1;
//ont="Organ_liver; Vector; pcMv-s809f6; Site_l: Oligo df.
Site_2: Salir_Cloned unidirectionally, Primer; Oligo df.
Average insert size 1.9 kb. Constructed by Life
Technologies, Motee this is a NCL_CGAP_Library."
Technologies, Motee this is a NCL_CGAP_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.00
1.907
50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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Gaps: 4
Percent Identity: 30.233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 919
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SOURCE
ORGANISM
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                       569 TTGACCTGGGCAAGTCTGCCAGGTAAGTCCATCTTGTATAATAGTGTGCT 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                369 CTTCCCAGCACGGGCACGTTCACCTCACAGTCATATCTGGTCAGTTCGGG 320
                                                                                                                                          419 GCACTGGTCCAGGGCTCTGAGGAGGTCCCCTCCTTGCAGGAGCTGTGGAG
                                                                                                                                                                                                                                                                                                                             519 GGCGTTATAAATACCTAGTTGCTTTTACAGTACGGAGAGAGTGAAGCTGT 470
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                                                                                                                                                                                                                                                                             42 euGlyGln.....CysAspAlaAspValProGlyPro...
                                                                                                                                                                                                                                                                                                                                                                       29 *SerLeu.....TrpAlaGluSerGluHis***LeuLysThrL 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ValThrTrpGlyProValThrGluAlaAlaIlePheTyrGluThrGln**
83 LeuThrGlyAspThrGlnGlyArgTyrArg.....
                                                                                         laGlnGluProValHisLeuAspSerProAlaIleLysHisGlnPheLeu 82
                                                                                                                                                                                   ........ProGlyAspSerArgLeuProAlaValGlnGlu.TrpGlyA 66
                                                                                                                                                                                                                                   TGGGACGGCGTCGGCAGAGGTGCCTGCCCAGGTAGAAGTCCTGGCTCAGGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mamumalian Gene Collection (MGC)
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NIH-MGC http://
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BF347835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: David N. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
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Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies, Inc cDNA Library Arrayed by: The I.M.A.G.E. Consortion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: brain; Vector: pcMv-sp6xF6; Site_1: NotI;
Site_2: Sall; Cloned unitdrectionally prince: Oligo dr
Perroge Insert size 2.3 kb. Constructed by Life
Technologies. Note: this is a NCI_GGAP Library."
a 222 c 216 g 224 t
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/clone-lib-"RAL_CAR_Ben67"
/tissue_type-"anaplastic oligodendroglioma with 1p/19g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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KEYWORDS
SOURCE
ORGANISM
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US-09-471-276-831 x AL597254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 LeuAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        225 GGCGTAGCACTGTGCGGGGAACCTGCTCTTGCTGTTCTCCCCGGGACTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 GACACCTTOTGGGCTCACGACAGTCTGTAGTCCTGGT.....ACTGGTT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 TCAGCAGGTAGTACTCAAATGAGGTCCCGAGCAGCCGGCTTGCCATGCCT 270
82
                                  1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rp***GlnLcu.....SerLysLeuLeuGluLeuThrGlyProLysVal 115
ATGACGCCCGCCTCACAGCCCTGCCTCTGCCTTGGGCTGAGTCTGGGCCC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....CysArgSerGlyLeuSerThrGlyT 101
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Am Klopferspltz 18a D-82152 Martinsried, Germany
This is the 5 sequence of the clone Insert
Clone from 5. Wlemann, Molecular Genome Analysis, German Cancer
Research Center (DKP2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No sl sequence available.
This clone (DKFSp313H512) is available at the RZPO in Please contact the RZPD: Ressourcenzantrum, Heubnerweg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata: Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 419)

Ansorge, W., Wirkner, U., Mewes, W., Well, B. and Wiemann, S.
EST (Ansorge, W., Wirkner, U., Mewes, H.W., Well, B. and Wiemann, S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Genome Project.
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1.482
41.353
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/db_xref~"taxon:9606"
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Gaps: 6
Percent Identity: 27.820
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6, 14059
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BASE COUNT	FEATURES H	SOURCE FORMATISM E FORMATISM E FORMATISM E FORMATISM FORMATISM	nent N	313 AAGA 89 yArg 1111 363 GAGA	69 63 76	51 Glyp 184 66 213 CGTG	1/ OVA1 132 CAGG 34 luSe 11 182 AG
~ ~ 0 ~ 0 0 ~ · · · · ~ ~ i	Tissue Procurement: ATC Tissue Procurement: ATC DNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.linl.gov Plate: LLAM10387 row: f column: 19 High quality sequence stop: 661. Location/Qualifiers 1. M62	C - B C B - C B	D_est2:BG257260 talliO_block:	ARAAAAAGGCCAGAFTETECKATUCCATECATECATEGAAAGGACAATGGGGG 382 yArgTyrArgCygarGlyLauSerThrfyTrp***GLAUSer 105		GlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGly65	ONAThroladaAlaIlePheTyrcluThrol1****SerLeuTrpAlaG 34

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Sequencing Center Clone distribution information can clone distribution: NCI-CGAP clone distribution information can close distribution of M A.C.B. Consortium/LLNL, send omail to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.n.h.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Nichael
R. Emmert-Buck, M.D., Ph.D. CONA Libzry Preparation: M. Bento
Soares, Ph.D. CDNA Libzry Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
BF195074
BF195074.1 GI:11081567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                              /organism="Homo sapiens"
//b_xref="taxon;906"
//b_xref="taxon;906"
//clone=!IMAGE:3643895"
//clone=!Ib="WI_CCAP_Ov18"
//clone_!Ib="WI_CCAP_Ov18"
//lab_host="DH10B (phage-resistant)"
//ab_host="DH10B (phage-resi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.50
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48.780
double-stranded cDNA was ligated to Eco RI adaptors
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Percent Identity: 36.585
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ORIGIN
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(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo.
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alignment_block:
US-09-471-276-831 x BF195074
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356 G 356
                                                                                     306 GCGTGCCTGAGTACTGCGCACGTTCATCAGGTGGTACCTGAGGGTGCCAC 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                           106 CTGATGTTCCACTGGGCAGGTGGGAGAATGCCCGAGCTCCGTTGAGCCCA 155
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                                                                                                                          76 AlaIle.....LysHisGlnPheLeuLeuThrGlyAspTh
                                                                                                                                                                                                                  59 roAlaValGlnGluTrpGlyAlaGlnGluProValHisLeuAspSerPro 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 TGGGGTCCAGTGTCAGAGAAGGGCAGTTACACAGAAACGGGGTTCAGTGT 79
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Maximum DB seq
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Perfect score:
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                                                                                                                                       Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                of hits satisfying chosen parameters:
                                                                                                                                                                   A.Geneseq_1101:*

1: /SIDS//gogdata/geneseq/yeneseqp/AA1981.DAT:*
2: /SIDS//gogdata/geneseq/yeneseqp/AA1981.DAT:*
2: /SIDS//gogdata/geneseq/yeneseqp/AA1981.DAT:*
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Copyright (c) 1993 - 2000 Compugen Ltd
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     Human 5' EST relat
House liver growth
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Human secreted pro
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Neisseria gonorrhe Human secreted pro C glittamicum prote Subtilopeptidase 9 Human novel protei Human secreted pro Human bone marrow S. epidarmidis ope S. epidarmidis ope S. epidarmidis ope Tumout necrosis fa Tumout necrosis fa Human secreted sol Human calcium chan Human alpha-2-delt Human secreted sol Human calcium chan Human alpha-2-delt Human secreted pro
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AAY90672
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AAU04379
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AAW23957
AAW48087
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AAU12254
AAM40835
AAY82703
 AAG90588
           AAG81483
                AAU03813
      AAG90137
Human G-protein co
Human G protein-co
Human mutant G pro
G protein-coupled
S. epidermidis ope
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PRO4343 pol
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ALIGNMENTS

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RESULT
AAY64670
01-FEB-2000
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                                                                                                                                         Novel secreted protein 5' expressed sequence tag sequences used diagnostic, forensic, gene therapy, and chromosome mapping proce
                                                                                                                                                                                           Dumas Milne Edwards J,
                                                                                                                                                                                                                           28-APR-1998;
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                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                    forensic; location; development; protein synthesis; stability, regulation; identification.
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                                                                                                                                                                                                                                                                                                                                    n; 5' EST; expressed sequence tag; secreted protein; diagnosis;
therapy; chromosome mapping; upstream regulatory sequence;
                                                                                                                                                                  AAZ42284
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98US-0069047
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RESULT
AAB48724
ID AAB4
XX
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                                                                                                                                                                                                                                                                                                                                                                               insertion of a polypeptide into a membrana, or importing a polypeptide into a ceil. The proteins encoded by the EST sequences may be useful in treating a variety of human conditions, secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAX42249 to AAX4224, and AX44244 to AX464650 represent
                                     AAB48724;
                                                                      AAB48724 standard; Protein; 512 AA
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                      nes 16; Conser
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hepatocellular lesion; hyperplasia; altered expression level; clo diagnostic marker; gipantism; acromegaly; diabetes; hepatotropic; transpenic animal; drug screening; drug discovery; murine; cytoplasmic protein; open reading frame; ORF. Mouse; growth hormone; GH regulatable gene; liver pathology; hypertrophy; heartrorellular lesion: hyperplasia; altered expression level; clone 5; Mouse liver growth hormone-induced clone 5 ORF #1,

SEQ IJ NO:8

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05-MAY-1999;
                                                                                                      05-MAY-2000; 2000WO-US12366
                                                                                                                                          09-NOV-2000
                                                                                                                                                                            W0200066787-A2
Kopchick JJ, Tiong
                                    (UYOH-) UNIV OHIO.
                                                                      9908-0132663
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comprising assaying growth transcriptional activity and protein expression level of hormone-regulatable liver genes, as diagnostic markers of liver pathology Diagnosing abnormal levels of growth hormone activity in liver

N-PSDB; AAC87257.

WPI; 2001-007239/01.

Claim 2; Page 53; 65pp; English.

The invention relates to a method of diagnosing ahnormal levels of growth bormone (GH) activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method involves correlating the level of expression of certain specific genes with the level of GH activity in the liver; or with an expected change in the condition of the liver as the result of GH activity. Excessive GH activity in the liver is thought to be deleterious to health, causing an increase in liver size as a consequence of both hyperplasia and hepatocyte hypertrophy, and hepatocellular lesions which progress with age. Studies in transgenic mice which express high levels of bowth age. Studies in transgenic mice which express high levels of bowthe growth bormone identified a number of genes whose expression in the liver is altered by high GH Levels. The genes which progress that the those encoding alpha fetoprotain, continosteroid binding globulin, fetuin, rab8-interacting protein, paraoxonase-3, cytochrome P450IIIA,

AN45238 represent the ESY-related proteins corresponding to AN42265 to AN4226

as

directing extracellular secretion of a polypeptide

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be

Claim 3; Page 603; 837pp; English

AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag

to human secreted proteins. AAY64651 to

(EST)

6

sequences,

corresponding

diagnostic,

procedures

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AAB66894
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Best Local
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New gene encoding proteins designated MO10, MO19, MO24, useful for diagnosis, prophylaxis and treatment of cancer, obesity, diabetes, osteoporosis, asthma, atherosclerosis and pulmonary disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nervous system disorder; pain; stroke; hypercholesterolaemia; etherosclerosis; chronic obstructive pulmonary disease; hyperlipidaemia; atherosclerosis; hyperlipoproteinemia; arteriosclerosis; coronary artery disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human M019 signal sequence
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                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                      WPI; 2001-112434/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; M010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M019; M024; cancer; obesity; diabetes; osteoporosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0345293
99US-0345680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%;
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Pred. No. 12;
1; Mismatches
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Claim 8; Page 93; 98pp; English

central and peripheral nervous system disorders, pain, stroke, chronic obstructive pulmonary disease, hypercholesterolaemia, hyperlipidaemia, hyperlipoproteinemia, atherosclerosis, arteriosclerosis and coronary

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Thes 8; Conserv
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                                                                          The present invention relation relates to novel human coding sequences and protoins designated M010 (AAR32082 and AAB66884), M019 (AAR32084 and AAB66895) and M024 (AAR32086 and AAB66895). M010, M019 and M024 proteins and compounds which modulate their activity or which bind M010, M019 and/or M024 are useful for prevention and treatment of a variety of disorders including cancer, obesity, diabetes, osteoporosis, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relation relates to novel human coding sequences and proveins designated M010 (AART2008 and AAR66889), M019 (AART2004 and AAR66889), M019 (AART2004 and AAR66889), M019 (AART2004 and M024 ART004 art
                                                                                                                                                                                                                                                                                                                                                 New gene encoding proteins designated MOIO, MOI9, MO24, useful for the diagnosis, prophylaxis and treatment of cancer, obesity, diabetes, osteoporosis, asthma, atheroscierosis and pulmonary disorders
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                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-112434/12
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30-JUN-1999;
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99US-0345680.
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72.7%;
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Pred. No. 1.2;
0; Mismatches
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The invention relates to a method of disgnosing abnormal levels of condition of the liver in response to abnormal levels of the condition of the liver in response to abnormal GH activity. The method involves correlating the level of expression of certain specific genes with the level of GH activity in the liver, or with an expected change of the two long of the liver as the result of GH activity. Excessive GH activity in the liver is thought to be delectrous to health, cousing an GH activity hypertrophy, and hepatocellular lesions which progress with expenses in liver size as a consequence of both hyperplasia and CH actease in liver is a consequence of both hyperplasis and CH actease in liver size as a consequence of both hyperplasis and CH actease in the special control of the special control of the special of the special control of the special of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosing abnormal levels of growth hormone activity in liver comprising assaying growth transcriptional activity and protein expression level of bormone-regulatable liver genes, as diagnostic markers of liver pathology
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N-PSDB; AAC87258.
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8; Conserv
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72.7%;
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Pred. No. 5;
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Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene

The present invention provides a number of nucleotide and protein

Claim 17;

SEQ

ID NO:

5936;

246pp + Sequence Listing; English

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AAG92182
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Best Local S
Matches 9
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07-APR-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising administering the drug to the transgenic animal; and preventing or treating a liver pathology in a patient comprising administering a drug which inhibits the expression of a GH-induced gone. The method of the invention is used for diagnosing abnormal levels of the activity in the liver or predicting a chape in the condition of the liver of predicting a chape in the condition of the liver in response to abnormal levels of GH activity. The GH-regulatable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     upon the same genes. The present sequence represents the protein encoded by the longest open reading frame of the novel mouse liver cDNA clone 45 The protein is thought to be membrane bound ad/or secreted, and has a Myc-type helix-loop-helix dimerisation domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isomerase appears to be downregulated. The invention also relates to transgenic nonhuman mammals comprising a GH-induced transgene which exhibit or have a propensity to develop a liver pathology; an assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organic acid synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum protein fragment SEQ ID NO: 5936
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WPI; 2001-376931/40.
N-PSDB; AAH67401.
                                                                           Tateishi
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                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                 18-DEC-2000;
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les 9; Conser
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2000JP-0159162.
2000JP-0280988.
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                                                                           Mizoguchi H,
Senoh A, Ik
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                                                                               Ando S, Hayashi
da M, Ozaki A;
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Pred. No.
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Mismatches
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25-APR-2000;
09-JUL-2000;
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
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                                      Novel nucleic acids and
such as central nervous
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Example 2; SEQ ID NO 6738; 10078pp; English
                                                                                                                  WPI; 2001-442253/47.
                                                                                                                                                                                                                                     (HYSE-)
                                                                                                                                                                                                                                                                                                                                                        19-JUL-2000;
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8; Conserv
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Wang Z,
Zhou P,
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2000US-0553317.
2000US-05598042.
2000US-0529312.
2000US-0529312.
2000US-053450.
2000US-0652191.
2000US-0593036.
2000US-0727344.
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Wehrman T,
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                                      polypeptides, u
system injuries
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Pred. No.
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Yang
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                                                         treating disorders
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Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human nucleic acids (AMIS7798-AMI61369) and the encoded polypeptides (AMMI612-AMMI6121) with mootropic, the encoded polypeptides (AMMI612-AMMI6121) with mootropic containing a polyperessant and cycostactic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as calcalised neuropathies and central nervous system diseases, such as a tabelner's, Perkinson's disease, Huntington's disease, amyotrophic calcalised neuropathies and central nervous system diseases, amyotrophic calcalised solerosis, and Shy-Drager Syndrome, other uses include the cutilisation of the activity, cancer disgone, the system suppression, can also thrombolytic activity, cancer disgonsts and therapy, drug screening, cassays for receptor activity, arthritis and inflammation, leukaemias and calcalisation of the activity, arthritis and inflammation, leukaemias and calcalisations.
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Matches 7
16 APR 1999
19 APR 1999
21 APR 1999
23 APR 1999
23 APR 1999
23 APR 1999
30 APR 1999
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01-APR-1999;
06-APR-1999;
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23-MAR-1999
25-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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                                                                                                                                                                                                                                                                                             05-MAR-1999
                                                                                                                                                                                                                                                                                                                                         25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                        termination sequence
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37 lavlvlllwgapw 49
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7; Conservative
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                                                                                                                                                                                                                                                                                                                                         2000EP-0301439.
              99US-0127462
99US-0128714
99US-0128714
99US-0129844
99US-0100077
99US-0100077
99US-01100510
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99US-0126264.
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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1; Mismatches
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29-OCT-1997;
29-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Althelmer's disease, ALS, neuropathies or Gencer PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tunor drugs. PRO253 may be used in the treatment of Usher Syndrome or Arrophia areata: PRO269 can be used as an anti-thrombotic agent: PRO289 polyapetides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                     06-MAR-2001
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                                                            AAB19404;
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97US-0065186.
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Pred. No. 64;
2; Mismatches
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treatment of diseases associated with altered expression of these proteins. The proteins are also useful for prention or treatment of platelet disorders, stem cell disorders, osteoporosas or osteoarthritis, burns, inclsions, ulcers, periodontal diseases, central and peripheral nervous system diseases and neuropathies, for healing fractured bones and to induce cartilage and/or bone growth in cosmetic plastic surgery.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted human proteins useful for stimulating blood cell generation in patients receiving cancer chemotherapy, treating bone marrow transplantation patients and for healing fractured bones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted protein; platelet disorder; stem cell disorder; osteoporosis; osteoarthritis; burn; Incision; ulcer; periodontal disease; neuropathy nervous system disease; bone growth; cosmetic plastic surgery;
                                                   The proteins are also useful for gut protection or regeneration treatment of lung or liver fibrosis, for stimulating blood cell generation in patients receiving cancer chemotherapy and for tr
                                                                                                                                                                                                                             types which express the proteins. The polynucleotide molecules can used as blomarkers for tissues or chromosomes and to elicit immune responses. The proteins and antibodies are useful in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-1999;
20-AUG-1999;
                                   of bone marrow transplantation patients.
                                                                                                                                                                                                                                                                                         are useful in assays to determine their biological activities. proteins can also be used as biomarkers to identify tissues or
                                                                                                                                                                                                                                                                                                                                  AAB19393-B19407 represent secreted human proteins.
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99US-0150054.
                                                                                            for gut protection or regeneration, for the
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RESULT 12
AAB18615
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Best Local Similarity
Thehes 7; Conserv
DNA encoding a human thioredoxin family active site molecule MP-4.
                        15-JAN-2001
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                                                                    AAB18615 standard; Protein; 280 AA
                                                                                                                               11 lavlvlllwgapw
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ardiovascular disease; hypertension; atherosclerosis; valvular disease; MP-4; thioredoxin family active site molecule; cellular redox reaction;

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Claim
                                  Novel nucleic acids encoding active site molecule useful f
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                          congestive heart failure
                                                                N-PSDB;
                                                                                           Khodadoust MM
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119..121
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                                  g MP-4 polypeptides of thioredoxin for treating cardiovascular disord
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English

06-OCT-1998; 02-DEC-1998; 10-MAR-1999;

98US-0172227. 98US-0155202. 99US-0123911.

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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                antiparkinsonian's; antisclerotic; anxiolytic; antischizophrenic; anti-inflammatory; antiarthritic.
          06-0CT-1999;
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          99WO-US23434
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277
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257
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221
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128
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RESULT 14
AAM40021
ID AAM400
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21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The polymeptides are useful for treating or preventing a disorder associated with decreased expression or activity of OME. Antaports of OME are useful for treating or preventing a disorder associated increased expression or activity of OME. The disorders include cell proliferative disorders (climbels, hepatitis), cancer (laukemia, melanoma), hypopitutisms and hyperpitutisms, hypothyroidism and hyperpitutism, hypothyroidism cetabolic disorders (Addisor's disease, cyclic fibrosis), reproductive disorders (Infertility, ovulatory doffects), neurological disorders (Adlsenmer's disease, Parkinson's disease)
                                                                                                                                                                       peripheral nervous system: neuropathy, central nervous system: CNS.
Alzheimer's, Parkitsor's disease; Huntington's disease; haemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amultiple sclerosis), mental disorders (anxiety, schizophrenia), autoimmune/inflammatory disorders (acquired immunodeficiency syndrome (AIDS), asthma, osteoarthritis), and viral infections. The polynucleotides may be used in Southern or Northern analysis, polymerase polynucleotides may be used in Southern or Northern analysis, polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 69-70; 97pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-303785/26
N-PSDB; AAA09375.
                                                          26-DEC-2000;
                                                                                                       WO200153312-AJ
                                                                                                                             Homo sapiens.
                                                                                                                                                               chemokinetic; thrombolytic;
                                                                                                                                                                                                                                 Human polypeptide SEQ
                                                                                                                                                                                                                                                         22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                  AAM40021;
                                                                                                                                                                                                                                                                                                      AAM40021 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain reaction (PCR), or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY92504-18 show OXRE-1 to -15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM
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                                                                                                                                                                                                                                                                                                                                                                                                              7; Conser
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JL, Bandman O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280
2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                          2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%;
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                                                                                                                                                                                                                                   ID NO
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                                                                                                                                                                                                                                   3166
                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB
Pred. No. 64;
2; Mismatches
                                                                                                                                                               drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme-linked immunosorbent assays (ELISA).
                                                                                                                                                                                                                                                                                                      280
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Y, Au-Young J, Yue H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an
                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The disorders include cell
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                                                                                                                                                               arthritis; inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 280;
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Lu DAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antagonists
                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   has identity
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AAB88357
ID AAB883
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                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
           08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-442253/47.
N-PSDB; AAI59177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
                                                                                                                                                  Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes.
                                                                                                                                                                                    Human membrane or secretory protein clone PSEC0085
                                                                                                                                                                                                            23-MAY-2001
                                                                                                                                                                                                                                                         AAB88357
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
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                                                                                                                            Homo sapiens
                                                                                10-JAN-2001
                                                                                                     EP1067182-A2
                                                                                                                                                                                                                                                                                                                11 lavlvlllwgapw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                                                                                                                                                                                       280 AA;
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2000US-0662191.
2000US-0693036.
2000US-0727344.
           99JP-0194179.
2000JP-0118775.
2000JP-0183766.
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC.
                                                        2000EP-0114090
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Wehrman T,
                                                                                                                                                                                                                                                         Protein:
                                                                                                                                                                                                                                                                                                                23
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                                                                                                                                                                                                                                                                                                                                                                          50.6%;
                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                     Score 44;
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immunosuppressant and cytostatic activity. The polynocleotides are useful in gene therapy. A composition containing a polypeptide or polynocleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathly and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amputrophic lateral sclerosis, and Shy-Doader Syndrome, Other uses include the utilisation of the activity, cancer disposals and therapy, constant activity, haemostatic and thrombolycic activity, cancer disposals and inframmation, leakemals and assays or receptor activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; SEQ ID NO 3166; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen R, Ma Y,
, Xu C, Xue AJ,
R, Drmanac RT;
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Yang Y,
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Mismatches
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          Length 280
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Gaps
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                profesh/membrane profein expression. The hickels acids and complementary sequences may also be used as DMA probes in diagnostic assays (e.g. polymerase chain reactions (PCN)) to detect and quantitate the presence of similar nucleak acids sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polymeptides and their role in metabolism. The polymeptides may be used as antipents in the production of antibodies against when and and assays to identify mediators (aponists and antisponists) of surges in a therepeutic agents to down regulate expression and board any. The antibodies may also be used as disposed as a contint. The antibodies and antisponists of surges in a samples and antisponists of surges in amples in amples in amples and antipolic agents in amples as of disposes which may be treated include rheumatoid erribititis and dispose of disposes which may be treated include rheumatoid erribititis.
                                                                                                                                                                                     antiparkinsonian nootropic; neur
antianglogenic; vasotropic; anti
antiarthritic; antiinfertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which encode human secretory or membrane proteins represented by ABM8317 - AAB8419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate the CDWA sequences of the invention. The invention also includes methods the production of antibodies directed against the proteins, and cDWA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development
22-FEB-2000; 2000WO-US04414
                                    18-JAN-2001
                                                                         WO200104311-A1
                                                                                                                                                                   ophthalmological; gene therapy;
                                                                                                                                                                                                                                               Human; PRO; dermatological;
                                                                                                                                                                                                                                                                                    Human PRO268 protein.
                                                                                                                                                                                                                                                                                                                           24-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                  AABB0267 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to nucleic acid sequences AAF93744 - AAF93916
                                                                                                                                                     ischaemia; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 laviviliwgapw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MLVVFLLLWGVTW 15
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai T, Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB
Pred. No. 64;
2; Mismatches
                                                                                                                                                                                                          antiasthmatic; antirheumatic; cancer;
                                                                                                                                                                                                                       antipsoriatic; cytostatic; antiinflammatory; neuroprotective; vulnerary; cardiant;
                                                                                                                                                                     skin disease;
                                                                                                                                                                                        antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
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                                                                                                                                                                   gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                        antiviral; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 280;
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AAY25756
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Best Local Similarity
Matches 7; Conserv
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Mather JP, Pa
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26-JUL-1999
28-JUL-1999
08-SEP-1999
08-SEP-1999
13-SEP-1999
15-SEP-1999
05-OCT-1999
29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1999;
20-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                   enterocolitis), neurodegenerative diseases (e.g., Alzheime's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. endomential bleeding angiogenesis, ischaemiss such as coronzy ischaemis, atherosciarosis), inflammatory disorders (e.g. askima, rheumatorid arthritis, multiple scierosis), infertility, AIDS and diabetes and retinal disorders such as retinitis pigmentosum, the PRO nucleic acids have applications in molecular biology, including the PRO nucleic acids have applications in molecular biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixty one nucleic acids encoding PRO polypaptides which are useful in the treatment of skin discases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     filvare
Godowski PJ, Grim
Godowski PJ, Grim
Godowski PJ, Grim
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of sixty one novel secreted and transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g.
                                                                                         04-OCT-1999
                                                                                                                                             AAY25756 standard; Protein; 281 AA
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 114; 393pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease) -
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16-DEC-1999;
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                                                                                                                                                                                                           11 lavlviliwgapw
                                                                                                                                                                                                                                     3 MLVVFLLLWGVTW 15
                                                                                                                                                                                                                                                                                                                                                        as hybridization probes, and in chromosome and gene mapping
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DB; AAF72428.
                                                                                                                                                                                                                                                                                                                                280 AA
                                                                                                                                                                                                                                                                Conservative
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong S, Gao W,
Grimaldi CJ, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US20944
99WO-US21090
99WO-US21547
99WO-US233089
99WO-US28214
99WO-US28313
99WO-US30095
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99US-0145698.
99US-0146222.
99WO-US20594.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-US30911
99WO-US30999
                                                                                                                                                                                                                                                                             50.6%;
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WF, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desnoyers L,
W, Gerber H,
                                                                                                                                                                                                                                                                           Score 44; DB
Pred. No. 64;
                                                                                                                                                                                                                                                                Mismatches
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Stewart TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DL,
                                                                                                                                                                                                                                                                                        Length 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IJ;
                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                     including
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Secreted protein; human; treatment; diagnosis; therapy; cancer; tumour; neurodegemerative disorder; developmental abnormality; blood disorder; fetal deficiency; blood disorder; leukemia, immune system; inflammantion; autoimmune disease; hepatic disease; renal disease; allergy; restenosis;

secreted

protein

encoded from

gene

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                                            B
                                                                    AAG28188
                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel human genes (see AAZ00410-Z00477) and the secreted proteins (see AAZ5711-Y25778) and fragments (see
AAY25719-Y25907) they encode. The polynucleotides and their corresponding
secreted polypeptides are useful for preventing, treating or ameliorating
medical conditions es, by protein or gene therapy. Also pathological
conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the amount of the new
CC polynucleotides to the invention, based on which tissues they are most
CC the new polynucleotides. Specific uses are described for each of the 67
CC polynucleotides of the invention, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis
CC overlapmental abnormalities and fetal officiencies, blood disorders,
CC developmental abnormalities and fetal officiencies, blood disorders,
CC question diseases of the immune system, autoimmune diseases, hepatic
CC and renal disease, inflammation, allergies, ischaemic shock, Alzheiner's
CC and cognitive disorders, senticophrenia, restenois, cardiovascular
CC disorders, wound healing, stroke, arthritis, obesity, asthma, seepsis,
CC cardiovascular transplant rejection, metabolic disorders, infections
CC and ADS. The polypeptides are also useful for identifying their binding
                                                                                            RESULT
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Best Local Similarity
Matches 7; Conserv
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     AAG28188;
                                            AAG28188 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                  Sequence
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Rosen CA, Ruben
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Human; secreted protein;
nutritional supplement;
                                                                  Human
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3 sflasfllgwgitig
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9; Conservative
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; cytokine; cell proliferation;
immune modulation; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                    . 68:
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Pred. No. 72;
1; Mismatches
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RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 55;
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     Human secreted protein; cytokine; cell proliferation;
                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                        autoimmune diseases, as heematopolesis regulators (treating mysloid or
lymphoid cell deficiencies), in the promotion of tissue growth, they mn
have chemokine or chemotactic activity, heemostatic or thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and rese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ALPH-) ALPHAGENE INC
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                               Human secreted protein SEQ ID
                                                           12-JAN-2001
                                                                                                              AAB23643 standard;
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|164 svltaflvlwlphwg 178
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nes 8; Conser
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DB; AAA93123.
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                                                                                                                                                                                                                                                                                                                             or anti-inflammatory activity.
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99US-0167822.
99US-0167823.
2000US-0298733.
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99US-0149639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regulation; tissue growth; haemostasis; inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0155686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= signal_peptide
29..372
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16..28
                                                                                                              Protein; 421
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                                                                                                                                                                                                                                                 50.6%;
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                                                                                                                                                                                                                                                 Score 44;
Pred. No.
                               NO:
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                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                            Length 372;
                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   research
                                                                                                                                                                                                                                                                                                                                                       they may
                                                                                                                                                                                                                                   Gaps
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       AAY57899
                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
                            Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder; reproductive disorder; smooth muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1999;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200049134-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nutritional supplement; immune modulation; autoimmune disorder; haematopolesis regulation; tissue growth; haemostasis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-NOV-1999;
15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1999;
17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2000;
                                                                                                                           23-MAR-2000
                                                                                                                                                     AAY57899;
                                                                                                                                                                             AAY57899 standard;
                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1999;
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|164 svltaflvlwlphwg
                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                         2 SMLVVFLLLWGVTWG 16
                  proliferative
                                                                                                                                                                                                                                                                                                   8; Conserv
                                                                                                                                                                                                                                                                                                                                                                    421 AA;
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99US-0157247.
99US-0167822.
99US-0167823.
2000US-0298733.
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yuan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0298733.
99US-0149639.
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                disorder
                                                                                                                                                                             Protein; 439
                                                                                                                                                                                                                                                                                                                53.3%;
                                                                                                                                                                                                                                                 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoffman
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Ξ, Hall J, Rapiejko

as well as nutritional sources or supplements New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research,

Disclosure; Page 304-305; 309pp; English

uses as nutritional supplements, as cytokinė or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as hematopoiesis regulators (treating mysloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, hemmostatic or thrombolytic activity, or anti-inflammatory activity. No information about sequences AAB2532-B3545 is given in the specification. similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have The proteins and coding sequences can be used in the isolation of present invention is concerned with a number of secreted proteins their coding sequences isolated from various human cDNA libraries.

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Score 44;
Pred. No.
 Mismatches
      , 99
              DB
              21; Length 421;
 Indels
0
Gaps
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Human transmembrane protein HTMPN-23

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RESULT
AAU14131
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Best Local
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02-JUL-1998;
02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT, I
Bandman O,
                                                 Human; novel protein; AntLanaemic; osteopathic; antlinflammatory;
Immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
anticonvulsant; antlarthritic; cerebroprotective; antifungal; antlviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX56698 to AAX56776 encode AAX59877 to AAX79525 which represent human transmembrane protein designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis treatment or prevention of immune, reproductive, smooth muscle, neurological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
Misc-difference 434
                      antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
                                                                                                           Human novel protein #2.
                                                                                                                                     24-OCT-2001
                                                                                                                                                                AAU14131;
                                                                                                                                                                                         AAU14131 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               gastrointostinal, developmental and cell proliferative disorders. The 
HYMPM's can be used to treat or prevent disorders associated with a 
decreased expression or activity of HYMPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 130-131; 229pp; English.
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             Parkinson's disease;
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                                                                                                                                                                                                                                                              164 svltaflvlwlphwg 178
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                                                                                                                                                                                                                                                                                         2 SMLVVFLLLWGVTWG 16
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DB: AAZ56720.
regeneration;
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCYTE PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                        439
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                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                    (first entry)
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98US-0109869
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98US-0091674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note: "unspecified"
                                                                                                                                                                                                                                                                                                                                   50.6%;
immune disorder
           inflammatory disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corgone
                                                                                                                                                                                           541 AA
                                                                                                                                                                                                                                                                                                                                 Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yue H,
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA,
                                                                                                                                                                                                                                                                                                                                 DB 21;
1e+02;
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                                                                                                                                                                                                                                                                                                                                            Length 439;
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                                                                                                                                                                                                                                                                                                                    Indels
           asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corley NC;
           osteoporosis.
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                  Gaps
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GENSET

11-SEP-2001

(first entry)

Human; secreted protein; gene therapy; vaccine; Human secreted protein, SEQ ID NO: 282.

treatment; diagnosis;

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Best Local Similarity
Thes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contractment of a mammal and prevention of disorders caused by the aberrant protein expression or activity protein explanate used as protein expression or activity. The polypeptides can be used as the polypeptides are used to identify compounds which bind to the compounds of the polypeptides are used to identify compounds which bind to the polypeptides of the poly
                                                                                                                                                                                                                                AAG89162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal infection or from autoimmunity, cancer, allergy, asthma,
graft-versus-host disease, eczema, haemophilia, thrombosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to polynucleotides encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-inflammatory diseases, nervous system disorders, and infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; Page 520-521; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (solated polypeptides useful for treating anti-inflammatory diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-2000; 2000US-0491404.
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                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                                                                                                                 2 SMLVVFLLLWGVTWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present sequence represents a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-451939/48
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                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 AA
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                                                                                                                                                                                                                            Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44;
Pred. No.
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3e+02;
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AAG89180
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Best Local
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        the patients own production of GENSET polypepides, Conversely, antisense nucleic acid molecules may be administered to down requisite the GENSET expression by binding with the calls, own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and constant of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or detections in a GENSET gene expression by rectifying mutations or detections in a patient; s genome that, affect the activity of GENSET or by supplementing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 21; Page 817-818; 921pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diseases, and for diagnosis of those diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Full length GENSET human nucleic acids encoding potentially secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1999; 99US-0169629
06-MAR-2000; 2000US-0187470
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              WO200142451-A2
                                             Homo sapiens
                                                                                      Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                  Human secreted protein, SEQ ID NO: 300.
                                                                                                                                                 11-SEP-2001
                                                                                                                                                                                                        AAG89180 standard; Protein; 541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                164 svltaflvlwlphwg 178
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                                                                                                                                                                                                                                                                                                             2 SMLVVFLLLWGVTWG
                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in gene therapy and vaccination against a variety of
                                                                                                                                                                                                                                                                                                                                                                                                                     541 AA;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                        53.3%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Length 541;
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RESULT :
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                                            Matches
                                                            Query Match
Best Local :
                                                                                                                                                                       antisense nucleic acid molecules may be administered to down regulate GRNSET expression by binding with the ceils' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence the determine which patients may be in need of restorative therapy. The GRNSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GRNSET polypeptide expression and activity. The present sequence is a GRNSET polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                        CRMSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 21; Page 829-831; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-1999; 99US-0169629
06-MAR-2000; 2000US-0187470
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                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       example, they be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEST ) GENSET
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  2 SMLVVFLLLWGVTWG 16
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DB; AAH64783.
                                         Similarity
8; Conserv
                                                                                                                                         541 AA;
                                         Conservative
                                                            50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bougueleret L,
                                         Score 44; DB 22;
Pred. No. 1.3e+02;
2; Mismatches 5;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jobert
                                                                             Length 541
                                         Indels
                                         0;
                                         Gaps
                                         0
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Human: secreted protein; gene therapy; protein therapy; cancer: weight tumour; chromosome mapping; forensic; haematological disease; allergy; inflammation; cell proliferation; viral infection; wound healing;

modulation; appetite; behaviour; food additive; preservative

Secreted protein encoded by gene 63 clone HJAAT30

W09903990-A1

Homo sapiens

28-JAN-1999. 15-JUL-1998;

98WO-US14613.

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                                                                                                                                                          consider for preventing treating or amailtowating modeles conditions e.g. by protein or gene therapy Pathological conditions can be also disagnosed by protein or gene therapy Pathological conditions can be also disagnosed by protein or gene amount of the new polypeptides. The anaple or by the sequences, or its fragments, are useful for chromosome identification and mappling; as antisense and triplex forming therapeutics; in gene therapy; for (foreasic) identify related sequences or specific marks; in concern therapy; for (foreasic) identify related sequences or specific marks; and concern therapy and contribute and to raise anti-DNA antibodies. Antibodies are useful as imminoassay reagents (including for in vivo imaging) and consecution of oligoners and to raise anti-DNA antibodies. A very therapeutically to inhibit or activate particular polypeptides. A very confidence of infections are consecutive or had a consecutive of the polynocleotide and contributed as quences, e.g. antichmune or haematological diseases, and consecutive or infections. The sequences may also be useful in wound healing to mobulate differentiation of embryonic siem cells, to modulate weight, papetite, behaviour etc. and as food additive or preservative. The
                                  Best Local Similarity
Matches 7; Conserv
                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1997;
22-JUL-1997;
22-JUL-1997;
18-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1997;
16-JUL-1997;
16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to nucleic acid sequences (AX22211 to AX22282) encoding human secreted proteins (AX20133 to AX20143). The secreted protein gene sequences are deposited with the ATCC under deposit number ATCC 20138, 209139 or 209141. Host cells containing vectors comprising the nucleic acid sequences are used for the recombinant expression of the secreted proteins. The polynucleotide and anno acid sequences are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding secreted human proteins - potentially useful for treating and diagnosing diseases and identifying specific
                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Page 238; 251pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX22281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greene JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (-AMUH)
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18-AUG-1997
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16-JUL-1997
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  1 MSMLVVFLLLWGVTW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feng P,
M, Hu J,
                                                                                                                   40
                                  Conservative
                                                                                                                                                 number and clone identification).
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97US-0055725.
97US-0055726.
97US-0055946.
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97US-0052875.
97US-0053440.
97US-0053441.
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9705-0052661.

9705-0052870.

9705-0052871.

9705-0052872.

9705-0052873.
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97US-0055985
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97US-0055683.
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Ni J, Rosen CA, Ruben SM,
                                                 49.48;
                                  ω.
                                                 Score 43; DB
Pred. No. 11;
                                  Mismatches
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                                                                    Length 40;
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В

22

mtllsvmallwkilw 36

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AAR80565
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                                                                                                                                                                                                                                         Query Match
Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                           AMUGAGI AMUGATZ represent Group B Streptococcus (Streptococcus an agalactiae) anno evid sequences of the invention. S. agalactiae is an encepsulated bacterium which is a major pathogo. of human cousing sepsis and meaning this is in secondaries when a adults. The S. agalactic antisent optypeptides are used to vacainate against Group B Streptococcus antisent for pathogolic composition is infections, particularly to prevent effection there been obtained arising from the maternal gential interies humannogenic composition is useful in the preparation of a medicament for the treatment prior art prohiphasis of group B Streptococcus infection. The invention does not have the disadvantages or varies response also associated with prior art capsid polysaccharide vaccination against Group B Streptococcus.
          EAV GL protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides derived from Streptococcus agalactiae are useful to provide detection of, and vaccination against, Group B Streptococcus infections, particularly to prevent infection in mematals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                      17-JAN-1996 (first entry)
                                                                        AAR80565;
                                                                                                     AAR80565 standard; Protein; 137
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Le Page RWF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2000; 2000WO-GB03437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis; meningitis; neonate; antigenic; vaccine; infection; genital tract;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group B Streptococcus antigenic protein, ID-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
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DB; AAS07097.
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5; Conserv
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                                                                                                                                                                                                                                                                                                                      65
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                         Score 43; DB
Pred. No. 19;
3; Mismatches
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Mora M; Scarselli M;

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RESULT
AAY74573
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Best Local
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              01-MAY-1998
31-JUL-1998
02-SEP-1998
02-SEP-1998
09-OCT-1998
09-OCT-1998
09-OCT-1998
25-FEB-1999
                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY74573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY74573 standard; Protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The DNA sequence equivalent to the entire EAV genome minus the first 18 bases and the poly-A tall is given in AAQ98814, and includes the GL protein coding sequence. Epitopes of GL are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 18; 31pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arteritis virus-mediated diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New equine arteritis virus peptide(s), conjugates, DNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ98814.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-1994;
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                                                                                                                                                                      30-APR-1999;
                                                                                                                                                                                                    11-NOV-1999
                                                                                                                                                                                                                                         W09957280-A2
                                                                                                                                                                                                                                                                        Neisseria gonorrheae.
                                                                                                                                                                                                                                                                                                           antibacterial;
                                                                                                                                                                                                                                                                                                                                                                          Neisserla gonorrheae ORF 152 protein sequence SEQ ID NO:620
                                                                                                                                                                                                                                                                                                                                                                                                             21-MAR-2000
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7; Conserv
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    are used as vaccines or diagnostic agents in

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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                              98US-0083758.
98US-0094869.
98US-0098994.
98US-00999062.
98US-0103749.
98US-0103794.
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                                                                                                                                                                                                                                                                                                      gene therapy.
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                  -0121528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB
Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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AAY74574
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Best Local
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                              01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX53015 to AAX54556, AAX54577 to AAX54615, and AAY14253 to AAY75941 represent novel Neisseria meningitis and n. gooverheae polynucleotides and polypeptides. AA554537 to AAX54576 and AAS54656 to AAX54573 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagants, and as immunogenic compositions. The polypeptides can be used in the treatment of the composition of the polypeptides can be used in the termination of preventing infection due to well-sential backeria; (a.g., meningitis and septicepsia), to detect the relationship of the polypeptides can be used in the composition of the polypeptides can be used in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 435; 1453pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel Neisserial polypeptides predicted to be useful antigens vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ53335
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                                                                                                                                                                                      30-APR-1999;
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                                                                                                                                                                                                                                                       W09957280-A2
                                                                                                                                                                                                                                                                                      Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                       antibacterial; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                      Neisserla meningitidis ORF 152 protein sequence SEQ ID NO:622.
                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY74574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY74574 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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(CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
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7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
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                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                              98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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                                                                                                                                                                                    99WO-US09346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Ratti
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Scalato E, S
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Best Local
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                                                              01-MAY-1998;
31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAX53015 to AAX54536. AAX54577 to AAX54015, and AAY14253 to AAY7504] represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAX5437 to AAX54576 and AAX54616 to AAX54737 represent FCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicament), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for aponists or antagonists, which may themselves have use as antiboterial agents. The polynucleotides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Praser C,
  (CHIR )
         (CHIR
                                                                                                                                                                                antibacterial;
                                                                                                                                                                                      Noisscria meningitidis; Neisseria gonorrheac; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septi
                                                                                                                                                                                                                                                      AAY74575;
                                                                                                                                                                                                                                                                       AAY74575 standard; Protein; 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                              09-OCT-1998;
                                                       09-OCT-1998;
                                                                                                          30-APR-1999;
                                                                                                                             11-NOV-1999
                                                                                                                                              WO9957280-A2
                                                                                                                                                               Neisserla meningitidis
                                                                                                                                                                                                                  Nelsseria meningitidis ORF 152 protein sequence
                                                                                                                                                                                                                                    21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel Neisserial polypeptides predicted vaccines and diagnostics
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Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENO-) INST
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CHIRON CORP.
INST GENOMIC
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B; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                be used in gene therapy protocols.
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Pizza M, Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                  218 AA;
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENOMIC RES
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                          98US-0083758

98US-009489

98US-0098994

98US-0099062

98US-0103749

98US-0103796

98US-0121528
                                                                                                                                                                               gene therapy.
                                                                                                          99WO-US09346
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                                                                                                                                                                                                                                                                                                                                                              48.9%;
  RES
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Pred. No. 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be useful antigens
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                                                                                                                                                                                        meningitis; septicaemia;
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Scalato E,
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                                                                                                                                                                                                                   NO:624
                                                                                                                                                                                                                                                                                                                                                                      218;
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  AAB64795
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Query Match
Best Local
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petersen
Tettelin
                                                                                                                                                                               be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 436; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Neisserial polypeptides predicted to vaccines and diagnostics
                                                                                                                                 Sequence
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DB; AAZ53337.
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J, Pizza M, Rappuoli R,
H, Venter JC;
                                                                                                                                     218
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Ratti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be useful antigens
                                                 21;
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Scalato E,
                                                 Length
                                                     218;
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hes 8; Conserv
50 llvfrlcwgi-wg
                 4 LVVFLLLWGVTWG
                                     Conservative
 61
                 16
                                   Score 42.5; [
Pred. No. 80;
2; Mismatches
                                     Indels
                                   1;
                                     Gaps
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23-MAR-2001
                                             AAB64795 standard; Protein;
                                                                    31
(first entry)
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Human secreted protein sequence encoded by gene 23 SEQ ID NO:81

antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nontropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; cerebrovascular disorder; infection; chemotaxinervous system disorder; coular disorder; skin aging; wound healing; food additive; tissue regeneration. 01-JUN-2000; 21-DEC-2000 WO200077256-A1 Homo sapiens. Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic; 2000WO-US14963 chemotaxis;

N-PSDB; AAF33117 WPI; 2001-032315/04 Rosen

CA,

Ruben SM,

Komatsoulis

(HUMA-) HUMAN GENOME SCI INC

99US-0138631

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RESULT
AAB76763
ID AAB7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
25-JUN-1999;
08-JUL-1999;
08-JUL-1999;
08-JUL-1999;
09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins AAB64773 - AAB64820. Fragments of the secreted proteins amino acid sequences which share homology with the fragments are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in preventing,
                                                                                                                                                                                                                                                                                                     Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                    membrane construction and membrane transport protein petroleum spill; mydrocarbon degradation; gram positive aerobic bacterium; marker; petroleum spill; degrabon; microcycanism; fine chemical production; transformation identification; microcycanism; fine chemical production; transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corynebacterium glutamicum MCT protein SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB76763 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide sequences AAF33095 - AAF33142 encode human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a human secreted protein
                                                                                                                                                    23-JUN-2000;
                                                                                                                                                                                                        04 - JAN - 2001
                                                                                                                                                                                                                                                     WO200100805-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium glutamicum; brevibacterium lactofermentum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 Sllafflilwg 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 SMLVVFLLLWG 12
                                                                                                                                                                                                                                                                                                                                                  mapping; genetic engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Similarity
7; Conserv
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                                                                                                                                                    2000WO-IB00926
99US-0141031.
99DE-1031454.
99DE-1031478.
99DE-1031563.
99DE-1032122.
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                                                                                                                                                                                                                                                                                                  glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                              fine chemical production; transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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AC AAG
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Best Local Similarity
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27-AUG-1999
27-AUG-1999
27-AUG-1999
27-AUG-1999
31-AUG-1999
31-AUG-1999
31-AUG-1999
31-AUG-1999
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27-AUG-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                ARF67743 to ARF6080 encode the Corynebacterium glutamicum membrane construction and membrane transport (MCT) proteins given in ARP7630 ARP76847. The MCT nucleic acids and proteins are useful in the identification of microorganisms which can be used to produce fine identificatio, for modulating fine chemical production in C. glutamicum commicals, for modulating fine chemical production in C. glutamicum commicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                       Corynehancterium glutamicum nucleic acids encoding membrane construction and membrane transport proteins or their portions, useful for typing or identifying C. glutamicum or related bacteria, and as markers for transformation .
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14-JUL-1999;
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09-JUL-1999;
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                related bacteria (e.g. Brevibacterium lactofermentum), the typing or identification of C. glutamicum or related bacteria, as reference points for mapping C. glutamicum genome, and as markers for transformation. AAF68082 and AAF68082 represent sequencing primers which are used in an
                                                                                                                                                                                                                                                                                                                                                               Claim
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AAG92801
                        AAG92801 standard; Protein; 449 AA
                                                                                                                                                                                                                     example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                      transformation
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                                                                                  377 ivifglawglkw 388
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                                                                                                            4 LVVFLLLWGVTW
                                                                                                                                                                                                                                                                                                                                                            20; Page 868-870; 1119pp; English
                                                                                                                                                                                               402 AA;
                                                                                                                                   Conservative
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99DE-1040832.
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99DE-1041378.
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99DE-1042077.
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99DE-1040765.
99DE-1040766.
99DE-1040830.
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99DE-1032125.
99DE-1032128.
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99DE-1032927
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99DE-1032228
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                                                                                                                                               48.3%;
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                                                                                                                                 Score 42; DB zz; ...
Pred. No. 1.8e+02;
Pred. No. 1.8e+03;
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                                                                                                                                                           DB 22; Length 402;
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RESULT :
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Best Local Similarity
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and annlysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium, coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, or anticolability of the producing anticolability in the producing anticolab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakagawa S,
Tateishi N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Coryneform bacterium; amino acid synthesis; vitamin; saccharide, organic acid synthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C glutamicum protein fragment SEQ ID NO:
                Octopus; rhodopsin; membrane; helix;
                                                  Octopus rhodopsin membrane protein.
                                                                                      13-SEP-1991
                                                                                                                       AAR12362;
                                                                                                                                                         AAR12362 standard; Protein; 455 AA
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     European
                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. In the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 17; SEQ ID NO: 6555; 246pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAH68020.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-2000; 2000EP-0127688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUN-2001
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                                                                                                                                                                                                                                               424
                                                                                                                                                                                                                                                                              4 LVVFLLLWGVTW 15
                                                                                                                                                                                                                                             ivifglawglkw 435
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                      449 AA;
                                                                                                                                                                                                                                                                                                                  Conservative
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2000JP-0280988.
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                                                                                   (first entry)
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Senoh A, Ik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0377484.
                                                                                                                                                                                                                                                                                                                                48.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ando
                                                                                                                                                                                                                                                                                                                                Score 42; DB 22
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S, Hayashi M,
Ozaki A;
                OR.
                                                                                                                                                                                                                                                                                                                                                 DB 22;
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                                                                                                                                                                                                                                                                                                                                                 Length 449;
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AAY09518
ID AAY095
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Best Local Similarity
Thehes 3; Conserv
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                                                                WPI; 1999-312943/26
                                                                                                    Blakely RD,
                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                             antiparasitic; psychoactive drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY09518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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         Novel C.elegans dopamine transporter proteins
                                                                                                                                      (UYVA-)
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                                                                                                                                      (AMCY ) AMERICAN CYANAMID CO
(UYVA-) UNIV VANDERBILT.
                                                                                                                                                                                          27-OCT-1997;
                                                                                                                                                                                                                            27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 lmlifvwmwsivw 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                  Eppler CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89JP-0260261
                                                                                                                                                                                          97US-0063282.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.38;
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Pred. No.
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A gene cassette is propd, by division of the OR membrane protein gene encoding helix structure polypeptides. A base sequence contraganth as sequence downstream to the tryptophan regulating per per per translation regulating base sequence, and the N-terminal Met of the tryptophan operanthe N-terminal Met of the tryptophane Met of the tryptophane Met of the tryptophane Met of the Met of t
                                                                                                                                                                                                                     C. elegans dopamine transport protein CeDAT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an expression vector for transformation of host cells. A or total OR membrane protein is produced by culturing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetic engineering of membrane protein - by division of protein
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elegans; dopamine transport protein; CeDAT2; CeDAT1; nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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ches 3;
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RESULT
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Best Local
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         The present sequence represents the C. elegans (nematode) dopamine transporter CobMT2. CobMT1 is a shortened version of CobMT2. The present invention also describes: (1) an expression vector comprising a DNA sequence operably linked to a control sequence which is compatible with a suitable host cell; (2) an expression system comprising a DNA to the comprising and the sequence which is compatible with a suitable host cell; (2) an expression system comprising a host cell transformed with the expression vector of (1); (3) a method of producing purified dopamine receptor; (4) an antibody to a dopamine receptor; (5) a DNA probe comprising a nucleic acid as defined above. The expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    purified dopamine receptor; (4) an antibody to a dopamine receptor. (5) a DNA probe comprising a nucleic acid as defined above. The expression system is used in a screening assay for dopamine transporter antagonists or stimulators. These can be used as antiparasitic or psychoactive drugs, specially antibulation of other dopamine transporter genes in an organism. The probe may be used for determine the presence of other dopamine transporter genes in an organism. The probe may be used for detecting genes encoding dopamine
                                                                                                                                                                                                                                                                                                                         (AMCY )
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                                                                                                                                                                  Claim 15; Page 33-35; 47pp; English
                                                                                                                                                                                                    Novel C.elegans dopamine transporter proteins
                                                                                                                                                                                                                                                           WPI; 1999-312943/26
                                                                                                                                                                                                                                                                                            Blakely RD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiparasitic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elegans; dopamine transport protein; CeDAT2; CeDAT1; nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        elegans dopamine transport protein CeDAT2.
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UNIV VANDERBILT.
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5; Conserv
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                                                                                                                                                                                                                                                                                          Eppler CM
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Pred. No.
assay for dopamine transporter antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7e+02;
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19-MAR-1999; 08-DEC-1999;

99US-0125363 99US-0169617

HUMA-) HUMAN GENOME SCI INC

Ruben SM,

Komatsoulis

16-MAR-2000;

2000WO-US06781

Claim 11; Page 387; 422pp; English.

Nucloic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating disorders such as Parkinson's and Alzheimer's diseases, cancers and infections .

WPI; 2000-602220/57.

acids, proteins, antibodies and (antiagonists are useful in the diagnosis treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastroinestinal tact, liver, lung or urogenital; (b) immune disorders e.g. addison's disease, allergies, autoimmune haemolytic anaemia, uvioimmune thyroiditis, diabetes mentitus combined of the second of the second arthritis and ulcorative croh's disease, multiple selecosis, theumatoid arthritis and ulcorative

colitis; (c) cardiovascular disorders such as myocardial ischaemias;

healing; (e) neurological diseases e.g. cerebral anoxia and (f) infectious diseases such as viral, bacterial, for

and

(d) wound

human secreted proteins encoded by the genes AAC59679-C59728. The genes and proteins are useful for preventing, amelicating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic

Sequences AAB38971-B39020 represent the amino acid sequences of 50

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or stimulators. These can be used as antiparasitic or psychoactive drugs, especially antihelminthic drugs. The nucleic acid can be used to determine the presence of other dopamine transporter genes in an organism. The probe may be used for detecting genes encoding dopamine
                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antiabatetrial; antifungal; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transporters.
                                                                                                                                                                                         Human secreted protein
                                                                                                                                                                                                                     02-FEB-2001
                                                                                                                                                                                                                                                  AAB39016;
                                                                                                                                                                                                                                                                           AAB39016 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                          28-SEP-2000
                                                     WO200056880-A1
                                                                                Homo sapiens.
                                                                                                         neurological disease; infection; human; secreted protein
                                                                                                                                                                                                                                                                                                                                              463 limewliiygttwg
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                        3 MLVVFLLLWGVTWG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        615 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                476
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                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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cches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 615;
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RESULT
AAM25231
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Best Local
                                                                                                                                                                                                                                                                                                                                                           23-DEC-1999;
21-JAN-2000;
25-APR-2000;
             cells they are expressed in, such as antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiagergeant; haemostatic; vulnerary; antibucer; osteopathic; dermatological; antiallargic; antiasthmatic; antidabetic; cytostatic; neuroprotective; antidepressant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotóctivo: antidepressant; noctropic; antiparkinsonia; infection; inmunostimulant; gene thoraby; antisense therapy; vaccine; inflammation; antianaphylectic; rheumatold arthritis; septic shock; parcestitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoletic disorder; platelet disorder; ashma; thrombocytopoenia; osteoporosis; severe combined immunodeficiency; altergic rhinitis; diabetes multiple solerosis; depression; altergic rhinitis; diabetes; multiple solerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; endocrine; cardiant; central nervous system; virucide; anti-milv; fungicide; anti-milv; cardiavascular; anti-ment; anaemia; anti-gregant; haemostatic; vulnerary; antilicer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
  antiparkinsonian;
                                                                                                               AAM25963.
                                                                                                                                                              Claim 20; Page 181; 1217pp; English
                                                                                                                                                                                             treatment
                                                                                                                                                                                                                                                              WPI; 2001-457603/49
                                                                                                                                                                                                                                                                                                                            (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antlinflammatory; antirheumatic; antiarthritic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 mhrlalwilglwgvmw 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSMLVVFLL-LWGVTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; ulcer; HTV infection; human immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
9; Conserv
                                                                                                                                                                                                                                              AAH99172
                                                                                                                                                                                                                                                                                                                            HYSEQ INC
                                                                                                             to AAH99904 encode the human proteins given in AAM25225 to . The proteins can have activities based on the tissues and
                                                                                                                                                                                             human polynucleotides encoding polypeptides, we thank diagnosis of e.g. cancer, ulcers and HIV
                                                                                                                                                                                                                                                                                             Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                           2000US-0488725
2000US-0552317
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                                                                                                                                                                                                                                                                                                                                                                                             99US-0471275
    and immunostimulant.
                                                                                                                                                                                                                                                                                             Drmanac
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                                                                                                                                                                                                                                                                                             RT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41.5;
Pred. No. 31;
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                                                                                                                                                                                             useful for
V infection
polynucleotides
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RESULT 39
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Best Local
           in vaccination, The nucleic actid (I) may be used to produce the Septembers (Pi) value production of vectors containing them which are used to produce hosts calls which express the polypoptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antitodies against the bacteria. The polypoptides may also be used to assay for other inabilitors of their activity and therefore identify companies that may be activity and therefore identify companies and the for the vaccinate subjects and the foreign identify companies and activity and therefore identify companies and confidence of the vaccination of vaccination of the vaccinatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, reheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, heamatopoletic disorders, anaemia, platelet disorders, transmouropopania, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic chintitis, asthma, diabetes, cancer, multiple scleonsis, depression, althelmer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 693; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for vaccinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAH53624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epidermidis open reading
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG82774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kimmerly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination;
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                                                                                                                                                                                                                                                                             (I) and (II) can have antibacterial activity and therefore can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 lvlfllewsv-wg
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hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-316495/33
                                                                                                                                                                                                                                                                                                304 to AAH53970 represent nucleic acids (I) encoding polypeptide given in AAGB1454 to AAGB3120, from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endocarditis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133
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                                                                                                                                                                                                                                                                                                                                                                                                                                           against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          frame protein sequence SEO ID NO: 2642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.5;
Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                               polypeptides
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polynucleotide sequences from the present invention.

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Best Local
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alphaZdelta-2, alphaZdelta-3 or alphaZdelta-4 sibhnit solible proteins which retain their affinity for radioactively labelled gabapentin, the alphaZdelta subunit is 1 of the components of the heteroamitimeric voltage-dependent calcium channel (VCC) complexes present in neuronal and non-neuronal tissues including heart and skeletal massler. Numerous soluble forms of the human calcium channel alphaZdelta subunits (AMU01014-AMU01024 and AMU01012-AMU01039) and 5 soluble-knows of the portine calcium channel alphaZdelta subunits (AMU01014-AMU01034 and AMU01014-AMU01034 and AMU01014-AMU01031) and 5 solubla-knows of the portine calcium channel alphaZdelta subunits (AMU01031-AMU01031) and 5 solubla-knows of the secreted soluble alphaZdelta subunit may be used in assays e.g. solublitation proximity assay (SRA), flashplate, miskel flashplate, filter binding or wheat germ lectin flashplate assays to detect or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AMB55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to 550 ID No:4454 so even though sequences are present for SEQ ID No:455 to 46472, no sequences are present for SEQ ID No:455 to 46472.
                                                                                                                                                                                                                The present sequence represents human secreted calcium channel alpha2delta subunit #7 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit (AAU01025) from which it is derived. The invention relates to truncated
                                                                                                                                                                                                                                                                                                                                               Calaium channel alphaZdelta subunits, useful in e.g. Flashplate assays, filter Wheat Germ Lectin Flashplate assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alpha2dolta-3; alpha2dolta-4; voltage-dependent calcium channel; VDCC; gabapentin; scintilation proximity assay; SR, nickol flashplate assay; filter binding assay; wheat germ lectin flashplate assay.
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                                                                                                                                                                                                                                                                                                             Disclosure; Page 84; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (WARN ) WARNER LAMBERT CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted soluble alpha2delta calcium channel subunit #7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01020 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 lvtillwgttlwg 137
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B; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908-0397550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              calcium channel alpha2delta subunit; alpha2delta-2;
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 22;
1.2e+02;
hes 2;
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                                                                                                                                                                                                                                                                                                                                                                  SPA assays,
binding assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227;
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RESULT
AAB62244
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                       measuring the level of binding of the labelled compound to alphadelta-1 subunit. The method is useful for screening ligands, preferably biologically active products that modulate a nervous system function, which bind a carebral cortical voltage-depandent calcium channel alphadelta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including path, epilepsy and anxiety. The present sequence represents a human calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Competitive binding assay for screening ligands which bind a cereby cortical voltage-dependent calculum channel alpha2-delta-1 subunit, where the ligands identified are useful for treating disorders of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure the binding or interaction of a ligand (e.g. gabapentin, L-Norleucine, L-Allo-Isoleucine, L-methionine, L-Leucine, L-Isoleucine,
                                                                                                                                                                                                                                                                                                                              preferably alpha2delta-1 subunit. The method comprises contacting a secreted soluble recombinant alpha2delta-1 subunit with a ligand of interest and a labelled compound which binds the subunit, followed by
                                                                alpha2delta subunit related
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new method for screening ligands which bind cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 84; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system, including pain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-257902/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bertelli F, Brown JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorder; pain; epilepsy; anxiety; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium channel alpha2delta subunit; alpha2delta-1; cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human calcium channel alpha2delta subunit related seg ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARN ) WARNER LAMBERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000; 2000WO-EP09136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               209 lvlfllewsv-wg 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LVVFLLLWGVTWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9905-0397549
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69.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dissanayake V,
                                                                sequence
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suman-Chauhan N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB 22;
1.6e+02;
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Query Match Best Local Similarity

47.78;

Score 41.5; DB 22; Pred. No. 1.6e+02;

Length 304;

Sequence

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AAU01021
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                                                                                                                                                                                                                                                                 cc alpha2delta subunit #8 which is soluble and retains the functional contaracteristics of the full length or wild type alpha2delta subunit (AMD01025) from which it is derived. The invention relates to truncated alpha2delta 2, alpha2delta is or alpha2delta is subunit soluble proteins which retain their affinity for radioactively libelied gabapenin. The cc alpha2delta subunit is 10 of the components of the heteromaltimeric voltage dependent calcium channel (VDC) complexes present in neuronal alpha2delta subunit sales including heart and skeletal muscle. Numerous soluble forms of the human calcium channel alpha2delta subunit mercous caluble forms of the human calcium channel alpha2delta subunit forms of the components of the soluble alpha2delta subunit soluble forms of the component is calcium channel alpha2delta subunit processor (AAMD0101*AAMD01024 and AAMD0102*AAMD01031) are concluded acclaim channel alpha2delta subunit may be used in assays concluded acclaims channel alpha2delta subunit soluble alpha2delta subunit solubl
                                                                          Query Match
Best Local
                                                 Matches
                                                                                                                                                                                                                          L-Valine, Spermine and/or L-Phenylalanine) of a calcium channel alpha2delta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Calcium channel alpha2delta subunits, useful in e.g. SPA assays, Flashplute assays, Nickel Flashplate assays, Filter binding assays or Wheat Germ Lectin Flashplate assays -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alpha2delta-3; alpha2delta-4; voltege-dependent calcium channel; VDCC; gabapentin; scintillation proximity assay; SRA; nickel flashplate assay; filter binding assay; wheat germ lectin flashplate assay.
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents human secreted calcium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 85-86; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (WARN ) WARNER LAMBERT CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted soluble alpha2delta calcium channel subunit #8 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01021 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209
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4 LVVFLLLWGVTWG
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                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS01411
                                                                                                                                                                            323
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          calcium channel alpha2delta subunit;
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                                                                          69
                                                                      28;
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                                             Score 41.5; DB 22;
Pred. No. 1.7e+02;
1; Mismatches 2;
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                                                                                           22;
                                                                                           Length 323;
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AAB62245
                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          secreted soluble recombinant alphaddelta Isubunit with a ligado of interest and a labelled compound which binds the subunit, followed by measuring the level of binding of the labelled compound to alphaddelta isubunit. The method is useful for screening ligands, preferably biologically active products that modulates a nervous system function, which bind a cerebral cortical voltage-dependent calcium channel alphaddelta-1 subunit. The ligands identified by the method are useful for treating disorders of the nervous system, including pain, cpliepsy and anxiety. The present sequence represents a human calcium channel alphaddelta subunit related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              competitive binding assay for screening lighted which bind a cerebral cortical voltage-dependent calcium channel alpha?-debita-1 subunit, where the lighted identified are useful for treating disorders of the
                 AAU01022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a new method for screening ligands which bind carebral cortical voltage-dependent calcium channel alpha/delta subunit, preferably alpha/delta-1 subunit. The method comprises contacting a
                                                                      AAU01022 standard; Protein; 350
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 85-86; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nervous system, including pain
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N-PSDB; AAF57548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bertelli F, Brown JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calcium channel alpha2delta subunit; alpha2delta-1; cerebral cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200120336-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nervous system disorder; pain; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB62245;
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9; Conserv
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69.28;
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RESULT AAB62246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents human secreted calcium channel alpha2delta subunit *9 which is soluble and retains the functional characteristics of the full length or wild type alpha2delta subunit (AAU01025) from which it is derived. The invention relates to truncated alpha2delta*2, alpha2delta*3 or alpha2delta*4 subunit soluble proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Calcium channel alpha2delta subunits, useful in e.g. SPA assays,
Flashplate assays, Nickel Flashplate assays, Filter binding assays or
Wheat Germ Lectin Flashplate assays .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha2delta-3; alpha2delta-4; voltage-dependent calcium channel; VDCC;
gabapentin; scintillation proximity assay; SPA; nickel flashplate assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which retain their affinity for radioactively labelled gabapentin. The alpha2delta subunit is 1 of the components of the heteromultimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 86-87; 160pp; English.
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11-JUN-2001
                                                                                                                                  AAB62246 standard; Protein; 350 AA
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      4 LVVFLLLWGVTWG 16
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Competitive binding assay for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2-delta-1 subunit,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a new method for screening ligands which bind a cerebral cortical voltage-dependent calcium channel alpha2delta subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 86-87; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nervous system, including pain
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Sequence
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Best Local Similarity 53.8%;
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SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09264419C
Patent No. 6174682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08676169 Patent No. 5773235
                                                                                                                                                                                     APPLICATION NUMBER: US/08/676,169
FILING DATE: 31-JUL-96
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: CLAWFORD, ARTHUR R.
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 26,937
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/264,419C
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVFLICANT: Khodsdoust, Mehran
TITLE OF INVENTION: No. 6174682el Thioredoxin Family Active Site Molecules and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MNI-076
                                                                                                     TELEFAX: (703) 816-4100 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTII: 280
                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC DOS/MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chirnside, Ewan Douglas
TITLE OF INVENTION: BOUNTS ARBEITIS VIRUS PEPTIDES; ANTIBODIES
TITLE OF INVENTION: AND THEIR USE IN A DIAGNOSTIC TEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                      LENGTH: 137 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Virginia
COUNTRY: U.S.A
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 No CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LAVLVLLLWGAPW 23
                                                                                                                                                                   TELEPHONE: (703) 816-4006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MLVVFLLLWGVTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: NIXON & VANDERHYE P.C.
1100 No. 5773235th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 4; Length 280;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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В
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; ORGANISM: L. lactis MG1363
US-09-068-195-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-068-195-24
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Best Local Similarity
Thehes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-024-868-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 24
LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Sanders, Jan W.
APPLICANT: Ledeboer, Adrianus M.
APPLICANT: Venema, Gerard
APPLICANT: Kok, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08024868 Patent No. 5386013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 46.0%;
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid
TITLE OF INVENTION: Batterium and IIs Used In allactic Acid Bacterium for
TITLE OF INVENTION: PRODUCTION of Darked Protein

EILE BEFERENCE: Sender: 60111/02522721red Protein

CURRENT APPLICATION: NUMBER: US-09/068,1958

CURRENT PILLA DATE: 198-07-29

EARLIER PILLA DATE: 198-07-29

EARLIER PILLA DATE: 197-08-20

EARLIER PILLA DATE: 196-09-05

EARLIER PILLA DATE: 196-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 614007
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                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                              ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                    APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vicek, Jan
TITLE OF INVENTION: Cytokine-Induc
TITLE OF INVENTION: Coding Therefor
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.24
                                                                                                                                  COUNTRY:
                                                                                                                                                              STATE:
                                                                                                                                                                             STREET: 419 Seventh Street, NW
CITY: Washington
                                                                                                                                                                                                                            ADDRESSEE: Browdy and Neimark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 LVFFLLLGGLLW 46
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    Mismatches

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Pred. No. 1.
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Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..8e+02;
3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/024,868

CLASSIFICATION: 435

FILING DATE:

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; MOLECULE TYPE: protein US-08-242-097-2
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REFERENCE/DOCKET NUMBER: VILC
TELECOMAUNICATION INFORMATION:
TELEPHONE: 1212-628-5197
TELEPHONE: 122-737-328
INFORMATION FOR SEG ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2,
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                                                                                                                                                                                                                                                                                      NAME: BROWNY ROGET L.
REGISTRATION NUMBER: 25.00
REGISTRATION NUMBER: 25.00
REFERRACE/DOCKET NUMBER: LEEZ
TELECOMMUNICATION INFORMATION: TELEPHONE: 212-628-3197
TELEPHONE: 212-797-358
                                                                                                                                                                                    TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAILIBLE

OPERATING SYSTEM: PC-TOS/MS-DOS

SOFTWARE: PALEONION DATA:
APPLICATION NUMBER: US/08/242,097

FILING DATE: 13-MAY-194

CLASSIFICATION: 435

CLASSIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lee, Tae Ho
APPLICANT: Wisniewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cytokine-Induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                       TOPOLOGY:
                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/642,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 LIYLFLLLWEDTQGWG 19
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                                                                                       linear
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50.0%;
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Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VILCEK-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
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                                                                                                                                  PCT-US96-11995-1
                                                                                                                                                 RESULT
          Sequence 1, Application PC/TUS9611995
GENERAL INFORMATION:
APPLICANT
APPLICANT
TITLE OF INVENTION: A Pharmaceutic
TITLE OF INVENTION: Protein for Tr
TITLE OF INVENTION: Methods of Usi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09206695 Patent No. 6210905
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                    Hest Local Similarity 50.0%; Matches 8: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 212-628-519
TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lee, Tae Ho
APPLICANT: Wishiewski, Hans Georg
APPLICANT: Vilcek, Jan
TITLE OF INVENTION: Cycokino-induced Protein, TSG-6, DNA Coding
TITLE OF INVENTION: Therefor and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/06
PFILING DATE: 13-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/242,097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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  NUMBER OF SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM, PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 419 Sever
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                     4 LIYLFLLLWEDTQGWG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 LIYLFLLLWEDTQGWG 19
                                                                                                                                                                                                                                          3 MLVVFLLLWGVT--WG 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                linear
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A Pharmaceutical Composition Containing TSG-6 Protein for Treating Inflammatory Diseases and Cancer-Relat Methods of Using same 9
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                                                                                                                                                                                                                                                                                                Score 39;
Pred. No.
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                            1.3e+02;
3;
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GENERAL IMPORMATION:
APPLICANT: MACOI, Shunji
TITLE OF INVENTION: NAW PROTEASE
FILE REFERENCE: 32290-144749
FULE REFERENCE: 32290-14749
CURRENT APPLICATION NUMBER: US/09/120,365
CURRENT FILING DATE: 1998-07-22
EARLIER FPLICATION NUMBER: US P-333 474
EARLIER FPLICATION NUMBER: US P-333 474
EARLIER FILING DATE: 1997-11-18
UNMBER OF SEO ID NOS: 101
SOFTWARE: PACHICIN Ver. 2.0
SEO ID NO 62 entil Ver. 2.0
SEO ID NO 62 entil Ver. 2.0
TENETIN: 339
                                                    Query Match
Best Local Similarity
----hes 5; Conserva
                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Sarcophaga cathepsin L
US-09-120-365-62
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Best Local Similarity
Thickes 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 62, Application US/09120365
Patent No. 6103514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/
APPLICATION NUMBER: US 60/
FILING DATE: 20-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWNY, ROGET L.
REGISTRATION NUMBER: 25,61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 212-628-5197
TELEFAX: 212-737-3528
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: WISNIEWSKI-1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 419 Sevent
CITY: Washington
STATE: D.C.
ZIP: 20004
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308 WGTTWG 313
                                11 WGVTWG 16
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419 Seventh Street, N.W., Suite 300
                                                                      Conservative
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63.3%;
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                                                                                        Score 39; DB 3;
Pred. No. 1.7e+02;
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Pred. No. 1.3e+02
                                                                    Mismatches
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                                                                                                       Length 339;
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SEQ ID NO 62
LENGTH: 339
TYPE: PRT
ORGANISM: Sarcophaga cathepsin
US-09-515-039-62
; APPLICANT: NALOTI, SHU11;
TITLE OF INCENTION, RIM PROTENSE
FILE REFERENCE: 32290-144749 S/09/515,039
CURRENT FILING DATE: 2000-03: 05
CURRENT FILING DATE: 2000-03: 05
EARLIER APPLICATION NUMBER: UP 9-333 474
EARLIER VILING DATE: 1997-11-18
NUMBER OF SEQ 1D NOS: 101
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; ORGANISM: Sarcophaga cathepsin
US-09-120-365-80
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APPLICANY: Natori, Shunji
TITLE OF INVENTION: NEW PROTEASE
FILE REFERENCE: 32290-144749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-120-365-80
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Best Local S
Matches 5
                                                                                                                                                   Sequence 80, Application US/09515039 Patent No. 6214599 GENERAL INFORMATION:
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APPLICANT: Natori, Shunji
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
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Patent No. 6103514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MEM PROTEASE
FILE REFERENCE: 32290-144149
CURRENT APPLICATION NUMBER: US/09/515,039
CURRENT PILING DATE: 0300-03-06
BARLIER APPLICATION NUMBER: JP 9-333-474
BARLIER FILING DATE: 1997-11-18
UNMER OF SEO ID NOS: 101
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Matches 5; Conserv
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CURRENT FILING DATE: 198-07-22
RAKLIER APPLICATION NUMBER: JP 9-333 474
RARLIER PILING DATE: 1997-11-18
NUMBER OF SEQ ID MOS: 101
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les 5; Conserv
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83.3%;
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Pred. No. 1.7e
0; Mismatches
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MOLECULE TYPE: po
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: NO
ORIGINAL SOURCE:
US-08-681-192-2
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Best Local Similarity 83.3%;
    Hatches 6; Conservative
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                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BERGSNA, DEKK
APPLICANT: ELSHOURBAGY, NABIL
APPLICANT: SARAU, HENRY
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR HNEDS78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 339
                                                                                                                                                                                                                                                                                                                     NAME: Schreck, Patricia A.
REGISTRATION NUMBER: 33,777
REFERENCE,DOCKET NUMBER: ATT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTMARE: PASTEEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
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CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SHILLIME Road compress: 709 Swedeland Road
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                                                                                                                                                                                                                                                                                                          TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/681,192
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                                                                                                                                                                           peptide
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           Score 39; DB 4; Lei
Pred. No. 1.7e+02;
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Pred. No. 1.7e+02;
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                                             Length 344;
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             Indels
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                                                        Sequence 4, Application US/08170558; Patent No. 6001621; GENERAL INFORMATION:
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                                                                                                              US-08-170-558-4
                                                                                                                                                                                                                                          Matches
         APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
APPLICANT:
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; Sequence 4, Application US/08445640
; Patent No. 5709858
                                                                                              Query Match 44.8%;
Best Local Similarity 38.5%;
                                                                                                                                                                                                                                                                            TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ 1D NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08 FILING DATE: 22-MAY 1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/170
PLICATION NUMBER: 08/170
PLICATION OATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TIPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/1
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
431 LLIIALMLWRLHW 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 AIMVVFLLMW 251
                                                                                                                                                                                         LENGTH: 913 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
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                                      3 MLVVFLLLWGVTW 15
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: California
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                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 28,616
                                                                          Score 39; DB 1; Le
Pred. No. 4.4e+02;
Pred. No. 4.3e+ches 3;
                                                                                                                 Length 913;
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                                                                          Gaps
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Baker, Kevin P

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US-08-447-314-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.8%; Score 39; DB 3; Best Local Similarity 38.5%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Scadden, David T.

APPLICANT: Baron, Will F.

APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PEIGR APPLICATION DANA.
APPLICATION NUMBER: 09/157563
FILING DAVIE: 23-NOV-1993
ATTORNEY/ACENT INFORMATION:
NAME: Hasak, Janet E. 28,616
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEO ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 913 amino acids
              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Centiceth)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/308/447,314
FILING DATE: 22-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 85-
TELECOMMUNICATION INFORMATION:
TELECHONE: 415/225-1896
TELECHAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALIA (Genentech)
CURRENT APPLICATION DAYA:
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                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 LLTIALMLWRLHW 443
                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                         ZIP: 94080
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/170,558
FILING DATE: 20-DEC-1993
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STREET: 460 Point San Bruno Blvd
City: South San Francisco
CLASSIFICATION:
                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
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Best Local Similarity 50...
Conservative
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                                                                                 PRIOR APPLICATION NUMBER: 08/70558

PRIOR APPLICATION NUMBER: 08/70558

PRIOR APPLICATION NUMBER: 09/157563

PRIOR APPLICATION NUMBER: 09/157563

APPLICATION NUMBER: 28.616

REGISTRATION NUMBER: 28.616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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INFORMATION FOR SEQ 1D NO:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TIPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: ISM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Protein Tyrosine Kinases
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 23-NOV-1993
                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Godowski, Paul J.
APPLICANY: Mark, Melanie R.
APPLICANY: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/445,461 FILING DATE: 22-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
TELEPHONE: 415/2...
TELEPHONE: 415/952-9881
                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/170558
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Baker, Kevin P.
Baron, Will F.
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TYPE: amino acids; TYPE: amino acids; TYPE: lamino acids; TOPOLOGY; linear US-08-445-461-4
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                                              RESULT 18
US-08-477-451-16
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US-08-336-343A-2
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                Sequence 16, Application US/08477451 Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 44.8%;
Best Local Similarity 38.5%;
Matches 5; Conservative
                                                                                                                                                                               Best Local Similarity
Matches 5; Conserva
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIEICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLUZZI, LAUTA A.
REGISTRATION NUMBER: 30,742
REFERRENCE/DOCKET NUMBER: 30,742
REFERRENCE/DOCKET NUMBER: 7683-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-990
TELEPHONE: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (212) 869-9741/88
TELEX: 66141 PENNIE
TELEX: BEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ullrich, Axel APPLICANT: Alves, Franke
                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 LLIIALMLWRLHW 443
                                                                                                                   431 LLIIALMLWRLHW 443
                                                                                                                                                                                                                                                                                                      TYPE: ami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                    3 MLVVFLLLWGVTW 15
                                                                                                                                                                                                                                                                                                                      amino acid
                                                                                                                                                                                                                                                                                                                                    919 amino acids
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                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                  38.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/336,343A
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Pred. No. 4.4e+02;
5; Mismatches 3
                                                                                                                                                                                                  Score 39; DB 1;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7683-065
                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                  DB 1; Length 919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 44.8%;
Best Local Similarity 40.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08131625B Patent No. 5695766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIPICATION: 435
ATTORNEY_AGENT INFOGMATION:
NAME: MCCIUM, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE_MOCKET NUMBER: 0335
TELECHONE: 31,010,12708
TELEPHONE: 310,601,2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      APPLICANT: LUM, MELISSA A.
APPLICANT: LUO, YOUG'S.
APPLICANT: LYO, YOUG'S.
TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
TITLE OF INVENTION: REPRODUCTIVE DISFASES, METHODS OF PROTECTING A PIG AGAINST
TITLE OF INVENTION: REPRODUCTIVE DISFASES, METHODS OF PROTECTING A PIG AGAINST
TITLE OF INVENTION: ADJECTED BY A RESPIRATORY AND REPRODUCTIVE
NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PAUL, PE
APPLICANT: HALBUR,
APPLICANT: MENG, XI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1786 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Helicobacter Pylori Cagi Region
                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    807 MRLLLVFFQAWATIW 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS.DOS
                                                                                                             ZIP: 22202
                                                                                                                                COUNTRY:
                                                                                                                                                                          STREET: 1755 S. CITY: Arlington
                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT. ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94608-2916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
SOFTWARE:
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Y: U.S.A.
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                                                                                                                                                                                                1755 S. Jefferson Davis Highway, Suite 400
PatentIn Release #1.0,
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                                                             Floppy disk
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XIANG-JIN
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Pred. No. 8.7e+02;
Pred. No. 8.7e+02;
Version #1.25
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Matches 9; Conserv
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                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: WFTHODS OF USE
                                                                                                REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: LAVAILEYE, JEAN-PAUL M.P. REGISTRATION NUMBER: 31.451
REFERENCE/DOCKET NUMBER: 4625-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            APPLICATION NUMBER: 08/287,941
FILING DATE: August 5, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                              NAME: Collins, John M. REGISTRATION NUMBER: 26,262
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: John M. Collins
STREET: 2405 Grand Blvd., Suite 400
CITY: Kansas City
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                                  LENGTH:
                                                                                  TELEFAX:
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                                                                                  474-9057
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Pred. No. 1s
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Best Local Similarity
Watches 9; Conserv
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SEQ ID NO 10
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/09113750A Patent No. 6294176 GENERAL INFORMATION:
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                             CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
RECISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 55
             TELECOMMUNICATION INFORMATION: TELEPHONE: (212)262-0400
                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
ADDRESSEE: John P. V
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                FILING DATE:
                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                   COUNTRY: U.
ZIP: 10036
                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                                                                                                                                                                                                                 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                   USA
(212)664-0525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.38;
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Pred. No. le
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Pred. No. le
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TITLE OF INVENTION: Recombinant Swinepox Virus FILE REFERENCE: 39119-H/JML
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERCENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                    APPLICANT: David E. Junker and Mark D. Cochran TITLE OF INVENTION: Recombinant Raccoonpox virus
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le+02;
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RESULT 23
PCT-US95-0927-11
Sequence 11 Application FC/TUS9509927
Sequence 11 Application FC/TUS9509927
SEMERAL INFORMATION:
APPLICATE MUTCHSUBH, Michael P.
1TITLE OF INVENTION: WE-2332 VIRAL NUCLEOTIDE SEQUENCE
TITLE OF INVENTION: METHODS OF USE
TITLE OF INVENTION: METHODS OF USE
PCT-US95-10904-17
; Sequence 17, Application PC/TUS9510904
; GENERAL INFORMATION:
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                                                   RESULT 24
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (816) 474-9057
INFORMATION FOR SEQ ID NO: 11:
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WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NAME: COllins, John M.
REGISTRATION NUMBER: 26122
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: John M. Collins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1101 Walnut, Suite 1400
CITY: Kansas City
STATE: Missouri
COUNTRY: USA
ZIP: 64106
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mes 9; Conserv
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STRANDEDNESS: sir
                                                                                                  73 LIMGAVVALLWGVYSAIETW 92
                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                   1 MSMLVVFLLLWGV----TW 15
                                                                                                                                                                                                                                                                                                    : 174 amino acids
amino acid
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                                                                                                                                                                                    Score 38.5;
Pred. No. 16
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                                                                                                                                                                                                                                                  Sequence 43, Application PC/TUS9510904 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 44.3%;
Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2200
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS:
APPLICANT: HALBUR, PATRICK G.
APPLICANT: LIM, ORDZOV, LOG.
APPLICANT: LIM, ORDZOV, LOG.
APPLICANT: LIM, ORDZOV, LOG.
TITLE OF ILVENTION: A POLYNUCLEIC ACID ISOLATED FROM A
TITLE OF ILVENTION: A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE
TITLE OF ILVENTION: PROTEIN ENCODED BY THE POLYNUCLEIC ACID OR
TITLE OF INVENTION: PROTEIN,
THE OF ILVENTION: PROTEIN,
MUNICIPAL OF SEQUENCES: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/131,625
FILING DATE: 05-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                       APPLICANT: PAUL, PREM S. APPLICANT: MENG, XIANG-JIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ZIP: 22:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                      73 LTMGAVVALLWGVYSAIETW 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
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LUM, MELISSA A.
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Pred. No. 1
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CORRESPONDENCE ADDRESS

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

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Best Local Similarity
Conserve
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 43:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            TITLE OF INMENTION: A POLYMUCLETC ACID ISOLATED FROM A TITLE OF INMENTION: PORCINE REPRODUCTIVE AND RESPIRATIONY SYNDROME VIRUS (PRRSV), TITLE OF INVENTION: A PROTEIN ENCOGED BY THE POLYMUCLEIC ACID, A VACCINE TITLE OF INVENTION: PREPARED FROM OR CONTAINING THE POLYMUCLEIC ACID OR TITLE OF INVENTION: PREPARED FROM OR CONTAINING THE POLYMUCLEIC ACID OR TITLE DE INVENTION: PROTEIN, NUMBER OF SEQUENCES: 77
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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APPLICATION NUMBER:
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CURRENT APPLICATION DATA;
APPLICATION NUMBER: PCT/US95/10904
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CITY: Arlington
STATE: Virginia
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                        COUNTRY:
                                                                                                                                                               CITY: Arlington
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                                                                                                                                                                                                                       ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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1755 S. Jefferson Davis Highway, Suite 400
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MOROZOV, IGOR
LUM, MELISSA A.
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PatentIn Release #1.0, Version #1.25
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45.0%; Pred. No. 1e
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Best Local Similarity
"hes 9; Conserve
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            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/131.625

FILING DATE: 05-0CT-193

ATTORNEY_ACRETI INFORMATION:

NAME: LAVALLEYE, JBEAN-PBULL M.P.

REGISTRATION NUMBER: 4625-021-5

REFERENCE_TOCCET MUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MOROZOV, IGOR
APPLICANT: LIM, MEISSA A.
ITTLE OF INVENTION: POSCINE
TITLE OF INVENTION: A PROTEIN
TITLE OF INVENTION: PREPARE
TITLE OF INVENTION: PREPARE
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Rolesse #1.0, Version #1.25
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STREET: 1/50 ...
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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REFERENCE/DOCKET NUMBER: 46:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                               CLASSIFICATION:
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248855 OPAT UR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PORCINE REPRODUCTIVE AND RESPIRATORY SYNDROME VIRUS (PRRSV)
A PROTEIN ENCODED BY THE POLYNUCLEIC ACID, A VACCINE
PREPARED FROM OR CONTAINING THE POLYNUCLEIC ACID OR
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                                                                                                                                                                                  PCT/US95/10904
               4625-021-55X CIP
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Pred. No. 1e+02;
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TELEPHONE:

(703) 413-3000

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Best Local
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                 TELEPHONE: (703) 413-300
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 4
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LENGTH: 174 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,451
REPERBNCE/DOCKET NUMBER: 4625-021-55X CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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MOLECULE TYPE:
                                                                                                                                           SEQUENCE CHARACTERISTICS
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NAME: Lavalleye, Jean-Paul M.P.
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Local Similarity 45.0%;
hes 9; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
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ZIP: 22202
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                                     TOPOLOGY:
                                                                                                           LENGTH:
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FILING DATE: 05-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                : 174 amino acids
amino acid
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1755 S. Jefferson Davis Highway, Suite 400
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LUM, MELISSA A.
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Pred. No. 1e+02;
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Best Local
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                                                                 Best Local Similarity
Matches 9; Conserv
                                                                                               Query Match
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 51:
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TITLE OF INVENTION: A POLYM
TITLE OF INVENTION: PORCINE
TITLE OF INVENTION: PREBAGE
TITLE OF INVENTION: PREBAGE
TITLE OF INVENTION: PREBAGE
TITLE OF INVENTION: PROTEIN,
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: Virginia
73 LIMGAVVALLWGVYSAIEIW 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/10904
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1755 S. Jefferson Davis Highway, Suite 400
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45.08;
                                                                               44.38;
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PORTURE REPRODUCTIVE AND RESPIRATORY
A PROTEIN ENCODED BY THE POLYMUCLEIC ACID, A VACCINE
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                                                                                 Pred. No.
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                                                                 Mismatches
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                                                                                 1e+02;
                                                                                                  DB 5;
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                                                                                               Length 174;
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                                                                 Indels
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RESULT 30 US-08-855-531D-37 ; Sequence 37, Application US/08855531D

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US-08-855-526B-37
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Best Local Similarity
---hos 9; Conserv
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                                                                                                                                                                                                                                                                  Sequence 37
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                          APPLICANT: PREM, PAUL S.
APPLICANT: HALBUR, PATRICK G.
APPLICANT: MENG, XIANG-JIN
APPLICANT: LUM, MELISSA A.
APPLICANT: LYOO, YOUNG S.
TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL TITLE OF INVENTION: RESPONSE AGAINST VINUSES CAUSING PORTICE RESPIRATORY AND TITLE OF INVENTION: REPRODUCTIVE DISEASES, METHODS OF PROFECTING A PIG AGAINSTITLE OF INVENTION: A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
                                                                                                                                                                                                                                                                                                                                                                                           87 LTMGAVVALLWGVYSAIETW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSMLVVFLLLWGV----TW 15
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FILING DATE: 30-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE

OPENATING SYSTEM: PC:DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
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RESEONSE AGIANST VIRUSES CAUSING POPCINE RESPIRATORY AND
REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAIN
A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE

A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PREM, PAUL S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/855,531D FILING DATE: 13-May-1997 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: LAVALLEYE, JEAN-PAUL M.P.
REGISTRATION NUMBER: 31,451
REFERENCE/DOCKET NUMBER: 4625-038-55X DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400 CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                     Application US/08855526B
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MENG, XIANG-JIN
LUM, MELISSA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.3%; Score 38.5; DB 3;
45.0%; Pred. No. 1.1e+02;
tive 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 188;
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                       AGAINST
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Patent No. 5695993
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                                                                                                                                                                                                                                                                                                                      GENERALI INFORMATION:

APPLICANT: Enkudome, Kenji
APPLICANT: Esmon, Charles T.

TITLE OF INVENTION: Cell Protein C/Activated Protein C Recep
TITLE OF INVENTION: Cell Protein C/Activated Protein C Recep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                 21P: 30306-3450
COMPUTER RANDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-005/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 30-OCT-1992
ATTOHNEY/AGENT INFORMATION:
NAME: LAVALLEYE, JEAN-PAUL M.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/969,071
FILING DATE: 30-OCT-1992
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COMPUTER READMALE FORM.

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                 CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                      STREET: 2800 OF STREET: Street
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  APPLICATION NUMBER:
                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 LTMGAVVALLWGVYSAIETW 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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TELEFAX: 703-413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/855,526B
FILING DATE: 13-MAY-1997
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                                                                                                                                                              Georgia
NY: US
                                                                                                                                                                                                                                          2800 One Atlantic Center,
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US/08/289,699A
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Pred. No. 1.
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; MOLECULE TYPE: US-08-878-283-4
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US-08-878-283-4
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Matches 7; Conserv
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TELEPHONE: (404)873-8795
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acids
                                                                                                                                                      FILLING DATE: 12-AUG-1994
APTORNEY_AGENT INFORMATION:
NAME: PABST, Pattreat.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OHRE
TELECHOMENICATION INFORMATION:
TELECHOMES: (40,4)833-2934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                         TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IHM PC COMPUTED:

OPERATING SYSTEM: PC CONS/MS-DOS

SOFTWARE: PALENLID Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/878,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Colning and Regulation of an Endothelial TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fukudome, Kenji
APPLICANT: Esmon, Charles T.
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MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
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MEDIUM TYPE: Floppy disk
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                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 335 amino acid
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sin
                                  TOPOLOGY:
                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
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                                                                     amino acid
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                                                                                    335 amino actos
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Pred. No.
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Best Local Similarity
Thehes 6; Conserv
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; ORGANISM: genomic
US-08-852-824-4
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Best Local Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08852824C Patent No. 6060272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/852,824C CURRENT FILING DATE: 1997-05-04 NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Human G-Protein Coupled Receptors FILE REFERENCE: 1488.1220000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Li.et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                              ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dlsk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     ADDRESSE: Townsend and Townsend Khourie and Crew STREET. Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 384
                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/288,510

PILING DATE: 10-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/193,372
                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,186
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adelman, John P
APPLICANT ASTROYA, MICHAEL J
APPLICANT, BOND, Chris T
TITLE OF INVENTION: DNA EMODING ATP-SENSITIVE POTASSIUM
TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 LMILLAFLYCWGPLFG 269
                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSMLVVFLLLWGVTWG 16
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                                                                                                                                             07-FEB-1995
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; MOLECULE TYPE: protein US-08-385-186-15
                                                                               US-08-614-801A-4
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                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-189
TELEPHON: (415) 399-3249
TELEFAX: (415) 399-3249
TELEX: 910 27729
INFORMATION FOR SEQ ID NO: 4:
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                          OMPOTTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release 41.0, Ve
CURRENT APPLICATION UNMER: US/08/614.801A
FILING DATE: 07-MAR-1996
CLASSIFICATION UNMER: US/08/066,371
PRIOR APPLICATION UNMER: US/08/066,371
FILING DATE: 21-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lester, Henry A.
APPLICANT: Movidson, No. 5744324man
APPLICANT: KOĆUJI, Paulo
TITILE OF INVENTION: INMARD RECTIFIER, G-PROTEIN ACTIVATED,
TITILE OF INVENTION: MAMALIAN, POTASSIUM CHANNELS AND USES THEREOF
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 407 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 543-9600
                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Four Embarce
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Kruse, No. 5744594man J. REGISTRATION NUMBER: 35,235
REFERENCE/DOCKET NUMBER: 14210
                                                                                                                      TOPOLOGY:
                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert STREET: Four Embarcadero Center, Suite 3400
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                                                                                                                   i: 414 amino acids
amino acid
CY: linear
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  43.78;
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Pred. No. 2.7e+02;
6; Mismatches 1
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Score 38;
Pred. No.
DB 1; 1
2.8e+02;
                   Length 414;
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; Sequence 1, Application US/08845566
; Patent No. 5912144
                                                                                                           US-08-845-566-1
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; MOLECULE TYPE: protein
US-08-385-186-13
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  GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
TITLE OF INVENTION: EDG-1 LJ
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                         Matches 5; Conser
                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acid
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APPLICATION NUMBER: 10-AUG-19

FILING DATE: 10-AUG-19

FRIOR APPLICATION DATA:

APPLICATION WINBER: US

FILING DATE: 08-FEB-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPALIBLE

OPERATING SYSTEM: PC-7005/MS-DOS

SOFTWARE: PALEATION DATA: 10.0, Version #1.25

CURRENT APPLICATION DATA: 05/08/385,186

APPLICATION NUMBER: US/08/385,186

FILING DATE: 07-FEB-1995

CLASSIFICATION: 435

CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Adelman, John P
APPLICANT: Ashford, Michael J
APPLICANT: Bond, Chris T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                95 LLIFVMVYTVTW 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kruse, No. 5744594man J. REGISTRATION NUMBER: 35,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                   425 amino acids
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(415) 543-5043
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                                                                                                                                                                                                                                                                        43.7%;
EDG-1 LIKE RECEPTOR
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Pred. No. 2.9e+02;
""" wismatches 1;
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                                                                                                                                                                                                                                                         Indels
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US-08-790-374-2
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                             Sequençe 2, Application US/08790374 Patent No. 5863734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, Lucy 3,
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMPHILICATION INFORMATION:
TELEPHONE: 415-855-0555
TELETHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/845,566 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                APPLICANT: Karaylorgou, Maria
APPLICANT: Gogos, Joseph A.
APPLICANT: Gogos, JOSEPH A.
TITLE OF INEMETION: METHODS OF TREATMENT FOR OBSESSIVE-COMPULSIVE
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 LMILLAFLVCWGPLFG 269
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Wir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                             CITY: Hackensack
                                                                                                                                                                                                                                                            ADDRESSEE: Klauber & Jackson STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE: 144690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                    CLASSIFICATION:
                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSMLVVFLLLWGVTWG 16
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                                                                                                                                                                                                                           New Jersey
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                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.78;
                                                           US/08/790,374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB 2;
Pred. No. 3.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF-0271 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 509;
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PCT-US96-10602-2
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US-08-790-374-2
PCT-US96-10602-2
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TELEPAX: 13521
INFORMATION FOR SEG ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1-ROSTH: 271 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application PC/TUS9610602 GENERAL INFORMATION:
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Best Local Similarity 58.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                     ATTORNEY/AGENT IMPORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
PRINTERN ACCOUNTY OF THE TELEPHONE: 617/542-5070
                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017,814
FILING DATE: 20-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: INHIBITION OF HEPATITIS B REPLICATION
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US96/10602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 LLVVLLLLLRHWG--WG 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                             346 amino acids
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Pred. No. 2.1e+02;
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Query Match Best Local Similarity

43.1%;

Score 37.5; DB 5; Pred. No. 2.7e+02;

Length 346;

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RESULT 42
US-08-747-863-2
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                                                                                                                                                    Ouery Match 43.1%; Score 37.5; DB 1; Length 2396; Best Local Similarity 44.4%; Pred: No. 1.9e+03; Matches 8; Conservative 2; Mismatches 5; Indels 3
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Patent No. 5620691
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                         1902 VQLLCVFFLLWRMMGHAW 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-7UN-1922
ATTORNEY/AGENT INFORMATION:
NAME: NAME: 15.579
REGISTRATION NUMBER: 16.579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-MAR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9
FILING DATE: 06-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.24
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICAMY: Medianberg, Johanna J
TITLE OF INVENTION: CASSITIVE ACENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pol, Johannes M
APPLICANT: Moorman, Robertus J
APPLICANT: Meulenberg, Johanna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/157,005
FILING DATE: 26-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (212) 977-9550
TELEFAX: (212) 315-1931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                  1 MSMLVVFLLLW---GVTW 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                           2396 amino acids
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Terpstra, Catharinus
Pol, Johannes M
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                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: EP 92200781.0
18-MAR-1992
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-747-863-2
                                                                            PCT-US92-00282-9
Sequence 9, Application PC/TUS9200282
GENERAL INFORMATION:
APPLICANT: OWENS, IDA S.
                                                                                                                                                                                                                                                            Query Match 43.1%;
Best Local Similarity 44.4%;
Matches 8; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (801) 531-91
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                      1902 VQLLCVFFLLWRMMGHAW 1919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
ATTORNEY/AGENT INFORMATION:
ANME: TULTHER; Allen C.
REGISTRATION NUMBER: 33041
REGISTRATION NUMBER: 33041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9
FILING DATE: 06-UN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 84111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wensvoort, Gert
APPLICANT: Pol, Johannes M
APPLICANT: Pol, Johannes M
APPLICANT: Mocrman, Robertus J
APPLICANT: Menlenberg, Johannes TITILE OF INVENTION: CAUSITIVE ACENT OF THE MYSTERY SMINE DISEASE,
MUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (801) 531-9168
TELEPAX: (801) 531-9168
TELEPAX: (801) 531-9168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: WINDOWS95
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STREET: 525 South 300 East
CITY: Salt Lake City
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/747,863
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                                                                                                                                                                                                                   1 MSMLVVFLLLW---GVTW 15
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                                                                                                                                                                                                                                                            Score 37.5; DB 4;
Pred. No. 1.9e+03;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                         Length 2396;
                                                                                                                                                                                                                                                                Gaps
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APPLICANT: RITTER, JOSEPH K.
TITLE OF INVENTION: THE GENETIC LOCUS UGT1 AND A MUTATION TITLE OF INVENTION: THERBIN.

NUMBER OF SEQUENCES:

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US-08-385-186-2
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Best Local Similarity 58.3%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5744594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS;
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Sceuart Street Tower, One Market Plaza
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                               APPLICANT: BOND, Chris T
TITLE OF INVENTION: DAM ENCODING ATP-SENSITIVE POTASSIUM
TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                   APPIJCANT: Adelman, John P APPLICANT: Ashford, Michael J APPLICANT: Bond, Chris T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-861-3000
TELEPHONE: 202-862-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, WATSON T.
REGISTRATION NUMBER: 26581
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CLASSIFICATION: 435
PRIOR APPLICATION UNMER: US 08/288,510
FILING DATE: 10-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20036-5601
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CITY: WASHINGTON
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                                                                   APPLICATION NUMBER: US/01
FILING DATE: 07-FEB-1995
                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                              STATE:
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Pred. No. 2.6e+02;
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; MOLECULE TYPE:
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: Patent No. 6005092
: GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Kruse, No. 5744594man J.
                                                                                                                                                                                     REGISTRATION NUMBER: 31,232
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                  SOFTWARE: FASTSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,636
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Shoseyov, Oded
APPLICANT: Shari, IX
TITLE OF INVENTION: GABIDOPSIS THALIANA ENDO-1,4-BETA-
TITLE OF INVENTION: GLUCANASE GENE, PROMOTER AND PROTEIN
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APPLICATION NUMBER:
                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 494 amino acid
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ATTORNEY/AGENI INFORMATION:
NAME: Baldwin, Geraldine F.
REGISTRATION NUMBER: 31,23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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Local Similarity 50.0%;
                                                                                                                                         TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
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                                                                  TYPE: amino acids
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                                                   STRANDEDNESS: single
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1155 Avenue of the Americas
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Pred. No. 3.9e+0
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Best Local Similarity 71.48; Pred. No. 4.6e+02;

MRTCHES 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Oy 9 LUNGVTW 15

Db 241 LUNGNSW 247

Search completed: January 7, 2002, 16:49:57

Job Lime: 286 sec

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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Maximum Match 100%
Listing first 100 summaries
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Copyright (c) 1993 - 2000 Comp
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hypothetical protein tir (repAl 3' C;Spccics: Escherichia coli C;Date: 30-Jun-1989 #sequence_revis C;Accession: S01095; C48662 A; Molecule type: DNA A; Residues: 1-243 <ARN> A; Cross-references: GB: AE001705; GB: AE000512; 밁 Ş C; Genetics: R; White, O.; Elsen, J.A.; Heidelberg, J.F.; Hickey, I. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, C;Species: Deinococcus radiodurans C;Date: 03-Dcc-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 8 ş A;Genc: TM0203 C;Superfamily: Synechococcus nitrate transport A.Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316 A;Accession: E72405 Garrett, M.M.; Stewart, A.M.; C.M. A; Map position: A; Gene: DR0634 A; Experimental source: strain A;Cross-references: GB:AE001921; GB:AE000513; NID:g6458330; PIDN:AAF10217.1; PID:g64583 A; Molecule type: DNA A; Residues: 1-98 <WHI> A; Title: Genome sequence of the radioresistant bacterium Deinococcus A; Reference number: A75250; MUID: 20036896 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999 C: Accession: H75494 hypothetical S01095 RESULT C; Genetics: A; Experimental source: strain A;Status: preliminary Nature 399, 323-329, 1999 A; Status: preliminary A; Accession: H75494 Query Match Best Local Query Match Best Local Matches Matches 97 -1 MSMLVVFLLLMGVTW 15 VSWLVVVIFLWGIGW 111 MSVLAVLLLMWAVTY 15 MSMLVVFLLLWGVTW 15 al protein · Deinococcus radiodurans (strain R1) Deinococcus radiodurans Similarity 8; Conserv Similarity 9; Conser Conservative Conservative #sequence_revision 30-Jun-1989 #text_change 17-Mar-2000 ; C48662 57.5%; 57.5%; Cotton, 2 MSBB ω Score 50; Pred. No. ų Score 50; DB Pred. No. 4.5; region) -ALIGNMENTS Mismatches Mismatches M.D.; Pratt, Gwinn, M.L.; E ; Pratt, M.S.; 2.3; Escherichia coli plasmids DB 2; NID:g4980694; PIDN:AAD35295.1; protein 2: 4. Length 243 Length 98; E.K.; Peterson, , L.; Utterback, Indels Indels Dodson, R.J.; Haft, D.H.; Hi; Phillips, C.A.; Richardson, Bacteria from 0; 0 J.D.; Dodson, T.; Zalewski, Gaps Gaps radiodurans (strain 0; 0 PID: 949807 genome sec MSB8) C.; M Hickey on, D.: 밁 Ó 밁 õ

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A;Experimental source: plasmid R1 R;Jiang, T.; Min, Y.N.; Liu, W.; W. J. Bacteriol. 175, 5350-5358, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Bravo, A.; de Torrontegui, G.; Diaz, Mol. Gen. Genet. 210, 101-110, 1987
C; Supertamily: Mycobacterium tuberculosis
                       A;Genome: plasmid
                                                     C;Genetics:
                                                                         A; Experimental source:
                                                                                                 A; Residues: 1-18 <JIA>
                                                                                                                                             A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                    A;Reference number: A48662; MUID:93374828
A;Accession: C48662
                                                                                                                                                                                                                      A; Title: Insertion and deletion mutations
                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X06240; NID:g45955; PIDN:CAA29583.1;
                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-217 <BRA>
                                                                         plasmid
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hypothetical protein
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      Rv0658c
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Query Match
Best Local Similarity
Conserv
9 LQFMLYMLAAWGISWG
             1 MSMLVVFLLLWGVTWG
                            Conservative
                                    37
24
             16
                                    .
50
                                   Score 49; DB
Pred. No. 5.7;
                             Mismatches
                                          2
                             S
                                           Length
                             Indels
                            0;
                           Gaps
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в86112

probable periplasmic binding protein yjeP [imported] - Escherichia coli (strain c;Species: Escherichia coli (strain c;Species: Escherichia coli (strain c;Species: Escherichia coli (c;batc: 16:Feb-2001 stext_change 31-Mar-2001 c;batc: 16:Feb-2001 stext_change 31-Mar-2001 c;Accession: B86112 R;Perrab, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Clasner, J.D.; Rose, D.J.; Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; 0157

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001

A.Fitle: Genome sequence of entorchemorrhagic Bacherichia coll 0157:H7 A.Faterence number: A85480; MUID:21074935; PMID:11205551 A.Facession: B86112

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1107 <STO>

A;Cross-references: GB:AE005174; NID:g12519144; PIDN:AAG59358.1; GSPDB:GN00145; A;EXperimental source: strain 0157:H7, substrain EDJ333 C;Cenetics: UWGP:

A;Gene: yjeP

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Matches
                                          Query Match
Best Local
1 MRLIITFLMAWCLSWG
                MSMLVVFLLLWGVTWG 16
                                 Similarity 37.
6; Conservative
                                          37.5%;
16
                                          Score 49;
Pred. No.
                                  Mismatches
                                                   DB
                                                   2
                                  4
                                                   Length 1107;
                                  Indels
                                  0
                                  Gaps
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N; Alternate names: hypothetical hypothetical 123.8 kD protein in genX-psd intergenic region - Escherichia coli N;Alternate names: hypothetical protein f1107 E65226 protein (strai

Cispecies: Becherichia coli
Cispecies: Becherichia coli
Cipato: 12-Sep-1997 *sequence_revision 17-Sep-1997 *text_change 08-Oct-1999
C.Accession. E65226; \$55387
C.Accession. E65226; \$55387
R.Blattiner, F.R.; Plumbett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A.; Ross__D.J.; Man, B.; Shao, Y. V.; Riley,

3

Science 277, 1453-1462, complete genome 1997 sequence of Escherichia col1 K-12

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Glodek, A.,
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A.;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92. A.;Reference number: S56310; NUID:55334362
A.;Reference number: S56310; NUID:55334362
                                                                                           hypothetical protein AF1221 - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C:Species: Archaeoglobus fulgidus C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999 C;Accession: D69402
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A;Molecule type: DNA
A;Residues: 1-1107 <BLAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: PA3789
C;Superfamily: Neisseria
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A.Moleoule type: DNA
A.Cross-references: GB:AE004797; GB:AE004091; NID:g9949950; PIDN:AAG07176.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.Y.
Nature 406, 959-964, 2000
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A;Start codon: GTG
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A:Mote: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
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A; Residues: 1-746,'X',748-1014,'A',1016-1107 <BUR>
                                                                          R; Klenk,
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A;Accession: E83173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E83173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA3789 [imported] - Pseudomonas aeruginosa (strain PAO1)
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Best Local
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Best Local
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           Reischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.;
Lodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonal
ture 390, 364-370, 1997
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                                                                    H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodsor
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8; Conserv
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37.5%;
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Larbig, K.; Lim
                                                  Kirkness,
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A; Molecule type: DNA
A; Residues: 1-389 <SIM>
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C: Genetics:
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A; Residues: 1-48 <KLE>
                             submitted to GenBank,
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Matches 6; Conserv
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6; Conserv
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A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343
A;Recession: D69402
A;Status: preliminary; nucleic acid sequence not shown; translat
                                                                                                                                                                        A;Cross-references: GB:AE001020; GB:AE000782;
                                                                                                                                                                                                                                                                                                              A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, Smith, H.O.; Woese, C.R.; Venter, J.C.
37 IVILLINGLSW 47
                                      5 VVFLLLWGVTW 15
                                                                            Conservative
                                                                                            54.0%;
                                                                                               Pred.
                                                                                                            Score 47;
                                                                            Mismatches
                                                                                            No. 3
                                                                                                                  DB 2;
                                                                                                                                                                        NID:g2689343; PIDN:AAB90036.1; PID:g264
                                                                            1;
                                                                                                                  Length 48
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C:SpecLes: Pseudomonas aeruginosa
C:Datche: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83138
                                                                                                              hypothetical protein PA3897 [imported] - Pseudomonas aeruginosa
                                                                                                                    (strain PAO1)
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A; Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, A; Reference number: A82950; MUID: 20437337R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ... Lory, S.; Olson, M. V.
Nature 406, 959-964, 2000 an opportunistic K.; L

A; Molecule type: DNA A; Molecule type: DNA A; Cross:references: GB:AE004807; GB:AE004091; NID:g9950076; PIDN:AAG07284.1; A; Reference number: A82950; A; Accession: D83158

strain

PAO1

GSPDB:GN

54.0%; Score 47; Pred. No. Mismatches DB Ν. Length Indels 0 Gaps 0,

LSLYLLTVLIWGTTW

C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 *sequence_revision
C;Accession: H82825 transport protein XF0281 [imported] - Xylella fastidiosa 20-Aug-2000 #text_change 20-Aug-2000 (strain 9a5c)

Seq

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151–157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below $A;Accession:\ H82825$

A;Cross-references: GB:AE003881; GB:AE003849; NID:g9105093; PIDN:AAF83094.1; GSPDB:GN A;Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A. A.; Camargo, L.E.A.; Carraro, D.M.; Carasa-Neto, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. A; Authors: Ferreira, V.C.A.; Ferro, June 2000 J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; nga, R. Carrer

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J.D.; Junquelra, M.L.; Komper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigi Chado, M.A.; Mudolra, A.M.B.N.; Madelra, H.M.F.; Martino, C.L.; Marques, M.V.; Marcins, E.A.; Mithors; Martins, E.R.; Mitacca, E.C.; Miyaki, C.Y.; A; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; G.F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodriques, V.; Rossa, A.J. de M.; de Rosa, T., V.E.; de Sa, R.G.; Santelli, R.V.; Savasa, A; A; Miracins, M.F.; Vellada, H.; Vandada, H.; V
                                                                                                                                                                                                                          R:Stover, C.K.; Pham, X.Q.; Erwin, A.I.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V. Mature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A:Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
A:Reference number: A70100: MUID:98065943
A:Accession: F70100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical integral membrane protein BB0006 - Lyme disease spirochete C;Specles: Borrelia burgdorferl (Lyme disease spirochete) C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000 C;Accession: F70100
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A;Cross-references: GB:AE004548; GB:AE004091; NID:99947102; PIDN:AAC04569.1; GSPDB:GN00:
A;Experimental source: strain PAO1
C:Genetics:
A:Gene: phoQ: PA1180
                                                                                                                   A; Molecule type: DNA
A; Residues: 1-448 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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A.Experimental Source: Erain BJ
G:Superfamily: conserved hypothetical protein H10338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Status: preliminary; nucleic acid sequence not shown: translation not shown
A.Molecule type: DNA
A.Mostdues: 1-374 <KLE>
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Bomman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch,
Nature 390, 580-586, 1997
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A;Gene: XF(
                                                                                                                                                                             A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-component sensor Pho0 PA1180 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A83498
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9; Conserv
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Pred. No. 17;
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Pred. No. 23;
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A; Accession: T36320
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A;Map position: 1
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A;Status: preliminary
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Best Local
                                                                                                                   179 VLAVSLLLTGATWG
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mes 9; Conserv
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9; Conserv
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A.;Kolecule type: DNA
A.;Kolasidues. 1-75 < VHID.
A.;Cross-references: GB:AE001882; GB:AE000513; NID:g6457865; PIDN:AAF09788.1: PID:g645
A.;Kyperimental source: strain R1
G.;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Accession: E7558

R;White, O.: Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Petarson, J.D.; Dodson, R.J., K.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1517-1577, 1999

N;Filte: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                         A.Molecule type: DNA
A.Molecule type: DNA
A.Gross-references: EMBL:AL049841; PIDN:CAB42747.1; GSPDB:GN00070; SCOEDB:SCE9.01
                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                       R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 *Sequence_revision 03-Dec-1999 *text_change 03-Dec-1999
C:Accession: T36520

    Streptomyces coelicolor (fragment)

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Pred. No. 30;
4; Mismatches
Pred. No. 35;
1; Mismatches
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Pred. No. 24;
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C:Species: Caenorhabditis elegans
C:Date: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 04-Mar-2000
C:Accession: T21591
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R:SIMBSON, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; ABRIONSON, A.J.G.; Reinach, F.C.; Arruda, P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P. Briones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, P. as-Netto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S., submitted to GenBank, Unce 2000
A; Authors: Rerreira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigy
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigy
Chado, M.A.; Madeira, A.M.B.N.; Medelra, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.A.; Martins, E.M.; Markins, F.A.; Martins, E.M.; R.C.; Pallyaki, C.Y.
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Pallyaki, C.Y.
Rodriques, V.; Rosa, A.J. de M.; de Rosa, J.T., V.E.; de Sa, R.G.; Santelli, R.V.; Savesta, A.M.; Tsuhako, M.H.; Vallada, H.; Ven Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., R.R.; de Silve, R.R.; de Sil
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A.JMar position: 1
A.JMartons: 4J.1: 81/3: 105/1: 130/3: 204/1: 274/3: 309/1: 430/1:
C.Superfamily: Caenorhabditis elegans hypothetical protein F3IC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A: Molecule type: DNA
A: Cross-references: EMBL; 292784; PIDN: CAB07196.2; GSPDB: GN00019; CESP:F31C3.6
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A;Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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A; Residues: 1-227 <SIM>
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                                                    153 MAMLTVLLVLLWDVRW 168
                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                1 MSMLVVFL-LLWGVTW 15
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Pred. No.
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Pred. No. 25
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C;Species: Homo sapiens (man)
C;Species: 13-11.1999 #sequence_revision 23-Jul-1999 #text_change 23-
C;Accession: T12471
C;Accessio
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A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77183
R:Kaneko, T.; Sato. S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamad NA, Res. 3, 109-136, 1956
                                                                                                                                                                                                                                                                                              probable integral membrane protein Cj1544c [imported] - Campylobacter jejuni (strain
C;Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Accession: F81301
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A; Note: DKFZp564E1962.1
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Tarches 12; Conserv
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A.Note: the nucleotide sequence was submitted to the EMBL Data Library, June
C;Superfamily: Synechocystis hypothetical protein s111698
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A; Residues: 1-126 <KAN>
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A;Accession: S77183
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reterence number: AB1250; MUID:20150912 A;Accession: FeB1301 A;Accession: FeB1301 A;Status: preliminary
                                                                                                                                                             RParkhill, J.; Wren. B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; Vanvliet, A.; Nature 403, 665-668, 2000
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A;Experimental source: fetal brain; clone DKFZp564E1962
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A; Accession: T12471
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Pred. No.
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A.; Whitehead,

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Yamada, M.;

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C:Superfamily: ADP.ATP carrier protein; ADP.ATP carrier protein repeat homology C:Keywords: duplication; transmembrane protein F76-171/Domain: ADP.ATP carrier protein repeat homology <ACP1> F.181-275/Domain: ADP.ATP carrier protein repeat homology <ACP2> F.181-369/Domain: ADP.ATP carrier protein repeat homology <ACP2> F.281-369/Domain: ADP.ATP carrier pr
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A;Gene: C;Genettos:
A;Gene: C;1544c
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
A; Map position: 4
A; Introns: 157/3; 281/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R:Saunders, D.C.; Harris, I
submitted to the EMBL Data
A:Reference number: Z21588
A:Accession: T35734
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Best Local Similarity
"had be be conserved."
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A; Residues: 1-379 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999
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C;Superfamily: proline aminopeptidase
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A; Rosidues: 1-323 <SAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T04608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADP, ATP carrier protein F2009.60 - Arabidopsis thaliana
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6; Conser
          Similarity 60.
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Data Library,
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                                         Score 44;
Pred. No.
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Entian, K.D.; Hoheisel, J.;
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               Mismatches
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43;
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                                                                             Length 379
          Indels
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     Gaps
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protein FIR22.10 |imported| - Arabidopsis thaliana Gispecies: Arabidopsis thaliana Grapecies: Arabidopsis thaliana Grapecies: Arabidopsis thaliana Grapecies: O2-Mar-2001 asequence_revision 02-Mar-2001 C:Accession: H96681 Asequence_revision 02-Mar-2001 R:Theologis. A.; Ecker, J.R.; Palm, C.J.; Federspie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain C; Genetics: A; Gene: BH0472
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A.Introns: 1873: 43/2: 87/3: 111/3: 151/3: 175/3: 222/3: 251/1: 399/2
C:Superfamily: Arabidopsis thaliana hypothetical protein F3C22.40
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A; Residues: 1-466 CPURS
A; Residues: 1-466 CPURS
A; Cross-references: EMBL:AL353912; GSPDB:GN00061; ATSP:F3C22.40
A; Experimental source: cultivar Columbia; BAC clone F3C22
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A.Tittle: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A.Reference number: A83650, MUID:20263314
A.Accession: H8708
A.Accession: H8708
A.Accession: H8708
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A;Gene: ATSP:F3C22.40
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A; Accession: T49017
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A;Experimental source: strain C-125
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A; Residues: 1-417 <STO>
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8; Conserv
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6; Conserv
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Pred. No.
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Mismatches
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          Federspiel, N.A.; Kaul, S.; White,
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A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Klaykin, C.A.; Li, J.A.; Liu, S.A.; Liu, S.A.; Liuros, J.S.; Maiti, R. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wenter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719

a:Resulus; preclaiminary
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R. Simpson, A.J.G., Reinach, E.C., Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; R

R. Simpson, M.J.G., Reinach, E.C.; Arruda, P.; Abreu, F.A.; Carnero, D.M.; Carrer, H

Briones, M.R.S.; Benon, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carrera, A.J.S.

as-Neto, E.; Becon, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carrera, A.J.S.

submitted to GenBank, June 2000

A. Authors: Rerreita, M.L.; Kenper, E.L.; Kitajira, J.P.; Krieger, J.E.; Kuramoe, E.E.; Laigi

J.D.; Junqueita, M.L.; Kenper, E.L.; Kitajira, J.P.; Krieger, J.E.; Kuramoe, E.E.; Laigi

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marrino, E.

A. Authors: Marting, E.M.F.; Marsukuma, A.Y.; Menck, C.F.M.; Miracoa, E.C.; Miyaki, C.Y.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa, T., V. E.; de Sa, R.G.; Sonteilli, R.V.; Savasa, M.; Tsuhako, M.H.; Vallada, B.; Van Sliva, A.M.; Silva, J.M.; Silva, J.; Wettore, A.L.; ?

i. Reference number; A59328
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A;Reference number: A82515; MUID:20365717
A;Rote: for a complete list of authors see reference number A59328 be
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A; Residues: 1-1197 <SIM>
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.S.; Maiti, R.;
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RESULT

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C. BEGG. S. Ogasawar. N. Moszer, I. Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; BEGG. S.; Ogasawar. N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, N.K.; A.; Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, A.; Ehrlich, S.D.; Emerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, Rature 90, 249-256, 1997n. P.T.; Entlan, M.; Fujita, Y.; Fumb, S.; Gallizi, A.; Gallich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A. Authors; Lauber, J.; Lazarevic, V.; Lee, S.M.; Leeine, A.; Liu, H.; Masuda, S.; Authors; Jauber, M.; Lazarevic, V.; Lee, S.M.; Leeine, A.; Liu, H.; Masuda, S.; Authors; Schleich, S.; Schroeter, R.; Scoffone, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl, A.; Athors; Schleich, S.; Schroeter, R.; Scoffone, F.; Schiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Farraka, H.; Zamelhi, A.; Yoshikawa, H.; Zamelhi, A.; Arītile: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
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C.Spacias: Synechocystis sp.
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C.Spacias: Synechocystis sp.
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C.Spacias: Synechocystis sp.
C.Straity: PCC 68037
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C.Spacias:
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A.Note: the nucleocide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein str0881
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-103 <K
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A; Accession: S77270
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A:ROSIGULES: 1-305 <KUN>
A:Cross-references: GBN-299121; GB:AL009126; NID:92635827; PIDN:CAB15405.1; PID:el1860
A:Experimental source: strain 168
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C;Date: 05-Dec-1997 #sequence_revision
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7; Conserv
Similarity
5; Conserv
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       Conservative
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                                                     Score 43;
Pred. No.
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Pred. No. 4
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                                                                                                          Length 103
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A.Gross-references: BMBL:X85194, NID:g18109: PIDN:GAA6311.1; PID:g181100
C:Supporfamilty, ADP_ATP carrier protein; ADP_ATP carrier protein repeat bomology
C:Reywords: duplication; bomodimer; mitochondrion; transmembrane protein
F;5-100/Domain: ADP_ATP carrier protein repeat bomology AGP19
F;109-204/Domain: ADP_ATP carrier protein repeat bomology AGP19
                                                                                                                                                                                                                                                                                                                                                                                  C:Pate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C:Accession: $20259 $20028  
R:Sharpe, JA.; DBY, A. A. WHAT AND THE CONTROL OF THE MEDICAL CONTROL OF THE M
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A:Title: Equine arteritis virus is not a togavirus but belongs A; Reference number: A39925; NUID:91237805
A: Accession: F39925
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C:Specles: la-reb-1992 #sequence_revision 14-Fab-1992 #text_change 08-Oct-1999
C:Accession: F39925
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A; Restdues: 1-365 KNED
A; Cross-references: EMBL: 234000; NID: 9496485; PIDN: CAA83969.1; PID: 9496488
A; Cross-references: EMBL: 234000; NID: 9496488
A; Mote: Only a part of the coding sequence is given in this paper
A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, Man A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, Man A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, Man A; Mote: the nucleotide sequence was submitted to the EMBL Data Library, Man A; Mote and Mote and Man A; Mote and Mote and Man A; Mote and Mote a
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A; Residues: 1-308 <SHA>
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A; Accession: S52775
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A; Residues: 1-255 <DEN>
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J. Virol. 6
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Species: Chloroflexus aurantiacus
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7; Conser
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Pred. No.
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hypothetical protein MJ0279
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A:Accession: Provo-
A:Molecule type: protein
A:Molecule type: protein
A:Residues: 303-313 <SEI
C:Superfamily: octopus rhodopsin
C:Superfamily: octopus rhodopsin
C:Reywords: chromoprotein; color vision; G protein coupled rec
C:Reywords: chromoprotein estatus predicted <TM2>
F:36-60/Domain: transmembrane #status predicted <TM3>
F:106-130/Domain: transmembrane #status predicted <TM3>
F:106-130/Domain: transmembrane #status predicted <TM4>
F:121-16/Domain: transmembrane #status predicted <TM4>
F:120-223/Domain: transmembrane #status predicted <TM5>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Seidou, M.; Kubota, T.; Hiraki, K.; Kito, Y. Biochim. Biophys. Acta 957, 318-321, 1986 A.Title: Amino acid sequence of the retinal binding A;Reference number: PT0063; MUID:89051045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A: Rolcoule type: mRNA
A: Relations: 1-448 CARRA
A: Cross references: EMBL: X70498; NID: 9397389; PIDN: CAA49906.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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A; Residues: 1-402 < NOE>
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R; Noel, P.J.; Cartwright,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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Best Local
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F;210-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
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212 NFLAAFLIGWGITIG
                2 SMLVVFLLLWGVTWG
                              Similarity
8; Conserv
                              Conservative
                                    49.4%;
                16
226
                             Score 43; DB
Pred. No. 50;
2; Mismatches
                                    50;
                               G.
                                             Length 308
                               indels
                              0
                              Gaps
                               0
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Drosophila translocation protein 1 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drosophila melanogaster C;Date: 15 -Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2
A.Gene: FlyBase:Trpl
A.Gene: FlyBase:FBgn0011584
C:Superfamily: Caenorhabditis clegans hypothetical protein C18E9
                                                                                                                          A;Cross-references: EMBL:238100; NID:9558180; PIDN:CAA86222.1; PID:9558181
C;Genetics:
                                                                                                                                                                                                                                                                                                                       A; Title: A Sec62p-related component of the A; Reference number: S51791; MUID:95045419 A; Accession: S51791
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 13, 5253-5261, 1994
                                                                                                                                                                                                                                                                                                                                                                                                          secretory protein translocon from Drosophi
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247 LIVFIIVWALTGG
              4 LVVFLLLWGVTWG
                            Similarity
6; Conserv
                            Conservative
259
              16
                                  46.28;
                                  Score 43;
Pred. No.
                            Mismatches
                                 DB
62;
                                           2
                            Ņ
                                          Length 402
                            Indels
                            0
                           Gaps
                            0;
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N;Alternate names: visual pigment protein
C;Speclas: Todarodes pacificus (Japanese flying squid)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: S29483; PT0063
A;Reference number: S29483; MUID:93154520
A;Accession: S29483
                                                                                                                          R;Hara-Nishimura, 1.; Kondo, M.; Nishimura, M.; Hara, R.; Hara, FEBS Lett. 317, 5-11, 1993
                                                                                       A; Title: Cloning and nucleotide sequence of cDNA
                                                                                                                                                                                                                                                                                                                                                                              rhodopsin [similarity] - Japanese flying squid
                                                                                       for rhodopsin of the squid Todarodes
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site

of

squid visual pigment. PID: g397390

receptor; glycoprotein;

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585 LLYFLICYGVTW 596

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R:Lin, X.; Kaul, S.; Bounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; VannAken, S.E.; Umayam, L.J. Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1939

A:Iltle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2948060 [imported] - Arabidopsis thaliana Cispecles: Arabidopsis thaliana (mouse-ear cress) C:pate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F:301-302/Domain: transmembrane *status predicted <TMY>
F:801-4322/Domain: transmembrane *status predicted F:8014/Binding site: carbohydrate (Asn) (covalent) *status predicted F:305/Binding site: retinal (Lys) (covalent) *status experimental F:336,337/Binding site: palmitate (Cys) (covalent) *status predicted
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ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein PB4.210 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C:Accession: T05361
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A; Residues: 1-621 <STO>
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A; Note: F8B4.210
                                                                                                                                                                                            A; Map position: 4
                                                                                                                                                                                                                    C;Genetics
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                                                                                                                                                                                                                                                          A; Cross-references: EMBL: AL034567
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-710 <BEV>
                                                                                                                                                                                                                                                                                                                     A; Accession: T05361
                                                                                                                                                                                                                                                                                                                                             A; Reference number: 215409
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Best Local Similarity
"~+~hes 5; Conser
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Best Local
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  4 LVVFLLLWGVTW 15
                                            7; Conserv
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7; Conser
                                                                                                                                                                     75/2; 137/2; 190/3; 246/1; 301/3; 359/3; 391/3; 450/3; 559/2
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                                               Conservative
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Pred. No. 86;
4; Mismatches
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                                                             Score 43;
Pred. No.
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Pred. No. 67;
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95;
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                                                                                  Length 710;
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Tallon, L.
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A; Residues: 1-218 <TE2>
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                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE002464; GB:AE002098; NID:g7226388; PIDN:AAF41544.1; PID:g722
A;Experimental source: serogroup B, strain MC58
  B81906
                    RESULT
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A; Map position: X
A:Introns: 51/3; 159/1; 476/1; 526/1; 1465/1; 1826/3; 1947/3;
                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-3345 < MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z17668
A; Accession: T13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A; Description: Sequencing the distal X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T13423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision
                                                                                                                                                                                                            A; Note: EG:30B8.4
                                                                                                                                                                                                                                                                            A; Cross-references: FlyBase: FBgn0000377
                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL009195; NID:e1355203; PID:e1248585; PIDN:CAA15708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 30B8.4 - fruit fly (Drosophila melanogaster)
1948 LQFIVTYIAPWQITWG 1963
                                                                                         hes 5; Conser
                                            1 MSMLVVFLLLWGVTWG 16
                                                                                                                                                                                                                                                                                                                                                                                        preliminary; translated from
                                                                                            Conservative
                                                                                                               49.4%;
                                                                                                                  Pred. No. 3.1e+02;
                                                                                                                                         Score 43;
                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              GB/EMBL/DDBJ
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                                                                                                                                         DB 2;
                                                                                                                                      Length 3345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                            Indels
                                                                                                                                                                                                                                  2081/1; 2196/3; 3007/3
                                                                                         0;
                                                                                         Gaps
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A; Experimental source: serogroup
A; Accession: F81115
                                                                                                                                                                                                                                                    A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: F81111
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R:Tettclin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elser Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Oin, H.; Vanathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C:Species: Neisseria meningitidis
C:Species: 31-War-2000 #sequence_revision 31-War-2000 #text_Change 19-Jan-2001
C:Accession: F81111; F81115
                                                      A;Cross-references: GB:AE002467; GB:AE002098; NID:g7226426; PIDN:AAF41579.1; A;Experimental source: serogroup B, strain MC58
                                                                                                                                                     A; Residues: 1-218 <TET>
                                                                                                                                                                                             A; Molecule type: DNA
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50 LLVFRLCWGI-WG
      4 LVVFLLLWGVTWG 16
                           Similarity
B; Conserv
                            Conservative
61
                                   61.5%;
                                  Score 42.5;
Pred. No. 4:
                            Mismatches
                                    45
                                          DB
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probable membrane protein NMA1368 (imported) - Neisseria meningitidis (strain 22491 s

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025035
hypothetical protein 2 - Escherichia coll plasmid Colla
C.Species: Escherichia coll
C.Species: 24-Jan-1988 *sequence_revision 24-Jan-1988 *text_change 18-Jun-1993
C.Date: 24-Jan-1988 *sequence_revision 24-Jan-1988 *text_change 18-Jun-1993
C.Accession: G.5035
C.Accession: G.5035
L. Bacceriol, J.A.: HBu, C.H.; Konisky, J.
J. Bacceriol, 168, 228-236, 1986
J. Bacceriol, 168, 228-236, 1986
                                                                                                    C:Genetics
A:Genome:
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M. Fittle: DNA and mano acid sequence analysis of structural and immunity gol A. Reference number: A91822; MUID:87008385

A. Accession: H25035
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A.78Eference number: A81775; MUID:20222556
A.Accession: p81906
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C:Species: Neisseria meningitidis
C:Accession: B81905
C:Accession: B81905
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A;Experimental source: serogroup A, strain 72491
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A; Residues: 1-218 < PAR>
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Pred. No.
                Score 42; DB 2;
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Mungall, K.; Quail,
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodur A; Reference number: A83650; MUID:20263314
A;Accession: A83755
                probable integral membrane transport protein - Streptomyces coelicolor C:pspecies: Streptomyces coelicolor C:Dato: 03-Dec-1999 #text_change 21-Jan-2000 C:Accession: T36979
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP001511; GB:BA000004; NID:g10173727; PIDN:BAB04880.1; GSPDB:G
A;Experimental source: strain C-125
C:Genetics:
A;Gene: BH1161
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A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A; Peterence numbor: A72450; MUID:99310339
A; Accession: E72636
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A;Molecule type: DNA
A;Residues: 1-406 <STO>
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C;Superfamily: unassigned
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A;Experimental source: strain Kl
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A; Residues: 1-338 <KAW>
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C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 17-Mar-2000
C:Accession: E72636
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D.; Bentley, S.D.;
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Pred. No. 74;
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Pred. No. 86;
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J.; Barrell, B.G.; Rajandream,
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F:30-46/Domain: transmembrane #status predicted <TM1>F:12-88/Domain: transmembrane #status predicted <TM2>F:112-128/Domain: transmembrane #status predicted <TM3>F:112-128/Domain: transmembrane #status predicted <TM3>F:138-134/Domain: transmembrane #status predicted <TM3>F:169-185/Domain: transmembrane #status predicted <TM3>F:169-185/Domain: transmembrane #status predicted <TM3>F:152-268/Domain: transmembrane #status predicted <TM3>F:153-334/Domain: transmembrane #status predicted <TM3>F:131-334/Domain: transmembrane #status predicted <TM3>F:131-334/Domai
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C;Superfamily: Streptomyces lividans chloramphenicol
                                                                                                                ribodopsin - giant octopus (;Species: Octopus Joifelni (giant octopus) (;Species: Octopus Joifelni (giant octopus) (;Ate: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 05-Jun-1998 (;Accession: S00610 (;Accession: S00610 R:Ovohinnikov, Y.A.; Abdulaev, N.G.; Zolotarev, A.S.; Artamonov, I.D.; Besp FEBS Lett. 232, 69-72, 1988
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A:Molecule type: DNA
A:Residues: 1:38 - AUE
A:Cross:references: EMBL:X62045; NID:g44771; PIDN:CAA43978.1; PID:g44772
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A;Reference number: S24065; MUID:92110434
A:Accession: S24065
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Biochimie 73, 683-688, 1991
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                                     A;Title: Octopus rhodopsin. Amino acid sequence deduced from cDNA A;Reference number: S00610; MUID:88211878
                                                                                                                                                                                                                                                                                                                                                       000CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
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Best Local Similarity
7; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 MMVIFCILFGLFW 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 MLVVFLLLWGVTW 15
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6; Conser
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Pred. No. 91;
5; Mismatches
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Pred. No. 86;
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                                                                                                                                                           I.A.;
                                                                                                                                                                           extreme acid resistance protein xasA - Escherichia coli
N;Alternate names; probable permease xasA
C:Species: Bacherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 17-Mar-2000
C:Accession: G64902; S78637
R:Blatther. P. R: Plunkett III. G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F
R:Blatther. P. R: Plunkett III. G.; Bloch, C.A.; Perna, N.T.; Burland, V.; F
Science 27, 1431-1462, 1997
A:Title: The Complete genome sequence of Escherichia coli K-12.
A:Accession: G6490; MUD5:7426617
A:Accession: G6490; MUD5:7426617
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A; Molecule type: DNA
A; Residues: 1-499 <BER>
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A;Cross-references: GB:AE000246; GB:U00096; NID:gl787764; PIDN:AAC74565.1; PID:gl7877
A;Experimental source: strain K-12, substrain MG1655
                                                                           A; Molecule type: DNA
A; Residues: 1-511 <BLAT>
                                                                                                                                                      A; Status: nucleic acid sequence not shown;
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R; Berks, M.
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Best Local :
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Matches 3; Conserv
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A. Molecule type: mRNA
A. Mesidues: 1-455 <0VC>
A; Cross: references: EMBI: X07797
A; Cross: references: EMBI: X07797
A; Note: the source is designated as Paroctopus deficini
A; Note: part of this sequence was confirmed by protein sequencing
C; Superfamily: octopus rhodopsin
C; Superfamily: octopus rhodopsin
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F:153-177/Domain: transmembrane #status predicted CTM3>
F:261-224/Domain: transmembrane #status predicted CTM5>
F:262-224/Domain: transmembrane #status predicted CTM5>
F:362-233/Domain: transmembrane #status predicted CTM5>
F:362-234/Domain: transmembran
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T3365.5 - Caenorhabditis elegans (fragment) C;Species: Caenorhabditis elegans C;Date: i2-Mar-1993 #sequence_revision 12-Mar-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 27/3; 134/2; 184/2; 215/3; 253/2; 332/3; 375/3; 409/1; 442/3 C;Superfamily: gamma-aminobutyric acid transporter
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379 LIMEWLIIYGTTWG
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                                                                                             3 MLVVFLLLWGVTWG
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5; Conserv
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23.1%;
392
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Pred. No. 93;
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                                                                                                                                                                                                                                                     Score 42; DB 2;
Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                        Length 499;
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G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, Y.

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translation not

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F:128-144/Domain: cransmembrane status predicted (TMA)
F:161-177/Domain: cransmembrane status predicted (TMA)
F:277/Domain: cransmembrane status predicted (TMA)
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A:Readdues; 402-489 AHERN
A:Cross-references; EMBL:U13204
A:NOte: the nuclectide sequence was submitted to the EMBL Data Library, August 1994
C:Cenetics:
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C;Function:
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A;Pitlo: A glutamate-dependent acid resistance gene in Escherichia coli. A.Reference numbor; $78627; MUID:96272279
A.Recession: $78627
A.Status; nucleic acid sequence not shown; translation not shown
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Search completed: January 7, 2002, 16:52:10 Job time: 227 sec
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Best Local Similarity 66./
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Pred. No. le+02;
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AB11_RABIT
I10S_MOUSE

UHPT_CHLMU
VES_PAPVE
X192_ECOLI
YBJG_ECOLI
YBJG_HCOLI
YBJG_HUMAN
I112A_HUMAN
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6 escherichia 2 mycoplasma 9 homo sapien 0 pelomedusa 7 caenorhabdi

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sus scrofa
sus scrofa
homo sapien
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homo sapien

FHUB_ECOLI Y281_BUCAI

buchnera escherichia escherichia brachydanio solea solea lithognathu

bacillus pseudomonas

GUDH_BACSU GUDH_PSEPU

OPSD_LITMO
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ITL2A_MOUSE
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chlamydia p chlamydia t bacillus su mus musculu homo sapien bacillus su drosophila methanococc

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9 escherichia
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gallus gall staphylococ sulfolobus lactococcus nus musculu rattus norv haemophilus

caenorhabdi drosophila

mus musculu

ALIGNMENTS

woodchuck h

macaca homo sapien caldocellum caenorhabdi

mula

MOTA_CHICK
PTSB_STAXY
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CYB_SULAC
YDNK_LACLC
YDNK_LACLC
YDN CAEEL
ITBN_DROME
YP84_CAEEL
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YR84_CAEEL
YR84_CALSA
GUNA_CALSA
KLK3_MACMU
COMT_HUMAN
VMSA_MHYW6

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MEDLINE~95334362; PubMed~7610040;
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REVISION TO 1015.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.,
                                                                                                                                                                                                                                                                       YIBP_ECOLI STANDARD; PRT: 1107 AA. P39285: PA5798: O1-FBB-1995 (Rel. 31, Created) I5-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last amountion update) HYPOTHETICAL PROTEIN YJEP PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL custation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bravo A., de Torrontegui G., Dlaz R., "Identification of components of a new stability system of plasmid R1, ParD, that is close to the origin of replication of this
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01-JAN-1990 (Rel. 13,
15-DEC-1998 (Rel. 37,
HYPOTHETICAL 24.3 KDA
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Pfam; PF02517; Abi; Abi.
Hypothetical protein; Plasmid.
SEQUENCE 217 AA; 24307 MW;
                                                                      "Analysis of the Escherichla coll genome region from 92.8 through 100 minutes."; Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                   Blattner F.R.;
                                                                                                                                                                                                                    Escherichia
                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X06240; CAA29583.1; -. PIR; S01095; S01095.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                       decarboxylase.";
J. Biol. Chem. 263:11516-11522(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Ros
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                 EMBL: U14003; AAA97058.1; -.
                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
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between the Swiss institute of Bioinformatics and the BMBL outsi
the European Bioinformatics institute. There are no restrictions
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                                                                                                                                                      Hypothetical
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W; . 5F52A2993B90532B CRC64;
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0003 FAMILY. STRONG,
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                                                                                                 Freser C.M., Casjons S., Huang W.M., Sutton G.G., Clayton K.A.,
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Reterson J., Kerlavoes A.R., Opadson R.D., Salzberg S., Hanson M.,
van Vugt R., Palmer A.R., Opadson D., Weidman J.,
Utterback T., Matthey I., Adbas M.D., Gocayne J.D., Meidman J.,
Garland S., Pujli C., Cotton M.D., Horst K., Roberts K., Hatch B.,
Smith H.O., Venicar J. C., Vetton M.D., Horst K., Roberts K., Hatch B.,
Gandin M.D., Weiner J. C., Vetton M.D., Horst K., Roberts K., Hatch B.,
Genonic Sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.—
The Buropean Bioinformatics institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agroement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BORBU
                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi (Lyme discase spirochete).
Bacteria; Spirochaetales; Spirochaetaceae; Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Transmembrane; Complete TRANSMEM 25 47 POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                        Nature 390:580-586(1997)
                                                                                         burgdorferi.
                                                                                                                                                                                                                                                                                                    NCBI_TaxID=139;
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                                             -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37 IVILLIWGLSW 47
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                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
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L PROTEIN BB0006.
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                                             THE UPF0118 (PERM) FAMILY.
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Pred. No.
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6AAB25353BB27BC1 CRC64;
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EMBL outstation -
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TRANSMEM
                           RuBL: Al109732; CAB52045.1; Totte:Pro: IPR000073; Abhydrolase.
InterPro: IPR000179; Est_lip_thioest_actsite
InterPro: IPR004179; Pro_amnorTase.
Pfam: Pr00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                     Actinomycetales;
NCBI_TaxID=1902;
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SC7H2.03C.
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                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S33.
                                                                                                                                                                                                                                                                                                                                              Rajandream M.A.
                                                                                                                                                                                                                                                                                                                                                             Saunders D.C., Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor
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              PRINTS; PR00793; PROAMNOPTASE
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POTENTIAL.
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Score 46; DB Pred. No. 15; u V Length 374 Indels 0 Gaps 0

20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last senotation update)
PROBABLE PROLINE IMINOPEPTIDASE (EC 3.4.11.5) (PIP) (PROLYL

Bentley S.D., Parkhill J., Barrell B Ģ,

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entitles requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. This SWISS-PROT entry is copyright. It is produced through a collaboration Swiss Institute of Bloinformatics and the There are no restrictions Usage ý and EMBL outstation for commercial on

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032256;
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Pfam; PF00892; DUF6; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                              SEQUENCE
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NCBI_TaxID-1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus subtilis
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                                                                                               SMLVVFL-LLWGVTW
                                                                ALLLAFLYIMWGVNW
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PROTEIN IN ARAR-LACA INTERGENIC REGION.
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Pred. No.
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BY SIMILARITY.
PROTON DONOR (BY SIMILARITY).
7BEF00133B353EEB CRC64;
                                                                                                                                           Pred. No. 28
                                                                                                                                                             Score 43.5;
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01-DEC-1992
01-DEC-1992
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                              ADT_CHLRE
P27080;
translocator gene from Chlamydomonas Mol. Gen. Genet. 237:134-144(1993).
                                                                             MEDLINE-93204887; PubMed-8455552;
                                                                                                STRAIN FUD44-R2;
                                                                                                                                                                                Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                 Eukaryota; Viridiplantae; Chlorophyta;
                                                                                                                                                                                                                       Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                             TRANSLOCATOR) (ANT).
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01-AUG-1992 (Rel. 23, La
01-OCT-1994 (Rel. 30, La
ADP,ATP CARRIER PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Envelope protein.
CARBOHYD 56 56 W-LINKED (GLCNAC.
SEQUENCE 255 AA; 28672 MH; 4310FFFFN117AF76
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InterPro: IPR001332; Ratteri_glycop.
InterPro: IPR003241; Equine_virus_ORF5
Pfam: PP00951; Arteri_glycop: 1.
ProDom: P0003371; Equine_virus_ORF5; 1
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Equine arteritis virus is not a togavirus coronaviruslike superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        den Boon J.A., Snijder E.J.,
Horzinek M.C., Spaan W.J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses, no DNA stage: Nidovirales:
Arteriviridae, Arterivirus.
NCBI_TaxID-11047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Last a HYPOTHETICAL 28.7 KDA PROTEI Equine arteritis virus (EAV)
                                                       Sharpe J.A., Day A.;
                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID-3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: X53459; CAA37544.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Virol. 65:2910-2920(1991).
-i- FUNCTION: POSSIBLE ENVELOPE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN- BUCYRUS;
                                      "Structure, evolution and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE 91237805; PubMed 1851863;
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7; Conserv
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25, Last annotation update)
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                                                                                                                                                                                                                                                                                 (ADP/ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB
Pred. No. 28;
3; Mismatches
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                                                                                                                                                                                                                                                                                 TRANSLOCASE)
                   of the mitochondrial ADP/ATP reinhardtil.";
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                                                                                                                                                                                                   Chlorophyceae;
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                                                                                                                                                                                                                                                                                 (ADENINE NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 255
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FUNCTION: CATALYZES THE EXCHANGE

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ADP

AND ATP

INNER MEMBRANE

MITOCHONDRIAL

between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no re

restrictions

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EMBL outstation

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RESULT
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Best Local
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P31356;
01-JUL-1993
01-JUL-1993
15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S30259; S30259.
InterPro; IPR002067; Mit_carrier.
InterPro; IPR001993; Mitoch_carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                               Todarodes pacificus (Japanese flying squid).
Enkaryota: Hetaroa: Mollusca: Cophalopoda: Coleoidea: Teuthoida:
Gesopsida: Ommastrophidae: Todarodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                       Hara-Nishimura I., Kondo M., Nishimura M., Hara R., Hara T.;
"Cloning and nucleotide sequence of cDNA for rhodopsin of the squid Todarodes partificus.";
FEBS Lett. 317:5-11(1993).
                                                                                                                                                                                                                                                                                                                                                                    RHO
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                                                                                                                                                                                                                                      MEDLINE-93154520; PubMed-8428633;
                                                                                                                                                                                                                                                        TISSUE-Retina
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                  NCBI_TaxID-6637
                                                                                                                                                                                                                                                                                                                                                                                   RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION:
                            OPSIN SUBFAMILY.
                                         BE PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY 1 OF
                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIPTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER
                                                                                                       PRINCTION: VISUAL PICHENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETIMAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION OF PHOSPHOLIPASE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INNER MEMBRANE
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8; Conser
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                38,
26,
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92
133
197
234
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                                                                                          INTEGRAL MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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D477CF0E72B7A53F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                           G-PROTEIN COUPLED
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                                                                                                                        ACTIVATION
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SWISS-PROT entry is copyright.

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SEQUENCE FROM N.A.

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PAGO_SALTY
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Best Local
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DOMAIN
SEQUENCE
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O30646;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00001; 7tm_1; 1.
Pfam; PF02162; Rhodopsin_C; 1.
PRTNTS; PR00237; GPCRRHODOPSN
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                                                                         15-JUL-1999 (Rel.
15-JUL-1999 (Rel.
20-AUG-2001 (Rel.
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InterPro; IPR001760;
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NCBI_TaxID=602;
               Salmonella
                          Bacteria; Proteobacteria;
                                    Salmonella typhimurium
                                                                PAGO
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5; Conser
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                                                                                                                            STANDARD;
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. 40, Last anno
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                          gamma
                                                                                                                                                                                                                                                                                                          MK.
                                                                           sequence update)
annotation updat
                                                                                                                                                                                                                                                       Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (POTENTIAL)
CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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3 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                               PALMITATE (BY SIMILARITY)
PALMITATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                       RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .).
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CYTOPLASMIC (
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                                                                                                                                                                                                                                           ore 43; DB
ed. No. 43;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; Vision;
                          subdivision; Enterobacteriaceae;
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                                                                                                       Auer J., Spicker G., Boeck A.; "Presence of a gene in the archacbacterium Methanococcus vannielli homologous to secy of eubacteria."; Biochimie 73:683-688(1991).
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SECY_METVA
This SWISS-PROT entry is copyright.
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                                                                                                                                                                 MEDLINE-92110434; PubMed 1764515;
                                                                                                                                                                                  SEQUENCE FROM N.A.
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SUBCELLULAR LOCATION. INTEGRAL ABBRANE PROTEIN.
SIMILARITY: BELONGS TO THE SECY/SECGI-ALPHA FAMILY.
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11 FUNCTION: VISION. PIGMENTS ANE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN. OPSIN, COVALENTLY LINKED TO CIS-RETINAL.

11 SUBCELLILIAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

11 TISSUE SPECIFICITY: NOD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATE
                                                                                                                                                                                                              Ovohinnikov Y.A., Abdulaev N.G., Zolotarev A.S., Artamonov I.D.,
Bespalov I.A., Dergachev A.E., Tsuda M.;
"Octopus rhodopsin, Amino acid sequence deduced from cDNA.";
                                                                                                                                                                                                                                                                                                   Octopus dofleini (Giant octopus).
Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
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Protein transport; Translocation;
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20-MG-2001 (Rel. 40, Last sequence update)
20-MG-2001 (Rel. 40, Last amnotation update)
AMINO ACID ANTIPORTER (EXTREME ACID SENSITIVITY PROTEIN).
XASA OR ACSA OR GADE OR 22216 OR ECS2097.
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EXTRACELLULAR.
7 (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR.
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CYTOPLASMIC.
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PALMITATE (BY SIMILARITY).
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1 (POTENTIAL)
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Maybaw G.F. Erwans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis M.H., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anancharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.*;
XASA_ECOLI STANDARD; PRT; p39183; p76131; p77384; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence
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'Complete genome sequence of enterohemorrhagic Escherichia coli
'157:H7 and genomic comparison with a laboratory strain K-12.*;
DNA Res. 8:11-22(201)
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MEDLINE-21074935; PubMed-11206551;
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MEDLINE-21156231; Pubb
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-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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Pred. No. 65;
1; Mismatches
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85DF72BD2529CE33 CRC64;
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Itob T. Kasai H. Kashimoto K. Kimura S. Kitakwa M. Kitagawa M. Makino K. Miki T. Mizobuchi K. Mori H. McMomara K. Makade S. Nakamura Y. Mashimoto H. Nishio Oshima T. Saito M. Sampai G. Seli Y. Stasundaram S. Takena J. Takena J. Takenato Y. Yanamato Y. Moriuchi T.; Yanamato Y. Moriuchi T.;
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Transmembrane; Inner membrane;
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or send an email to license@isb-sib.ch).
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corresponding to the 28.0-40.1 min region on the linkage map.";
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AMINO ACID ANTIPORTER
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O ACID ANVIPORTER (EXTREME ACID SENSITIVITY PROTEIN)
OR ACSA OR GADC OR B1492.
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H., Nishio Y.,
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AMINO ACID ANTIPORTER
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                                                                            POTENTIAL
          Score 42; DB
Pred. No. 65;
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Pred. No.
                                                       POTENTIAL.
8369AEA15AF1523D CRC64;
                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                  Transport;
   Mismatches
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                                                                                                                                                                                                   Amino-acid transport
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                                                                                                                                                                                                                                                                                      Usage
                     Length 511;
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MBL outstation -
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RESULT 16
DAL5_YEAST
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                                               Matches
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01-APR-1990
01-OCT-1996
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TRANSMEM
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                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                            Transport;
                                                                                                                                                                                                                                                                                                                   EMBL; M24098; AAA34555.1;
EMBL; Z49652; CAA89685.1;
PIR; A28671; A28671.
SGD; S0003913; DAL5.
                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88086880; PubMcd-3275614; Rai R., Genbauffe F.S., Cooper T.G.; Structure and transcription of the allantoate permease gene (DAL5) from Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALLANTOATE PERMEASE
DAL5 OR UREP1 OR YJI
                                                                                                                                      CARBOHYD
                                                                                                                                                     CARBOHYD
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 154 MLAVFIVIWGM 164
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                      3 MLVVFLLLWGV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE ALLANTOATE PERMEASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nitted (SEP-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: COMPONENT OF THE ALLANTOATE TRANSPORT SYSTEM
                                             Similarity
6; Conser
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124 145
155 171
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14, Last sequence update)
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                                                       48.38;
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                                                                                                      W.
                                             Score 42; DB
Pred. No. 68;
4; Mismatches
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RESULT 17 NTDO_CAEEL

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Waterson R.,
Wohldman P.;
"2.2 Mb of co
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EMBL; Z19158; CAA79575.2; -.
EMBL; Z19156; CAA79575.2; JOINED
EMBL; Z19156; CAA79564.2; -.
EMBL; Z19158; CAA79564.2; JOINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DUIDIN R.;

SUBMITTED (OCT-2000) to the EMBL/GenBank/DDBJ databases.

II FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS HIGH-
II FUNCTION: TERMINATES THE ACTION OF DOPAMINE BY ITS TRAINALS.

AFFINITY SODIOM-DEFENDENT REDPTAKE INTO PRESYMAPTIC TRAINALS.

I SUGCELLIANE LOCATION: LITERSTAN EMBHARA PROFESS PROTEIN (FORDABLE).

I MISCELLANEOUS; THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR
I MISCELLANEOUS; THIS PROTEIN IS THE TARGET OF PSYCHOMOTOR

I SIMILARITY: BELONGS TO THE SODIUM: NEUROTRANSMITTER SYMPORTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          datreille P., Lightning J., Lloyd C., Mortimore B., O'Ccallaghan M. Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen Stas M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R. Ainscough R. Ainderson K. Baynes C. Berks M. Bourson Great M. Couled M. Copsey T. Cooper J. Coulson Bonfield J. Burton J. Connell M. Copsey T. Cooper J. Couled Greaton M. Fraser A. Dear S. Du Z. Durbin R. Powello A. Fraser M. Fraser M. Fraser M. Johnston L. Cardone A. Green P. Hawkins T. Hillier L. Johnston L. Jones M. Kristen J. Laissler M. 
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Eppler M., Blakely R.D.;
"The Caenorhabditis elegans gene T23G5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98440631; PubMed-9765501;
MEDLINE-98440631; Apparsundaram S., /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT)
                                                                                Wormben, 72365.5; G225124.
ILLEEPPO, IRBOO0175; Na_neurotran_symport.
Pram, PP00209; SNF: 1.
PRINTS; PR00176; NA_NEUROTRAN_SYMP_1; 1.
PROSITE; PS00610; MA_NEUROTRAN_SYMP_1; 1.
PROSITE; PS00754; MA_NEUROTRAN_SYMP_3; 1.
PROSITE; PS00754; NA_NEUROTRAN_SYMP_3; 1.
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MEDLINE=94150718; PubMed=7906398;
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Neurotransmitter transport;
Symport.
DOMAIN 1 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                        Transport;
    CYTOPLASMIC (POTENTIAL)
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                                                    Transmembrane; Glycoprotein;
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Best Local
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Q1-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIM MAYUT.

MEDILINE-93077448; PubMed-1332940;
Allaout A., Sansonettl P.J., Parsot C.;

*MAIJ, a lipoprotein involved in secretion of Shigella ipa invasins.

*MAIJ, a lipoprotein involved in secretion factor of the Yersinia Yop
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SEQUENCE
                                                                          InterPro; IPR003282; SecIIIOMPK.
InterPro; IPR002920; YscJ_F11F.
Pfam; PF01514; YscJ_F11F; 1.
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DOMAIN
                                   Virulence; Plasmid; Transport; Protein transport; Outer membrane
                                                          PROSITE; PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                          EMBL; M98390; AAA26532.1; -. PIR; C45271; C45271.
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                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid 210 kb invasion
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SIMILARITY: BELONGS TO THE YSCJ FAMILY OF LIPOPROTEINS.
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  Lipoprotein.
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Last annotation update
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (PO'
N-LINKED (GLCNAC. . .) (PO'
N-LINKED (GLCNAC. . .) (PO'
DDA2876EB3AC8049 CRC64;
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Pred. No. 75;
7; Mismatches
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(POTENTIAL).
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75;
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RESULT 20
YIJE_ECOLI
ID YIJE_E
AC P32667
DT 01-OCT
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MXIJ_SH
ID MX
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Best Local S
Matches 8
                                                                                                                                            Query Match
Best Local
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YIJE_ECOLI STANDARD;
P32667;
01-OCT-1993 (Rel. 27, Created)
                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
LIPID
SEQUENCE
                                                                                                                                                                                                                                                            InterPro: IPR003282; SecIIIOMPK.
InterPro: IPR002520; YSCJ_FIIF.
Pfam: PP01314; YSCJ_FIIF; J.
PROSITE: PS00013; PROKAR_LIPOPROTEIN;
                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HH-95;
STRAIN-HH-95;
SLIMHILED (MAY-1995) LO THE EMBL/GenBank/DDBJ databases.
SLIMHILED (MAY-1995) IN THE SCREETION OF THE IPA ANTIGENS.
-1- FUNCTION: INVOLVED IN THE SCREETION OF THE JPA ANTIGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSIUS
                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                  Virulence; Plasmid; Transport; Protein
                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Electrone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella sonnei.
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                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                      TIPID
                                                                                                                                                                                                                                                                                                            EMBL; D50601; BAA09148.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE YSCJ FAMILY OF LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                       -1- SUBCELLULAR LOCATION: ATTACHED TO THE OUTER MEMBRANE
ANCHOR (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPOPROTEIN
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                                                                                     MAVLVVILLVWAFKTG
                                                                                                          MSMLVVFLLLMGVTWG
                                                                                                                                  Similarity
B; Conser
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8; Conser
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PRECURSOR.
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27523
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50.08;
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                                                                                                                                                                                         LIPOPROTEIN MXIJ.
N-ACYL DIGLYCERIDE
MW; 1FB3D62033A31B20
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Pred. No. 49;
3; Mismatches
                                                                                                                                            Score 41;
Pred. No.
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3D20D62033A30898
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                           PRT;
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RESULT POPULATION OF THE POPUL
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Best Local
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Q9YGZ7;
20-AUG-2001
20-AUG-2001
20-AUG-2001
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TRANSMEM
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TRANSMEM
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                                                                                               Liza saliens (Leging mullet).

Eukaryota; Metazoa: Chordeta; Craniata; Vertebrata; Euteleostomi;
Eckaryota; Metazoa: Chordeta; Craniata; Vertebrata; Neoteleosteni;
Actinopterygii; Neopterygii; Percomorpha; Mugilomorpha; Mugilidae;
                                                                                                                                                                                                                                                                                                                                                                             LIZSA
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InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U00006; AAC43049.1; ALT_INIT. EMBL; AE000468; AAC76925.1; ALT_INI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids res. 21:5408-5417(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Analysis of the Escherichia coli genome. region from 89.2 to 92.8 minutes.";
                                                                                                                                                                                                         RHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli
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      SEQUENCE FROM N.A
                                                   NCBI_TaxID-48192;
                                                                                                                                                                                                                              RHODOPSIN
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7; Conserv
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92
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46.78;
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POTENTIAL.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                     353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 301;
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OPSD_MUGCE STANDARD: Q9YGZ9; 20-AUG-2001 (Rel. 40, Created)

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SOFT THE TENENT REPORT OF THE

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                                                  RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN,
LINKED TO CIS-RETINAL.

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-1. TISSUB SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WH:

-1. TISSUB SPECIFICITY OF THE CARBOXYL-TERMINAL SER OR THR I

-1. PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR I
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1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT ABSORBING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; PROSITE; PS00238; OPSIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Retina;
Archer S.N., Hirano J.;
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00237; GPCRRHODOPSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y18670; CAA77252.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                         257
                                                                                                                                        Local Similarity
les 8; Conserv
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SIMILARITY: BELONGS TO FAMILY 1 OF
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                                                                                         MVVAFLICWCPYAGVAW 273
                                                                                                                 MLVVFLLLW----GVTW 15
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134
153
177
                                                                                                                                          Conservative
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202
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353
                                                                                                                                                     47.18;
                                                                                                                                                                                                         39566
                                                                                                                                                                                                         MW;
                                                                                                                                        Score 41; DB
Pred. No. 66;
2; Mismatches
                                                                                                                                                                                                                            N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
RETINAL CHROMOPHORE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                               7 (POTENTIAL).
CYTOPLASMIC.
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                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR
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                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                         A155664649079E3C CRC64;
                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor
                                                                                                                                                                   1.
                                                                                                                                          ω
                                                                                                                                                                 Length 353;
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Query Match
Best Local Similarity
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DOMAIN
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DOMAIN
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostel; Euteleostet, Neoteleostel;
Acanthomorpha; Acanthopterygil; Percomorpha; Mugilomorpha; Mugilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; PROSITE: PS00238; OPSIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR0002760; Opsin.
Pfam; PF00001; 7tml; 1.
PRINTS: PR00237; GPCRRHODOPSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for comme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative analysis of opsins in Moditerranian coastal (ish."; Submitted (JAN-1999) to the CMEL/GonBank/DDBJ detabases.
--- FUNCTION: VISUAL PICKENTS ARE THE LIGHT-ABSORBING MOLECULES MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALE
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PRINTS; PR00579; RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL. SUBGELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES VISION IN DIM LIGHT.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 40,
                                                                                                                N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipoprotein;
          47.18;
47.18;
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Last annotation update)
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                                                                             MW.
                                                                                            CYPOPLASHIC:

N-LINKED (GLCHAC. .) (POTENTIAL).

N-LINKED (GLCHAC. .) (POTENTIAL).

N-LINKED (GLCHAC. .) (POTENTIAL).

RETINAL CHOMOPHORE (BY SIMILARITY).

BY SIMILARITY.
                                                                                                                                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
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EXTRACELLULAR.
3 (POTENTIAL)
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Pred.
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7 (POTENTT
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EXTRACELLULAR
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                                                                                                                                                                                                                         (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Glycoprotein; Vision;
       N 1
     DB
66;
                         1;
                         Length 353
                                                                             CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coupled receptor
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RESULT 23
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01-NOV-1997 (Rel. 35. Last sequence t
01-NOV-1997 (Rel. 35. Last annotation
NADH-UBIQUITANE OXIDOREDUCTASE CHAIN
NDS OR NADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NU5M_CHLRE
P08739; Q34
                                                 EMBL; X54860: CAA38641.1; ALT_INIT
EMBL; U03843; AAB93442.1; -.
EMBL; X64843; CAA47113.1; -.
EMBL; X03464; CAA27181.1; -.
                                                                                                                                                           entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vahrenholz C., Pratje E., Michaelis G
"Mitochondrial DNA of Chlamydomonas r
arrangement of URF5 and the gene for
                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMBL outstation - the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence and mode of transcription.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The URF 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Short dispersed repeats localized reinhardtli mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN- CW15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CW15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1995) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gray M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CW15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of a protein coding region in Chlamydomonas reinhardtii mitochondrial DNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87016388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Viridipiantae: Chlorophyta; Chlorophyceae: Volvocales Chlamydomonadaceae: Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86164259; PubMed-3007117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN CW15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91330346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Gen. Genet.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genet. 19:309-312(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Gray M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gray M.V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201:213-224(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii mitochondria: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14:7506-7507(1986).
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TASE CHAIN 5 (EC 1.6.
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reinhardtii: sequence and
r cytochrome oxidase subunit I.";
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PIR: B24707; B24707

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Best Local
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P98196;
30-MAY-2000
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Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, 30-MAY-2000 (Rel. 39, 20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase;
                                                                                                                                                                                 PROSITE; PS00154;
                                                                                                                                                                                                                                                                    MIM: 605868;
                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Prediction of the coding sequences of unidentified human genes. XI The complete sequences of 100 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tanaka A., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99397452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                        Pfam; PF00702; Hydrolase;
                                                                                                                                                                                                                            InterPro; IPR001757; E1-E2_ATPase.
InterPro; IPR001454; Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
ATPASES). SUBFAMILY IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           large proteins in vitro.";
Res. 6:197-205(1999).
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PF00662; oxidored_q1_N; 1.
                                                                                                                                                                                                                                                                                        AB028944; BAA82973.1;
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6; Conserv
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IPR001750; Oxidored_q1.
IPR001516; Oxidored_q1_N.
                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                546 AA;
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545
578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD; Ubiquinone; Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10470851;
T., Ishikawa K.-I., H
H., Nomura N., Ohara
                                                                                                                                                                                 ATPASE_EL
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                                                                                                                                                             Phosphorylation;
                                                                                                                                                                                    E2;
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Pred. No.
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                                                         EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                    POTENTIAL.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                 (POTENTIAL
                                                                                                 (POTENTIAL)
                                                                                                                                                             Magnesium;
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LSHB_TRIVU
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Best Local
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O46482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METAL
METAL
SEQUENCE
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DOMAIN
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DOMAIN
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DOMAIN
                                                                                        EMBL;
                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab
between the Swiss Institute of Bioinformatics and the EMBL outst
the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "cDNA cloning of luteinizing hormone subunits from brushtail and red kangaroo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Pituitary;
MEDLINE=98345424; PubMed=9680384;
Harrison G.A., Deane E.M., Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trichosurus vulpecula (Brush-tailed possum).
Trichosurus vulpecula (Brush-tailed possum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammmalia; Metatheria; Diprotodontia; Phalangeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
10TROPIN BETA CHAIR PRECURSOR (LUTEINIZING HORMONE BETA SUBUNIT) (LSH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawrence S.B., McNatty K.P., Fidler A.E.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETA) (LSH-B) (LH-B).
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Pfam; PF00007; Cys_knot; 1.
SMART; SM00068; GHB; 1.
                                            InterPro; IPR001545;
                                                                  InterPro; IPR000359; Cys_knot
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: PROMOTES SPENANTOGENESIS AND OVULATION BY STIMUL
THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mamm. Genome 9:638-642(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VVFLLLW-GVTW
                                                                                                                                                                                                                                                                                                                                                                                      CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY LUTROPIN, FOLLITROPIN AND GONADOTROPIN. SIMILARITY: BELONGS TO THE GLYCOPROTEIN HOPEL CONFERENCE OF THE GLYCOPROTEIN
                                                                                     AF017448; AAC96019.1;
AF090388; AAC63526.1;
P01233; 1HRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
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75.0%;
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Pred. No. 1.5e+02;
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MAGNESIUM (BY SIMILARITY).
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                                                                                                                                                                                                                                                    as its content
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Trichosurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Poulsen L.K., Larsen N.M., Molin S., Andersson "Analysis of an Escherichia coli mutant strain killing function encoded by the gef gone family Mol. Microbiol. 6:895-905(1992).
                                                                             or send an
                                                                                                            modified
                                                                                                                                                                                     Science
                                                                                                                                                                                                                                             Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                         Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                         MEDLINE-97426617; PubMed-9278503;
                                                                                                                                                                                                                                                                                                           STRAIN-K12 /
                                                                                                                                                                                                                                                                                                                                                                      Nashimoto
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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X72336; CAAS1063.1; ALT_INIT.
D64044; BAA10910.1; ALT_INIT.
U36841; AAA79822.1; ALT_INIT.
AE000342; AAC75613.1; ALT_IN
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7; Conser
                                                                          and this statement is not removed requires a license agreement (Sec an email to license@isb-sib.ch).
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EIN IN PURL-DPJ INTERGENIC REGION
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BY SIMILARITY
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                                                                                                                                                                                                              Escherichia coli K-12.";
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No. 44;
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                                                                                           (See http://www.isb-sib.ch/announce/
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MEDLINE 95191401; PubMed 7533882;
Bronner D., Clarke B.R., Whitfield C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O-ANTIGEN EXPORT
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Q48475;
                                                                                                                                                                                                                                                           Pfam; PF01061; ABC2
PROSITE; PS00890; A
                                                                                                                                                                                                                                                                                                       EMBL; L31775; AAC98411.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the cytoplasmic membrane of Klebsiella Mol. Microbiol. 14:505-519(1994).
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8; Conser
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                                                                                                                                                                                                                            transport;
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of an ATP-binding cassette transport system required for translocation of lippopolysactheride O-antigen side-chains across the cytoplasmic membrane of Klebsiella pneumoniae serotype Ol.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOGENE: EG11371; yfhB.
HYDOLTheLical protein: Complete proteone.
SEQUENCE 211 AA: 24439 MH; 908E95FE54A3AA2D CRC64;
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35, Last sequence update)
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TRANSMEM 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oin H., Allen R., Knaff D.B.;
"Primary structure of genes encoding light-harvesting
center proteins from Chromatium vinosum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last annotation update)
REACTION CENTER PROTEIN L CHAIN (PHOTOSYNTHETIC
                                                                                                                                                                                                                                                                                                   EMBL; AB011811; BAA32740.1; -. EMBL; D50647; BAA09314.1; -. HSSP; P02954; 4RCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
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30-MAY-2000 (Rel.
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PROSITE; PS00244; REACTION_CENTER;
                                                                                                                                                                                                                                                                             Pfam; PF00124; photoRC;
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                                                                                                                                                                                                                                                                                        InterPro; IPR000484; Photo_RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO BACTERIOPHEOPHYTINS, TWO UBIQUIDONES, ONE ITON, AND TWO HIGHLY HUROPHOBIC POLYPEPTIDE CHAIMS (DESIGNATED L AND M). SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA PSBD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        s SWISS-PROT entry is copyright. It is produced through a comeon the Swiss institute of Bioinformatics and the BMBL Buropean Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS.
                                                                                                                                                                                                                                                                                                                                                     non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  PR00256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .E., Nagashima K.V., Matsuura K.,
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          IRON (NON HAEM) (BY SIMILARITY).

IRON (NON HAEM) (BY SIMILARITY).

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G -> V (IN REF. 2).

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E -> N (IN REF. 2).
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EVENT IN THE ELECTRON TRANS
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15-JUL-1998
15-JUL-1999
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PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; l.
PROSITE: PS00238; OPSIN; l.
PROSITE; PS00238; OPSIN; l.
PROSITE; PS00238; OPSIN; l.
PROCOFECEPCO; Retinal protein; Transmembrane; Glycoprotein; Vision:
                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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between the Swiss Institute of Bioinformatics and the BB
the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                  *Parapinopsin, a novel catfish opsin localized to the organ, defines a new gene family.*;
J. Neurosci. 17:803:8092(1997).
-1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING
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Siluriformes; Ictaluridae; Ictalurus.
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                                                                                                                                                                                                                                                             modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blackshaw S., Snyder S.H.;
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4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (
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InterPro; IPR001993; Mitoch_carrier
Pfam; PF00153; mito_carr; 3.
                                                                                                                                                                                                                                                                                                                                                          modified and this Statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A Kluyveromyces lactis gene homologue t
Saccaromyces cerevisiae opi mutation.",
Curr. Genet. 27:229-231(195)
-1- FUNCTION: CATALYZES THE EXCHANGE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-95254664; PubMed-7736606;
Viola A.M., Galeotti C.L., Goffrini P.,
                                             TRANSMEM
                                                                                                                                     TRANSMEM
                                                                                                                                                                                PRINTS; PR00927; ADPTRNSLCASE.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kluyveromyces lactis (Yeast).
Eukaryota; Fungi; Ascomycota;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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RETINAL CHROWOPHORE (BY SIMILARITY).
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PALMITATE (BY SIMILARITY).
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REPEAT: Transmemb:
1 (POTENTIAL).
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7 (POTENTIAL).
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cetaceae; Kluyveromyces
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Cobalamin
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                                                                                                                                                                                                                                                                                                                                                                                     of Salmonella typhimurium.";
J. Bacteriol. 175:3303-3316(1993).
-:- FUNCTION: INVOLVED IN THE CONVERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93273696; PubMed-8501034;
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TISSUE-Retina;
                                                                                                        Chelon labrosus (Thicklip grey mullet). Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sofia H.J., Burland V., Daniels D.L.,
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MEDLINE-94316500; PubMed-8041620;
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HYPOTHETICAL PROTEIN YHHT.
Archer S.N., Hirano J.; "Comparative analysis of opsins in Mediterranian coastal fish.";
                                                                        Chelon
                                                                                  Acanthomorpha; Acanthopterygii;
                                                                                           Actinopterygil; Neopterygil; Teleostel; Euteleostel; Neoteleostel;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00263; G_PROTEIN_RECEP_F1_2;
PROSITE: PS00238; OPSIN; 1.
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SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPSIN SUBFAMILY
MYVAFLYCWCPYAGVAW 273
                                   Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                     PR00237; GPCRRHODOPSN. PR00238; OPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                         IPR000276; GPCR_Rhodpsn
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134
153
177
203
277
285
310
                                   Conservative
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                                                                               A
                                                                                                                                                                                                                                                                        Lipoprotein; Palmitate; G-protein coupled receptor 36 EXTRACELLULAR.
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                                          46.08;
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                                Score 40; DB
Pred. No. 90;
2; Mismatches
                                                                                                                                                                      EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
                                                                                                                                                                                                          3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
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                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
RETINAL CHROMOPHORE (BY SIMILARITY)
                                                                                                                                            7 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                               EXTRACELLULAR
                                                                                                                                                                                                                                     EXTRACELLULAR
                                                                                                                                                                                                                                                      CYTOPLASMIC
                                                                                                 PALMITATE (BY SIMILARITY).
                                                                               SIMILARITY.
8C4B6F4847B3C632
                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                         Transmembrane;
                                         DB
90;
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                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                         Glycoprotein; Vision;
                                                  Length 353;
                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUPLED
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L outstation -
                                  Gaps
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Query Match
Best Local S
Matches
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SEQUENCE
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BINDING
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TRANSMEM
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Ekkaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Actinopterygii: Reopterygii: Teleostei: Euteleostei; Reoceleostei;
Acanthomorpha: Acanthopatrygii: Percomorpha: Perciformas: Percolodi;
Sparidae: __clognathus.
                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRO0238; OPSIN.
PRINTS: PRO0579; RIODDSIN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE: PS50023; G_PROTEIN_RECEP_F1_2;
PROSITE: PS500238; OPSIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to licensedisb-sib.ch).
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Submitted (JAM-1999) to the EMEL/CenBank/DDBJ databases
- I- FUNCTION: VISUAL PICHENTS ARE THE LIGHT ABSORBING MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE Retina;
Archer S.N., H
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PRINTS; PR00237; GPCRRHODOPSN.
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InterPro; IPR001760; Opsin.
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PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER
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SUBCELLULAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: ROD SHAPED
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SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
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                            Score 40;
Pred. No.
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3 (POTENTIAL)
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
RETINAL CHROMOPHORE (BY SIMILARITY)
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CYTOPLASMIC.
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EXTRACELLULAR
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BY SIMILARITY.
3BFB29AAD00EFF87
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                        90;
                                                                                                                                                                                                        SIMILARITY).
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                                                         Length 353;
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Gaps
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(POTENTIAL) (POTENTIAL)

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RESULT 35
OPSD_LIZAU
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CARBOHYD
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TRANSMEM
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DOMAIN
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PRINTS; PRO0579; RHODD/SIN.
PROSTIE; PRO00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PRS00237; G_PROTEIN_RECEP_F1_2;
PROSITE; PRS00238; OPSIN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Comparative analysis of opsins in Mediterranian coastal fish., submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through at between the Swiss Institute of Bioinformatics and the EMBA the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liza aurata (Golden grey mullet).
Eukeryota: Metazoa: Chordeta: Craniata: Vertebrata: Euteleostomi
Actinopterygii: Neopterygii: Teleostei: Euteleostei; Neoteleostei;
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InterPro; IPR001760; Opsin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
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20-AUG-2001
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VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE PHOSPHORYLATED
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Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHAPED PHOTORECEPTOR
CYTOPLASMIC.
N-LINKED (GI
N-LINKED (GI
                                                                                                   5 (POTENTIAL)
CYTOPLASMIC.
6 (POTENTIAL)
                                                                                                                                                                                                                                               CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
                                                                 EXTRACELLULAR
7 (POTENTIAL)
                                                                                                                                                                     EXTRACELLULAR
                                                                                                                                                                                                          3 (POTENTIAL)
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                     Palmitate; G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                 (POTENTIAL).
                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELLS WHICH MEDIATES
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Best Local
Phosphorylation;
DOMAIN 1
TRANSMEM 37
DOMAIN 62
TRANSMEM 74
DOMAIN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPSD_SOLSO
Q9YGZ5;
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOLSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archer S.N., Hirano J.;

"Comparative enalysis of opsins in mediterranian coastal fish.";

Submitted (JAN-199) to the EMHL/Genhank/DDJ databases.

1- PUNCTION: VISUAL PICHENTS ARE THE LIGHT-ARSOBBING MOLECULES THAT

1- EMEDIATE VISION. THEY CONSIST OF AN APOPROTEIN. OPSIN, COVALENTLY

LINKED TO CLIS-RETINAL.

1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1- TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES

VISION IN DIM LIGHT.

1- PIM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SMISS-PROT entry is copyright. It is produced through a collaboratin between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on i
                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this steenant is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleost
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Solea solea (Common sole).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BINDING
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                                                                                                                                                                                                                                   Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; Y18672; CAA77254.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soleoidei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-AUG-2001
20-AUG-2001
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                                                                                                                                        Photoreceptor; Retinal
                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR001760; Opsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 MLVVFLLLW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE PHOSPHORYLATED.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MVVAFLVCWCPYAGVAW 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
8; Conser
                                                                                                                                                               PS00237; G_PROTEIN_RECEP_F1_1; PS50262; G_PROTEIN_RECEP_F1_2; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
296
322
110
353 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soleidae;
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-GVTW 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
39530
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296
322
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47.1%;
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                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
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Pred. No.
EXTRACELLULAR.

1 (POTENTIAL).

CYTOPLASMIC.

2 (POTENTIAL).

EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PALMITATE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
RETINAL CHROMOPHORE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata;
                                                                                                                    Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D07AC0DC0B55EF9F
                                                                    (POTENTIAL).
                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
                                                                                                              G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                     Glycoprotein; Vision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
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                                                                                                                 coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neoteleostei;
                                                                                                                 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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RESULT 37
OPSU_BRARE
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Best Local
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DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994
01-JUN-1994
20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPSU_BR
P35359;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota: Metazoa: Chordata; Cranitata; Vertebrata; Euteleostomi:
Actinopterygli; Neoterygli; Teleostei; Euteleostei; Ostariophysi;
Gypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last annotation update) ULTRAVIOLET-SENSITIVE OPSIN (ULTRAVIOLET CONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
             This
                                                                                                                                                                             "Temporal and spatial patterns of (panio rerio)."; Vis. Neurosci. 12:895-906(1995).
                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                   MEDLINE=93317613; PubMed=8327475; Robinson J., Schmitt E.A., Harosi F.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZFO2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                     MEDLINE=96244282; PubMed=8924413;
Robinson J., Schmitt E.A., Dowling J.E.;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                      "Zebrafish ultraviolet visual pigment:
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZFO2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                             MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPS LINKED TO CIS-RETINAL. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. TISSUE SPECIFICITY: THE COLOR PICALEUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MLVVFLLLW----GVTW 15
                                                     BE PHOSPHORYLATED (BY SIMILARITY)
MISCELLANEOUS: THIS OPSIN HAS AN
SIMILARITY: BELONGS TO FAMILY 1 O
                                                                                                                                                                                                                                                                                                          localization."
                                            OPSIN SUBFAMILY
                                                                                                PHOTORECEPTOR CELLS.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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7; Conser
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1 (Rel. 29,
1 (Rel. 40,
                                                                                                                                                                                                                                                                                             Acad. Sci. U.S.A. 90:6009-6012(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114
134
153
177
203
231
253
277
285
310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
200
200
296
322
187
187
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152
176
202
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353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
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N-LINED (GLCNAC. .) (POTE
N-LINED (GLCNAC. .) (POTE
RETINAL CHROMOPHORE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY (BY SIMILARITY)
W: B25570A75EBB20FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR.
7 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
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CYTOPLASMIC.
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                                                       AN ABSORPTION
1 OF G-PROTEIN
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                                                                                                                                                                   APOPROTEIN, OPSIN,
                                                                                                                                                                                                                                                                                                                        absorption spectrum,
                                                       G-PROTEIN
                                                                                                                                                                                                                       gene
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RESULT 38
GUDX_ECOLI
ID GUDX_ECOLI
AC Q46915;
DT 01-NOV-1997
DT 01-NOV-1997
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Best Local S
Matches 7
Gregor
    STRAILW-KIZ / GG655;
STRAILW-KIZ / GG655;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhow G.F.,
Riley M., Collado-Vides J., Glasner J.D., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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                                                                                              SEQUENCE FROM N.
                                                                                                                                             Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                           GUDX OR B2788.
Escherichia coli
                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, GLUCARATE DEHYDRATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000276; GPCR_Rhodpsn
InterPro; IPR001760; Opsin.
Pfam: PP00001; 7tm_1; 1
PRINTS; PR00238; OPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCRDb; GCR_0754; -.
ZFIN; ZDB~GENE-990415-271;
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EMBL; AF105152; AAD14679.1;
                                                                                                                           NCBI_TaxID 562;
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                                                                                                                                                                                                                                                                                                                                                                     257
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7 (Rel.
1 (Rel.
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Last annotation updat
RELATED PROTEIN (EC 4
                                                                                                                                                                                                                                                      Created)
                                                                                                                                                          gamma
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EXTRACELLULAR
5 (POTENTIAL)
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CYTOPLASMIC.
BY SIMILARITY.
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CYTOPLASMIC.
6 (POTENTIAL).
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2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
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N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
295DB19B3C0CB0F0 CRC64;
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                                                                                                                                                                                                                                                                                        PRT:
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                                                                                                                                                          subdivision; Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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(EC 4.2.1.-) (GDH-RP) (GLUCDRP).
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RESULT 39
GUDH_PSEPU
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Best Local :
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                                          Biochemistry 37:14358-14368(1998).

-i- FUNCTION: CATALYZES THE DEMYDRATION OF GLUCARATE TO DEDXY-D-GLUCARATE F. KDGLUC).

-i- CATALYTIC ACTIVITY: D-GLUCARATE - 5-DEHYDRO-4-DEOXY-
                                                                                                                                                        Gulick A.M., Pelmer D.R., Babbitt P.C., Gerlt J.A., Rayment I.;
"Royalution of enzymatic activities in the enclase superfamily;
crystal structure of (D) glucarate delydratase from Pseudomonas
                                                                                                                                                                                                                                                                                                   "Nucleotide sequence of genes for glucarate dehydratase and 5-keto-4-deoxyglucarate dehydratase from Pseudomonas putida Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32,
01-NOV-1995 (Rel. 32,
20-AUG-2001 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000362; AAC75830.1; -
ECOGENE; EGI1186; gudX.
InterPro; IPR001354; MR.MLE.
Pfam: PF00188; MR.MLE. 1
PROSITE: P500908; MR_MLE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-98447506; PubMed-9772161;
                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-PP3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GUDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science
- I - PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                Burlingame R.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID~303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: DOES NOT SEEM TO HAVE AN IN-VIVO ACTIVITY ON G PUNCTION: ITS REAL SUBSTRATE IS UNKNOWN.
SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCONATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
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5; Conser
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FIRST STEP IN
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                                                                                                                                                                                                                                                                                                                                                                          K.C.;
                                                                                                                                                                                                                                                                                                                                                                                                Lauer G.D., Platz J.G.,
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83.3%;
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Last sequence update)
Last annotation update)
(EC 4.2.1.40) (GDH) (GLUCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Pseudomonadaceae;
GLUCARATE
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Pred. No. 1
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CATABOLISM
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                                             5-DEHYDRO-4-DEOXY-D-GLUCARATE +
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SUBUNIT: HOMOTETRAMER.
SIMILARITY: BELONGS TO THE MANDELATE RACEMASE LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.

MUCONATE

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20-AUG-2001
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                                                                                                                       Lyase; Co
SEQUENCE
                                                                                                                                               EMBL; D30808; BAA06470.1;
EMBL; Z99105; CAB12043.1;
Subtilist; BG11161; gudD.
                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95219079; PubMed-7704254;
Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
"Determination of a 21548 bp nucleotide sequence around the degrees region of the Bacillus subtilis chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GUDH_BACSU
P42238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M69160; AAA25868.1; -. PDB; 180G; 18-MAY-99.
                                                                                                                                                                                                                                                                                                                                                                                                    MICROBIOLOGY 141:269-275(1995).
-!- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GUDD
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                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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342
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CATALYTIC ACTIVITY: D-GLUCARATE = 5-DEHYDRO-4-DEOXY-D-GLUCARATE
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WGLTWG
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhow G.F.,
Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rôse D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujita N., Mori H., Yura T., Ishihama A.;
"Systematic sequencing of the Escherichia coll genome: analysis of
the 2.4-4.1 min (110,917-93.643 bp) region.";
Nucleic Acids Res. 22:1637-1639(1994).
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01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last anotation update)
FERRICHROME TRANSPORT SYSTEM PERMEASE PROTEIN
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Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O
Laashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
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MEDLINE=97426617; PubMed=9278503;
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Koester W., Braun V.;
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SIMILARITY: MITH INTEGRAL MEMBRANE COMPONENTS OF OTHER BINDING-
PROTEIN-DEPENDENT TRANSPORT SYSTEMS. BELONGS TO THE FECCD
                                                                                                                                                                                                                                                                                                                                                                     . Gen. Genet. 209:49-55(1987). FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN THE HIGH-
                                                                                                                                                                                                   SUBFAMILY.
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Pfam; PF01032; FecCD_family; 2.
ProDom; PD001557; FecCD; 2.
                                                 "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.".
Nature 407:81-86(2000).
                                                                        MEDLINE-20445173; PubMed-10993077; Shigenobu S., Watanabe H., Hattori
                                                                                         SEQUENCE FROM N.A. STRAIN-TOKYO 1998;
                                                                                                                         symbiotic bacterium).
Bacteria; Proteobacteria; gamma
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0927N9; 093019;
20-XNG-2001 (Rel. 40, Created)
20-XNG-2001 (Rel. 40, Last sequence
20-XNG-2001 (Rel. 40, Last sequence
20-XNG-2001 (Rel. 40, Last sequence)
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        Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F.
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comporison of whole genome sequences of Chlamydia pneumo
                                                                                                              "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                       Gwinn M., Nelson W.,
Eisen J., Fraser C.M
                                                                                                                                                 Read T.D., Brunham R.C., Shen C., Gill S.R., Heldelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weldman J., Khouri H., Craven B., Dowman C.,
Ginn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
                                                                                                                                                                                                                     STRAIN-AR39
                                                                                                                                                                                                                                                       Kalman S., Witchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grim-ood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-CWL029;
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                                                                                                                                                                                                       MEDLINE 20150255; PubMed 10684935;
                                                MEDLINE - 20330349;
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                                                                          SEQUENCE FROM N.A.
                                                                                                   Nucleic Acids Res.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Transport; Sugar transp
                                                                                                     Chlamydia trachomatis.";
Science 282:754-759(1998)
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Bacteria: Chlamydiales: Chlamydiaceae: Chlamydia
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-i- FUNCTION: TRANSPORT PROTEIN FOR SUGAR PHOSPHATE UPTAKE
                                                                                                                                                Davis R.W.;
                                                                                                                                                          Stephens R.S., Kalman s
Mitchell W.P., Olinger
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL SIMILARITY: BELONGS TO THE SLC37A FAMILY OF TRANSPORTERS.
                                               SIMILARITY: BELONGS
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SUBCELLULAR LOCATION:
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                                                                                                   Mike Y., Pujita Y.;
Sequencing of a 65 kb region of the Bacillus subtilis genome containing the lic and cel loci, and creation of a 177 kb contig covering the gnt-sacXY region.",
Microbiology 12:3113-2134(196).

11- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                           Schroegel O., Krispin O., Allmansberger R.;
"Expression of a pepT homologue from Bacillus subtilis.";
FEMS Microbiol. Lett. 145:341-348(1996).
                                                                                                                                                                                                                                                                                                                                                            Bacillus/Staphylococcus
NCBI_TaxID=1423;
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OSMWNZ:
01-MAY-2000 (TrEMBLrel. 13, Created)
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MEDLINE:20036896; PubMed:10567266; White O., Elson J.A., Heidelberg J.F., Hickey E.K., Motoson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Rimotfat K.S., Qin H., Jiang L., Pamphile W., Crosby
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
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MEDLINE-99287316; PubMed-10360571;

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dedson R.J.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotten M.D., Pratt M.S., Phillips C.A., Richardson D.,

Meidelberg J., Sulton G.G., Fleischmann R.D., Elsen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C. Frence C.M., White O.,

Evidence for lateral gene transfer between Archaea and Bacteria from

genome sequence of Thermotopa maritima.";

Mature 359:123-339(1991).
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09WY46: PRELIMINARY: PRT: 243 AA.
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Science 286:1571-1577(1999).
SMLL; AEGO1921: AAF10217.1; -
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TICR: DR0634; -
Hypothetical protein; Complete proteome.
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Makarova K.S., Aravind L., Daly M.J., Minton K.W.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O.,
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BMBL, AJ131925; CAM10529.1; oytc_asm.
InterPro. IPR003537. cytc_asm.
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EMBL, A1163672; CAB8734.1; -
SEQUENCE 443 AA; 47464 MW; 1CEA47D3C453D4FC CF
                                                                                                                                                         STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
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Bacteria; Firmicutes; Actinobacteria;
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                    MEDILINE-20637337, PubMed-10984043;

Stover C.K., Pham X.O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Minagle M.O., Kowalik D.J., Lagrou M. Garber M.L., Goltry L., Tolentino E., Mesbrock Hodman S., Yuan Y., Brody L.L., Coulter S.N., Fölger K.R., Kas A., Larbiy K., Lim R.M., Santh K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen IT.T., R.M., Relzer J., Salar M.H., Bancock R.E., Lovy S., Olson M.V., Romphete Jenome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogan.
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KUTOGA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayash
Cul L., Oguchi A., Aoki K.I., Nagal Y., Lian J., Ito T., Kanal
Marisumaru H., Maruyama A., Murakami H., Hosoyama A., Mizukani
Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
Yamashita N., Oshima K., Euruya K., Yoshino C., Shiba T., Hat
Ogasawara N., Haysshi H., Hiramatsu K.,
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NCBI_TaxID=158879;
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Bacteria; Firmicutes; Bacillus/Clostridium gro
Bacillus/Staphylococcus group; Staphylococcus
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Yoneyama H., Nakae T.;
"Protein C (oprC) of the outer membrane copper regulated channel protein.";
Microbiology 142:2137-2144(1996).
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EMBL; AP003136; BAB43262.1;
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17,
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Last annotation update
C.
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Last annotation updat
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Pred. No. 1
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RESULT
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Best Local
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Submitted (JAM-1996) to the EMBL/GenBank/
EMBL: U6988 (AM50279.1]:
InterPro: IPRO01332: Arteri_91yoop.
InterPro: IPRO01341: Equine_Virus_ORF5.
Pfam; PF00951; Arteri_91yoop: 1.
PF00Dm; PD002371; Equine_Virus_ORF5; 1.
PS0UENCE 255 AA; 28709 MM; 13129B6A9/
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Best Local
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Submitteed (JAN-1996) to the EMBL/GenBank,
EMBL, UKG999, ABESG001;
ThesePro (IPRO01312; Bruteri_g)ycop
ThesePro (IPRO01312; Bruteri_g)ycop
ThesePro (IPRO01312; Bruteri_g)ycop
ThesePro (IPRO01312; Bruteri_g)ycop
Promom; PRO002371; Bruteri_g)ycop
Promom; PRO002371; Bruterytrus_DRFS; 1
SEQUENCE 255 AA; 2662 MH; 8DBA5667A;
                                                                                                                                                                                                                                                                                                                          P97640 PRELIMINARY;
P97640;
01 MAY-1997 (TERMILEEL 03. Lac
01 MAY-1997 (TERMILEEL 17. Lac
01 JUN-2001 (TERMILEEL 17. Lac
STRAIN 19933 (MFS.
Equine afteritis virus (EAV);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P87639 PRELIMINARY;
P87639; O1-MAY-1997 (TrEMBLrcl. C
O1-MAY-1997 (TrEMBLrcl. C
O1-UN-2001 (TrEMBLrcl. C
STRAIN 11958 ORFS.
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                                                                                                                                                                                              STRAIN-19933;
                                                                                                                                                                                                                                                                                 Viruses: ssRNA positive-strand viruses, Arteriviridae; Arterivirus.
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Viruscs; ssRNA positive-strand viruses,
Arteriviridae; Arterivirus
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                                                                                                                                                                     Archambault D., St-Laurent G.,
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           NCBI_TaxID-11047;
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8; Conser
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8; Conserv
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Pred. No. 29;
3; Mismatches
                                                                                                                                               EMBL/GenBank/DDBJ
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Pred. No.
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         8DBA5667A1DA3C08 CRC64;
                                                                                                                                                                     Lepage
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Matches
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01-MAY-1999
01-MAY-1999
01-JUN-2001
                J. Virol. 0:0-0(1996).
BMBL: U81027; AADD0496.1;
InterPro: IPR001322; ArterL_glycop.
InterPro: IPR003241; Equine_virus_ORF5.
                                                                                                                 "Sequence Analysis and Phylogenetic Characterization of Two Strains of Equina Arteritis Virus Isolated from Persistently Infected Stallions on the Same Ranch in California.";
                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TREMBLEE). 10. Last sequence u 01-JUN-2001 (TREMBLEE). 17. Last annotation CA95GS ORFS 5. 6 AND 7 GENES, COMPLETE CDS. Equine arteritis virus (EAV). Viruses; seakh postitue-strand viruses, no Arteriviridae; Arterivirus.
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ProDom; PD002371; Equine_virus_ORF5; 1
SEQUENCE 255 AA; 28695 MW; 099008C;
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*Sequence Analysis and phylospenetic Characterization of Two Strains of Equinc Arteritis Virus [solated from Persistently Infected Stallions on the Same Ranch in California.";

on the Same Ranch in California.";

J. VICO. 0.0(1996).

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Ol-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation update)
STRAIN CA95C ORF5, ORF56 AND ORF57 GENES, COMFLETE CDS.
Equine arteritis virus (EAY).
Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Arteriviridae; Arterivirus.
                                                                                                                                                                                    Balasuriya U.B.R., Hedges J.F., Patton J.F., Ti
McCollum W.H., Hullinger P.J., Maclachlan N.J.;
                                                                                                                                                                                                                                          STRAIN CA95GS;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Q9QKG5;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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Q9QKG7;
01-MAY-2000
01-MAY-2000
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Vertical Transmission (in an Outbreak of Equine Viral Av
J Gen. Virol. 800:1949-1958(1999).
EMBL. AR18072: AMD54698.11
InterPro. 1FR001313: Arteri_glycop.
InterPro. 1FR001314: Equine_Virus_ORP5.
ProDom: PP000521A. Terulay/Yoop: 1.
ProDom: PP000521A. Equine_Virus_ORP5: 1.
SEQUENCE 255 AA; 2910 NH; AMD$FDBFD00D685B CRC64:
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SEQUENCE 255 AA; 28661 MW; 0EB8D43
MEDLINE-99394666; PubMed-10466790;
Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum W.H.,
Timomey P.J., MacLachian N.J.;
"Genetic Stability of Equine Arteritis Virus during Horizontal and
Vertical Transmission in an outbreak of Equine Viral Arteritis.";
J. Gen. Virol. 80:1949-1958(1999),
EMBL; AF18774; ADDS4710.1; "-
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(TrembLrel. 17, Last annu
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01-MAY-2000
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NCBI_TaxID=11047;
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InterPro; IPR001341; Equine_virus_ORE5.
Pram; PP00951; Arter1_d|ycop; 1
Probom; PD002371: Equine_virus_ORE5; 1.
SEQUENCE 255 AA; 28730 MM; D0EBB7|CD605C66B CRC64;
MEDLINE-99394666: PubMed=10466790;
Balasuriya U.B.R., Hedges J.F., Na
Timoney P.J., WacLachlan N.J.;
"Genetic Stability of Equine Arter
                                                                                                                                                   Arteriviridae; Arterivirus.
NCBI_TaxID=11047;
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Arteriviridae; Arterivirus.
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Balasuriya U.B.R., Hedges J.F., Nadler S.A., McCollum
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                                                                                                                                                                                                                                                            (TrEMBLrel.) (TrEMBLrel.
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                                                                                                            N.A
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                                          Hedges J.F., Nadler S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
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Last annotation updat
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                                                                                                                                                                                                                                                               Last
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Pred. No.
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      Arteritis Virus
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                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                viruses,
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Matches
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOWNSHIP TO THE MECLACITIEN N.J.;

*Genetic Stability of Equine Atteritis Virus during Horizontal and Vertical Transmission in an outbreak of Equine Viral Arteritis.*;

J. Gen. Virol. 80:1149-1158(1999).

EMBL. AFI18759. AAD34680.1;

EMBL. AFI18770. AAD34680.1;

EMBL. AFI18770. AAD34680.1;

EMBL. AFI18770. AAD34680.1;

EMBL. AFI1870. AA
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Q9PWZ4;
Q1-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                 Q9PWV4;
Q9PWV4;
01~MAY~2000
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J. Gen. Virol. 80.1949-1958(1999).

EMBL; AF118776; AAD54722.1.

Interfro: IPR001332; Arteri_glycop.

Interfro: IPR001341; Equine_Virus_ORP5.

Pfdam; PF00951; Arteri_glycop: 1.

Probom: PF00951; Arteri_glycop: 1.

Probom: PF00951; Arteri_glycop: 1.

Probom: PF00951; Arteri_glycop: 1.

PRODOM: PF009371; Equine_Virus_ORP5.
                                                                          Viruses; ssRNA positive-strand viruses, Artoriviridae; Artorivirus. ACBI_TaxID~11047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3, A1, AND A2;
MEDLINE-99394666; PubMed-10466790;
Balasuriya U.B.R., Hedges J.F., NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Equine arteritis virus (EAV). Viruses; ssRNA positive-strand viruses, Arteriviridae; Arterivirus.
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     SEQUENCE FROM N.A
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hes 8; Conserv
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                                                                                                                                                                                                                                                                                         (TremBirel. 13, Created)
(TremBirel. 13, Last seq
(TremBirel. 17, Last ann
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(TrembLrel. 13, Last sequence update)
(TrembLrel. 17, Last annotation updat
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Last annotation updat
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Pred. No. 29;
3; Mismatches
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                                                                                                                                                                DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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X MEDITRE-9939466; PobMedi-10466790;
A Ballssurlya U.B.R., Hedges J.F., Modler S.A., McCollum W.H.,
A Timoney P.J., McCachlan N.J.;
A Timoney F.J., McCachlan N.J.;
A Cen. Virol. 80:1949-1958(1999).
B Cen. Virol. 80:1949-1958(1999).
B EMBL; AFI18781; ANDS4704.1;
B EMBL; AFI18781; ANDS4704.1;
B F.J., McCachlan N.J.;
B F.J., McCachlan N.J., McCachlan N.J., McCachlan N.J., McCachlan N.J., McCachlan N.J., McCachlan N.J., Mc
                         Query Match
Best Local
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Best Local Similarity
Matches 8; Conser
   Matches
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Q66483;
                                                                                                                                                                                                                                                              Balasuriya U B R., Hedges J.F., Patton J.F., Thmoney P.J., McCollum H.H., Hullinger P.J., MacLachlan N.J.:
McCollum H.H., Hullinger P.J., MacLachlan N.J.:
Sequence Analysis and Phylogenetic Characterization of Two Strains of Equine Arteritis Virus isolated from Persistently Infected Stallions on the Same Ranch in California.";
J. Virol. 0.0 0(1996).
EMBL: UBS04. AAA928991;
EMBL: UBS04. AAA928991;
EMBL: UBS04. AAA928991;
EMBL: UBS04. AAA928901;
EMBL: UBS04. AAA928901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-RAY CANES (FIELD ISOLATE);
MEDLINE-9613015; Pubmed-8535754
Balasuriya U.B., Timoney P.J., McCollum H.H., Maclachlan N.J.;
"Phylogenetic analysis of open reading frame 5 of field isolates
equine arteritis virus and identification of conserved and
monconserved regions in the GL envelope glycoprotein.";
virology 214:990-697(1955).
                                                                                                                                InterPro: JPR001332; Arteri_qlycop.
InterPro: JPR003241; Equine_Virus_ORF5
Pr0am; PF00951; Arteri_qlycop; 1.
Pr0bom: PD002371; Equine_virus_ORF5; 1.
SEQUENCE 255 Aa; 28668 Mm; 800685A
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Viruses; ssRNA positive-strand viruses,
Arteriviridae; Arterivirus.
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EAV CAN86 ORP5 (FIELD STRAIN
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Q995W1;
01-JUN-2001
Q995V9 PRELIMINARY;
Q995V9;
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                      Larsen L.E., Storgeard T., Holm E.;

"Phylogenic characterization of the GL protein of equine arteritis virus isolated from semen of asymptotic stallions and fatal cases equine viral arteritis.";

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL: AF247548; AKX37631.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL. AF247547, ARAT91500,1; SEDUFUNCE 255 AA; 28760 MW; 55DE905C49960EE4 CRC64;
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"Phylogenic characterization of the GL protein of
virus isolated from semen of asymptotic stallions
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Viruses; ssRNA positive-strand viruses,
Arteriviridae; Arterivirus.
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Equine arteritis virus (EAV)
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and fatal cases (
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O9HXB6.

O1-MAR-2001 (TreMBLrel. 16, Cr
O1-MAR-2001 (TreMBLrel. 17, Lr
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Q98VL6;
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"Phylogonic characterization of the GL protein of equine arteritis virus isolated from semen of asymptotic stallions and fatal cases coquino virul arteritis.",

submitted (MAR-2000) to the BMBL/GenBank/DDBJ databases.

EMBL. ARS47541. ARS47624.11.

EMBL. ARS47541. ARS47624.1.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ data EMBL; AF247549; AAK37632.1; -.
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Viruses; ssRNA positive-strand viruses,
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"Phylogenic characterization of the GL protein
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gamma subdivision; Pseudomonadaceae;

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RESULT RESULT REPORTED RESULT 
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Best Local Similarity
Matches 6; Conserv
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Nature 406;959:944(2001).
EMBL, AED04807, AACD7284 1;
InterPro. TPR000620; DUF6.
Pfam; PF00892; DUF6. 2
Pfam; PF00892; DUF6. 2
SEQUENCE 300 AA: 32291 MN; 3
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O9PGL7;
O1-OCT-2000 (Trembl
O1-OCT-2000 (Trembl
O1-JUN-2001 (Trembl
TRANSPORT PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20437337; PubMed-10984043;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 w
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Last annotation update)
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Pred. No. 33;
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390033DEC9185B1C CRC64;
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Best Local
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                                                                                                                                            Q914F8
Q914F8;
Q91-MAR-2001
01-MAR-2001
01-JUN-2001
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018736;
01-JAN-1998
01-JAN-1998
01-JUN-2001
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warn Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowallk D.J., Gairber R.L., Golfry L., Tolentino E., Westbrock Wadman S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2001 (TrEMBLrel. 17, UDP-GLUCURONOSYLTRANSFERASE.
                                 MEDLINE 20437337; PubMed 10984043;
                                                                                                                                     01-MAR-2001 (Tremblrel. 16, 01-MAR-2001 (Tremblrel. 16, 01-JUN-2001 (Tremblrel. 17, TWO-COMPONENT SENSOR PHOQ.
                                                                                                                                                                                                                                                                                                                                                 Transferase.
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-1997) to the EMBL; AB008677; BAA23359.1; InterPro; IPR002213; UDPGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 389 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zago M.A., Zatz M., Meddanis J., Setubal J.C.
"The genome sequence of the plant pathogen Xy
Mature 406:151-159(2000).
EMBL. AE003081; -.
InterPro., PR002549; UPP0118.
                                               STRAIN PAOL
                                                                                                                 Pseudomonas
                                                                                                                            PHOQ OR PA1180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Cetarliodactyla;
                                                        SEQUENCE FROM N.A.
                                                                               NCBI_TaxID~287;
                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00375; UDPGT; 1.
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Yokota H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9913;
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                                                                                                                                                                                                                                                  VSVAVFFLALMGFTLG
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9; Conserv
                                                                                                                                                                                                                                                                                            Similarity
9; Conser
                                                                                                                 aeruginosa
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                                                                                                   gamma subdivision; Pseudomonadaceae;
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                                                                                                                                                                      Created)
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pred. No. 73;
2; Mismatches
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Pred.
                                                                                                                                                                                             PRT;
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No. 41;
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RESULT
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Matches 6
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Best Local
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Pfam, PP00727; DUF5;
Pfam, PP007218; HATPASS—C: 1.
Pfam, PP00512; Signal;
Pfam; PF00512; Signal;
Pfam; PF00514; ECTRUSENSOR.
SMATT; SM00387; HATPASS—C: 1.
SMATT; SM00388; HISKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Q39398;
Q39398;
Q1-NOV-1996
Q1-JAN-1998
      P95489;
P95489;
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR000658; DUF5.
InterPro; IPR003594; HATPase_c.
                                                                                                                                                                                                 Ozone-induced defense reactions in EMBL; x97994; CAA66633.1; NON_TER 1 1
                                                                                                                                                                                                                                                                                                   Betula verrucosa (Mhite birch) (Betula pendula).
Eukaryota; Virdidplantes; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fagales; Betulaceae; Betula.
MCBL_TaxID-3505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen."
Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                 Kiiskinen M.;
                                                                                                                                                                                                                                                                     STRAIN-KL-5-M;
                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE HOMOLOGUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome; Kinase; Phosphorylation; Sensory transduction
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                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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9; Conserv
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    Q66481;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                         Archambault D., St.Laurent G., Lepage N.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
EMBL: U46952: AAB50283.l.;
InterFro: IPR001332; Arteri_glycop.
InterFro: IPR001341; Equine_virus_ORF5.
PFdam; PF00951: Arteri_glycop; 1.
PFdam; PF00951: Arteri_glycop; 1.
SEQUENCE 255 AA; 28635 MN; 563D3ADBJ77035D5 CRC64;
                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand
Arteriviridae; Arterivirus.
NCBI_TaxID=11047;
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01-MAY-1997 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                               P87643;
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PRINTS; PR01386; CCMCBIOGNSIS
NON_TER 177 177
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Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases EMBL, U85716, AACG5583.1;
InterPro: IPRO03541: Cytc_sam.
InterPro: IPRO03577; Cytc_blog_CcmC.
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                                                  Q66481
                                                                                                                                                                                                                                                                                          STRAIN-VIENNA;
Archambault D.,
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Equine arteritis virus (EAV)
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Pred. No. 54;
3; Mismatches
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Q66495;
Q1-NOV-1996
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Virology 214:690-697(1995),
EMGL: U38592: AAA93887.1:
InterPro: IPRO01332: Arter1_glycop.
InterPro: IPRO01341: Equine_virus_ORP5.
Pfam: PP00931: Equine_virus_ORP5.
PFam: PP00931: Equine_virus_ORP5.
Probom: PP00931: Equine_virus_ORP5.
Probom: PP00931: Equine_virus_ORP5.
PRODOM: P000371: Equine_virus_ORP5.
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MEDLINE-963 2016; Pulmed-9553578 Balasuriya U.B., Timoney P.J., McCollum W.H., Maclachlan N.J.;
Phylogenetic analysis of open reading frame 5 of field isolates of equine arteritis virus and identification of conserved and
Q66482; Q9YV80;
                                                                                                                                                                                                                                                                                           STRAIN:PAY SM264 (FIELD ISOLATES);
MEDLINE:96130216; Pubmed-0555758;
Balssurlya U.B., Timoney P.J., McCollum W.H., Machachian N.J.;
"Phylogenetic anallysis of open reading frame 5 of field isolates
equine arteritis virus and identification of conserved and
                                                                                                                                                                                          Pfam; PF00951; Arter1_glycop; 1.
ProDom: PD002371; Equine_virus_ORF5;
SEQUENCE 255 AA; 28649 MW; DEC277
                                                                                                                                                                                                                             nonconserved regions in the GL envelope glycoprotein.
Virology 21:690-697(195).
RMBL. U38609: AAA92014.1:
InterPro; IPR0031312. Arteri_glycop.
InterPro; IPR003211; Equino_virus_ORP5.
                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.
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EAV SWZ64 O
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SWZ64 ORF5.
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Pred. No.
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              PRT:
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Balasuriya U.B., Evermann J.F., Hedges J.F., McKeirnan A.J.,
Mitten J.Q., Beyer J.C., McCollum W.H., Timoney P.J., Maclachlan N.
'Serologic and molecular characterization of an abortigenic strain
equine arteritis virus isolated from infective frozen semen and an
aborted equine fectus.";
J. Ample Assoc. 213:1586-1589(1998).
EMBL: U38593; AAA92898.1.
                                                                                                                             White O., Elsen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffet K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Wanathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., McKarova K.S., Aravind L., Daly M.J., Mitton K.W., Pleischmann R.D., McKarova K.S., Aravind L., Daly M.J., Mitton K.W., Pleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Deinococcus radiodurans.
Bacteria: Thermus/Deinococcus
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STRAIN-EAV AZ87 (FIELD ISOLATE);
MEDLIME-96130216; PubMed-8553578;
Balasuriya U.B., Timoney P.J., McCollum W.H..
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Arteriviridae, Arterivirus.
NCBL_Tax1D·11047;
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EAV AZ87 ORF5
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ProDom; PD002371; Equine_virus_ORF5; 1.
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Virology 214:690-697(1995).
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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InterPro: IPR003241; Equine_virus_ORF5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01,
01,
17,
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5 of field isolates
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radiodurans R1."; Science 286:1571-1577(1999).

AE001882; AAF09788.1; -

"Genome sequence of the radioresistant radiodurans R1.":

bacterium Deinococcus

Fraser C.M.;

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062194
ID 0
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Best Local S
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Best Local
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                     01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                          062194;
01-AUG-1998
                                                                                                                                                                                                                                                             Kinashi H., Hopwood D.A.;

*A set of ordered cosmaids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.*;

Mol. Microbiol. 21:77-96(1996).

EMBL, A1045841: Ch847747.1;

EMBL, A1045841: Ch847747.1;
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01-NOV-1999 (TIEMBLIE1. 12, Last Sequence update)
01-NOV-1999 (TIEMBLIE1. 12, Last annotation update)
HYPOTHETICAL 47.7 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9XBH4;
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9X8H4
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F31C3.6 PROTEIN F31C3.6.
                                                                 062194
                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                   James K.D., Parkhill J.,
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                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                              A set of ordered cosmids and a detailed genetic and physical map
the 8 Mb Streptomyces coelicolor A3(2) oltromosome ";
submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oliver K., Harris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Streptomycineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.
                                                                                                                                                                                                                                                    Hypothetical protein
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                                                                                                                      179 VLAVSLLLTGATWG
                                                                                                                                                               Local Similarity
les 9; Conserv
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                                                                                                                                           3 MLVVFLLLWGVTWG
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8; Conser
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                                                                 PRELIMINARY;
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the EMBL/GenBank/DDBJ databases
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                                                                 PRT;
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                     Last sequence update)
Last annotation update)
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Pred. No.
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RESULT
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Best Local Similarity
Thehes 5; Conserv
Simpson A.J.C., Williams P., Abreu F.A., Accentio M.,
RA Alvarenga R., Alves L.M.C., Aryal J.E., Bala G.S., Baptissa C.S.,
RA Barros M.H., Bonaccosi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccosi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccosi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Benno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Coultnin L.L., Cristofani M., Dias-Nato E. Docena C.R., Costa Meco C.M.,
RA Fraga J.S., Franco S.C., Franco M.C., Frohme M., Furian L.R.,
RA Fraga J.S., Franco S.C., Franco M.C., Frohme M., Furian L.R.,
RA Krieger J.E., Kurame E.E., Ladgret F., Lambais M.R., Leite L.C.C.,
RA Krieger J.E., Kurame E.E., Ladgret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Hemos M.V.F., Loppes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B., Madeira H.M.F., Mathain A.Y.,
RA Marques M.Y., Martins E.A.L., Martins E.M.F., Mathain A.Y.,
RA Marques M.Y., Magai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Mani A. Jr., Nobega F.G., Nunes L.R., Oliveira M.A.,
RA Marques M.Y., Ge Oliveira R.C., Palmeiri D.A., Paris A.,
RA Mani A. Jr., Nobega F.G., Nunes L.R., Oliveira M.A.,
RA Mani A. Jr., Nobega F.G., Nunes L.R., Slive M.A. Jr.,
RA de Souza A.P., Terenzi M.A., Verjovski H.R.Y., Sansaki H.E.,
RA de Silva A.C., da Silva A.M., da Silva R.M., Jeb Souza A.N.,
RA de Souza A.P., Terenzi M.F., Truffi D., Taai S.M., Tshako M.H.,
RA Wallada H., Van Silva M.A., Verjovski H.Jmeida S., Vettore A.L.,
RA Mature Sequence of the plant pathogen Xylcila fastidiosa.*;
RI Mature 406:151-159(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9PAE4;
Q9PAE4;
01-OCT-2000
01-OCT-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          investigating biology,";
Science 282:2012-2018(1998).
EMBL; 792784; CAB07196.3; .
SEQUENCE 554 AA; 62566 MW;
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Matches 12
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Q66484;
Q1-NOV-1996 (TrEMBLTG1. 0
Q1-NOV-1996 (TrEMBLTG1. 0
Q1-NOV-1996 (TrEMBLTG1. 0
Q1-JUN-2001 (TrEMBLTG1. 1
EAV ITA92 ORF5.
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P73694;
01-FEB-1997 (
01-FEB-1997 (
01-JUN-2000 (
HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDILINE-97061201; PubMod-8905231;
Kaneko T., Sato S., Kolani H., Tanaka A., Asamizu E., Nakamura Kaneko T., Sato S., Kinura T.,
Miyajima N., Hirosawa M., Sugiara M., Sissamoto S., Kinura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okum
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicollular cyanobacterium Syncchocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.": BMA 1791-136(1995). BMA 1791-11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AE004064; AAPB5371.1; -
InterPro; IPRO00326; PA_PTPase.
Pfam; PF01569; PAP2; 1.
SMART; SM0014; acidPrc; 1.
Hypothetical protein; Complete
SEQUENCE 227 AA; 25665 MW;
                  SEQUENCE FROM N.A.
STRAIN-RAY ITA92 (FIELD ISOLATE);
MEDLINE-96130216; PubMed-8553578;
Balasuriya U.B., Timoney P.J., McCollum
                                                                                                              Equine arteritis virus (EAV).
Viruses; ssRNA positive-strond viruses,
Arteriviridos; Arterivirus.
NCBI_TaxID:11047;
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SEQUENCE 1:
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Synechocystis sp. (strain PCC 6803)
Bacteria; Cyanobacteria; Chroococca
NCB1_TaxID-1148;
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  Phylogenetic
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Local Similarity 62.5
es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
12; Conserv
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126 AA; 14220 MW; 42CF97B3378A9919
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analysis
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Pred. No. 58;
1; Mismatches
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Last annotation update
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l; Mismatches
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59C79A14CD9B4A43 CRC64;
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Maclachlan N.J.;
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RESULT
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Q995W5
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virolopy 214:690-697(1995).
EMBL: U38598; ANA92903.1;
InterFro; IPR001332; ArterL_91ycop.
InterFro; IPR001332; ArterL_91ycop.
Pfam: PF00951; ArterL_91ycop; 1
PF00m; PD002371; Equine_virus_ORF5; 1.
SEQUENCE 255 AA; 28731 MW; 21587DC4FF
                                                                                                        O9H3N1 PRELIMINANA...
O9H3N1 PRELIMINANA...
O1H3N1:
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 17, Last annotation update)
O1-JUN-2001 (TREMBLREL 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q995W5;
01-JUN-2001
01-JUN-2001
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Virus isolated from semen of asymptotic
equine viral arteritis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses: ssRNA positive-strand Arteriviridae; Arterivirus. MCBI_TaxID-11047;
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
"Identification
                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF247539; AAK37622.1; -. SEQUENCE 255 AA; 28756 MW; F1897CF4D3797EC
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                          Matsuo
                                    SEQUENCE FROM N.A.
                                                             NCBI_TaxID-9606;
                                                                                                   Homo sapiens (Human)
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2 LSMTVLLFLLWGV
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of a
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                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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Novel Thioredoxin-related Transmembrane
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Pred. No. 74;
4; Mismatches
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Pred. No.
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"highes 7; Conserv
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Best Local :
                                                                                                                                                                                                                                                                                                      QSPMC5 PRELIMINA...,
QSPMC5,
QSPMC5,
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
01-UN-2001 (TrEMBLRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U1-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 32.5 KDA PROTEIN (FRAGMENT).
DKRZP5648162...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09Y4T6;
09Y4T6;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF(
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saplens (Human).

**Romo saplens (Human).
STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K.,
                                                                                                                                                                                                                                                                                            Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; ALO80080; CAB45700.1; - HSSP; P07237; 1MEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Redox-active center; Transmembrane.
SEQUENCE 280 AA; 31791 MW; A57E222481A997DE CRC64;
                                                                                                                                                                                                                            Campylobacter.
                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00085; thiored; 1.
PRINTS; PR00421; THIOREDOXIN.
PROSITE; PS00194; THIOREDOXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blum H., Bauersachs S., Mewes H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB048246; BAB20629.1;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                          NCBI_TaxID-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Redox-active center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MLVVFLLLWGVTW 15
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TE; PS00194; THIOREDOXIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
7; Conser
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53
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                                                                                                                                                                                                                                                     epsilon subdivision; Campylobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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         Ketley J.M., Churcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gassenhuber J.,
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049447; 01-UN-1998 (TIENBLIFEL. 06, Created)
01-UN-1998 (TIENBLIFEL. 06, Last sequence update)
01-UN-2001 (TIENBLIFEL. 17, Last annotation update)
ADP, ATP CARRIER-LIKE PROTEIN.
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Nature 403:655-668(2000).
Nature 403:655-668(2000).
                                                                                                                                                                                                                                                         Pfam; PF00153; mito_carr; 3.
PRINTS; PR00926; MITOCARRIER.
PROSITE; PS00215; MITOCH_CARRIER; 2.
                                                                                                                                                                                                                                                                                                                                            INNER MEMBRANE (BY SIMILARITY)

INSTALLABLE TO THE MITOCHONDRIAL EMBL. AL021749: CAN16877.1:

EMBL. AL021749: CAN16871.1:

EMBL. AL021749: CAN16871.1:

EMBL. AL021749: CAN16871.1:

INCEPTO. IPR001993: MITOCh.carrier.

INCEPTO. IPR001993: MITCChricer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F2109.60 OR AT4G28390.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                     Inner membrane; Mitochondrion; SEQUENCE 379 AA; 40718 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000)
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Rose M., Hempel S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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1 Similarity 46.2
6; Conservative
                                                           Similarity
9; Conserv
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Entian K.-D., Mewes H.W.,
DD) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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                                                                                   50.6%;
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                                                   Score 44; DB
Pred. No. le+C
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB
Pred. No. 85;
4; Mismatches
                                                                                                                                                                                                     Repeat; Transmembrane; Transport. C865FEAD6968A2A9 CRC64;
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le+02;
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databases.
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09KFK7;
01-0CT-2000 (TrEl
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BH0472 PROTEIN.
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OD: MAR-2001 (TEEMBLrel. 16, Created)

OD: MAR-2001 (TEEMBLrel. 16, Last sequence update)

OD: MAR-2001 (TEEMBLrel. 16, Last sequence update)

OD: MUN-2001 (TEEMBLrel. 17, Last annotation update)

OPENTYPE UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE.

ACTINOBACILIUS pleuropheumoniae (Hoemophilus pleuropheumoniae).

Bacteria: Proteobacteria: gamma subdivision: Pasteurellaceae:

Actinobacilius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; nucleic Acids Res. 28:317-4331(2000).

BMGL: AP001508: BAB04191.1.
InterPro: IPN001508: BAB04191.1.
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                                                                                                                                                                                                                     Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AP39452; AMG45943; 1:
InterPro, IPB003362; Bact transf,
InterPro, IPB003939; Mitcoh_carrier.
Piam; PF02397; Bact_transf; 1.
                                                                                                                                                                                                                                                                                                                                                                                  Labrie J., Kloux S., Wade M.M., Champlin F.R., Holman S.C., Wilson W.W., Savoye C., Kobisch M., Galarneau C., Jacques M.; Wilson H.W., Savoye C., Kobisch M., Galarneau C., Jacques Actinobacillus Tidentification of genes involved in biosynthesis of Actinobacillus pleuropneumoniae serotype 1 O-antigen and biological properties of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN "C-125 / JCM 9153;
MEDLINE 20512582; PubMed 11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN C-125 / JCM
                                                                                                                                     PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN_1.
Transferase.
SEQUENCE 471 AA; 55192 MW; C5B445ABD7BE3
                                                                                                                                                                                                                                                                                                                                                               rough mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-4074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID 715;
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|104 VILRLLWGIAW ||14
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Last annotation update)
                          Score 44; DB 2; Length 471;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 1.1e+02;
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Oy 10 LWGVTWG 16
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Db 110 LWGLTWG 116
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Search completed: January 7, 2002, 16:51:30 Job time: 277 sec

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Search information block:
Ouery Us-09-471-276-831_COPY_1_16
Ouery length: 16
Database: GeoEmbl: *
Database sequences: 1472140
Database length: -34114437
Search time (sep): 1331.940000
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sb. ltg x6012233
pb. ltg x6012233
pb. ltg x60122433
pb. ltg x6012433
pb. ltg x6012433
pb. ltg x6012729
pb. ltg x601286
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pb. ltg x601391
pb. ltg x6013872
pb. ltg x6013872
pb. ltg x6012435
                                        gb_pr:AC012410
gb_ln:CEP127E9
gb_ln:CEP127E9
gb_ln:AC084471
gb_pr:HS191E19
gb_pr:AC0757945
gb_hrg:AC068151
gb_hrg:AC068151
gb_hrg:AC0623766
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-(0-/cgn2_1/108F0C_spool)(US084121676/runat_07012002_142445_19882/app_query.fasta_1.274
-(0-/cgn2_1/108F0C_spool)(US084121676/runat_07012002_142445_19882/app_query.fasta_1.274
-DB-GenBmb1 -OEMT-fastap -SUFFIX-ryge -GAPOP+12.000 -GAPEXT-4.000
-MINARTH-0.100 -LOOPCI-0.000 -LOOPEXT-0.000 -GAPEXT-0.000
-GAPEXT-0.000 -YGAPOP-10.000 -YGAPEXT-0.500 -FGAPOP-6.000
-CGAPEXT-0.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-0.000 -START-1 -MATRIX-DIOSUM62 -THE MAX-100 -THE,MIN-0
-LIST-100 -DOCALIGN-200 -THE,SCORE-PGC -THE MAX-100 -THE,MIN-0
-ALIGN-100 -DOCALIGN-200 -THE,SCORE-PGC -THE MAX-100 -THE,MIN-0
-ALIGN-100 -DOCALIGN-200 -THE,SCORE-PGC -THE MAX-100 -THE,MIN-0
-MAXLEN-2000000000 -USER-US09471276_GCGN1_1_6345
-NCPU-6 -CCPU-3 -LONGUOG_DEV_TIMEDUT-120 -MARN_TIMEDUT-30
-NO_XLPXY -MAIT -THREADS-1
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11 AC057944 Homo suplens BAC cil
29 AC06815 Homo suplens Chromc
20 AC09146 Homo suplens Chromc
21 AC021766 Homo suplens Chromc
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AC084471 Caenorhabditis brigo
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AC022937 Homo sapiens clone
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                                                                                                                               SOURCE
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9b. bis : SCES0

9b. htg : ACC23011

9b. pl : ACC011675

9b. pt : AL139102

9b. htg : ACC015661

9b. htg : ACC05661

9b. htg : ACC05660

9b. htg : ACC07400

9b. pt : ACC07400
                                                                                                                                                                                                              9b_om:AF055546
9b_ba:PPU131925
9b_pr:AF044311
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gb_brig: ACO7542
gb_pr: HUU59743
gb_brig: ACO759743
gb_htg: ACO375674
gb_htg: ACO32414
gb_htg: ACO325718
gb_htg: ACO375611
gb_htg: ACO375631
gb_htg: ALI353782
gb_htg: ALI353782
gb_htg: ALI353783
gb_htg: ALI353783
gb_htg: ALI358706
gb_th: AEO35324
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9b_htg:AC034140
9b_htg:AC074107
9b_htg:AC064842
9b_pr:AC068812
9b_htg:AC018450
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gb_htg:AC025642
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gb_pr:AC008790
gb_pr:HS18111
gb_htg:AL139261
gb_htg:AC015598
gb_htg:AC009173
gb_htg:AL133543
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gb_ba:AE001921
gb_ba:AE001705
gb_pr:AL391420
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gb_pr:HS512B11
gb_htg:AL590044
gb_pr:AC006061
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7.2e+03
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595.89
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AB0017951 Delnococciis raddo
AB001795 Thermotoga maritti
AL391420 Human DNA sequenc
AL156172 Streptomyces coel
AC023011 Homo sapiens clon
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AC001975 Homo sapiens clon
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AC058071 Homo sapiens chr
AC068378 Homo sapiens chr
AC025868 Homo sapiens chr
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AJ000388 Homo sapiens mRNA
1 AC019542 Drosophila melano
1 AL031058 Human DNA sequenc
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AC006061 Homo sapiens Xp22
AC008852 Homo sapiens chr
AC008790 Homo sapiens chr
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gb_pr:AK027222

ACCESSION VERSION seq_documentation_block:
LOCUS AK027222
DEFINITION Homo sapiens AK027222 2175 | Homo sapiens cDNA:

AK027222 AK027222.1 GI:10440301 bp mRNA : FLJ23569 fis, PRI clone LNG11861.

29-SEP-2000

oligo capping; fis (full insert sequence). Homo sapiens human lung cDNA to mRNA, clone_lib:LNG clone:LNG11861 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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JOURNAL
REFERENCE
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KEYWORDS
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US-09-471-276-831_COPY_1_16 x AK027222/rev
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LOCUS AC012313 1
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Unpublished
2 (bases 1
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Sugano, Institute of Medical Science, University of Tokyo.
Laboratory of Gonome Structure Analysis, Human Genome Center:
Shirokane-dsi. 4-6-1 Minato-ku, Tokyo 108-6699, Japan
(E-maillicinal@lmsju-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Tanigami, A., Matsumura, K., Nakajima, Y., Mizuno, T., Morinaga, M., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Okawara, Y., Isogai, T., Tanaka, T., Nakamura, Y., Isogai, T., and Sugano, S.
NEDO human cDMA sequencing project
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                                              Direct Submission
                                                                      1 (bases 1 to 186451)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                  HTG; HTGS_PHASE2; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                             AC012313.6 GI:15145671
                                                                                                                                                                                                                                                                       AC012313
                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 19 clone CTD-2619J13, PROGRESS ***, 2 ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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(bases 1 to 186451)
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/note∵"cloning vector pME18SFL3"
598 c 626 g 431 t
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                                                                                                                                                                                                                                                                                                                                          ONA
                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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LOCUS AC022955 1
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US-09-471-276-831_COPY_1_16 x AC012313/rev
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TITLE
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 conting. Caps beckeen the conting are represented as rins of N. The order of the pieces
                       unordered pieces.
AC022955
                                                                         Homo sapiens clone
AC022955.3 GI:7249299
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181942: contig of 181942 bit in length
181943 182042: gpp of unknown length
182043 1826451: contig of 4009 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Is believed to be correct as given, however the sizes
of the gaps between them are based on estimates that have
provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence will be replaced
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/clone.*CTD-2619J13*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 184784 bases at least Q40 Consensus quality: 18594 bases at least Q40 Consensus quality: 185487 bases at least Q20 Estimated insert size: 194270; agarose-fp estimation Estimated insert size: 194270; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Project Name: 835906
Center clone name: CTD-2619J13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
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                                                                         RP11-153B10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 82.353
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                                                                         DRAFT SEQUENCE, 44
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16-MAR-2000

		TITLE JOURNAL COMMENT	SOURCE ORGANISM ORGANISM REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS
consists of 44 conclips. The true order of the pieces 1s not known and their order in this sequence record is arbitrary dags between the conclips are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved 1065 contig of 1065 bp in length 1066 1165: gap of 100 bp 1073 3813 3812: gap of 100 bp 108 3713 3812: gap of 100 bp 109 568 5765: gap of 100 bp 109 5768 3737: contig of 1855 bp in length 109 5768 3737: contig of 100 bp 109 5768 3737: contig of 100 bp 109 5768 3737: gap of 100 bp 109 5768 3737: contig of 1070 bp in length 109 5768 3737: contig of 1070 bp 109 5768 3737: contig of 1070 bp 109 5768 3737: gap of 100 bp 109 5768 3737: contig of 2072 bp in length	.mit.edu reads of reads of reads t 040 t 030 t 020 t 020 t 020	Norman, C.H., O'Connor, T. O'Donnell, P., Olivar, T. M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Nohman, D., Royano, Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, M., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vessillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Ilmer, A. and Zody, M. Limer, A. and Zody, M. Limer, A. Wo, A., Wu, X., Wyman, D., Ye, W.J., Ilmer, A. and Zody, M. Limer, A. Wu, X., Wyman, D., Ye, W.J., Ilmer, A. and Zody, M. Carles, Street, Cambridge, M. O2141, USA on Mar 16, 2000 this sequence version replaced gi:7108171. All repeats were identified using Repeatwasker: Smit, A.F. A. & Green, P. (1996-1997) http://fip.genome.vashington.edu/RN/Repeatwasker.html	HTGS_PHASE1; HTGS_DRAFT. human. buman. buman
91346 91643; gap of 100 bp in length 96878 65973; gap of 100 bp in length 96878 65973; gap of 100 bp in length 10230 10229; gap of 100 bp in length 10230 10229; gap of 100 bp in length 10756 107561; contri of 5322 bp in length 10756 207661; gap of 100 bp in length 11245 11252; gap of 100 bp in length 11245 11252; gap of 100 bp in length 11253 11253; gap of 100 bp in length 117674; contri of 5122 bp in length 117674; contri of 6122 bp in length 117675 11774; gap of 100 bp in length 125917; contri of 6275 bp in length 125918; gap of 100 bp in length 13288; 13284; gap of 100 bp in length 13760 137719; gap of 100 bp in length 1360 13719; gap of 100 bp in length 144499 144598; gap of 100 bp in length	\$397. 9ap of 3083 by \$6460: 9ap of 100 bp \$6460: 9ap of 100 bp \$6460: 9ap of 100 bp \$6711: control of 4281 bp \$6810: 9ap of 100 bp \$6504: control of 4183 bp \$6504: control of 4418 bp \$6522: control of 4418 bp \$6522: gap of 100 bp \$7622: 9ap of 100 bp \$7623: 9ap of 100 bp \$76313: cantrol of 3240 bp \$7613: gap of 100 bp \$1253: gap of 100 bp \$1254: control of 5252 bp	2836 2836 2836 2837 bp in length 3086 31092: gap of 100 bp in length 3086 31092: gap of 100 bp in length 3202 34301: contrig of 329 bp in length 34202 3474: contrig of 329 bp in length 34302 3474: contrig of 3173 bp in length 37475 27574: gap of 100 bp in length 3755 40724: contrig of 3150 bp in length 40725 4084: gap of 100 bp in length 40825 43315: contrig of 3291 bp in length 43416 46746: contrig of 3291 bp in length 4674 4686: gap of 100 bp 4674 6874 6896 290 cf 100 bp 46874 49973: contrig of 3297 bp in length 49874 49973: contrig of 3297 bp in length 49874 49973: gap of 100 bp	9829: gap of 10097; gap of 110997; gap of 12097; gap of 1433: contil 13950; contil 13950; contil 15950; contil 15950; contil 15950; contil 15950; contil 17958; gap of 12095; gap of 12095; contil 12095; gap of 12095; contil 120

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ACCESSION
VERSION
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Ratio:
   AC022937.3 GI:7249297
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                        unordered pieces
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9830. .10997
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37575 .40724
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24221. .26233
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30963. .34201
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20196. .22180
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17799. .20095
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2506. 3712
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/clone~"RP11-153B10"
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/db_xref…"taxon:9606"
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159560: contig of 8971 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (07-FBB-2000) Whitehead Institute/AIT Center for Genome Research, 320 Charles Street, Cambridge M. 02141 USA On Mar 16, 2000 this sequence version replaced gi:6997314. All repeats were identified using RepeatMasKer: smit. A.F.A. & Green, P. (1996-1997)
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Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
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Anderson, S., Baldwin, J.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-577C21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Chemistry: Dyo-terminator Big Dyo: 100% of reads
Assembly program, Phrap; version 0 60731
Consensus quality: 174164 bases at least 040
Consensus quality: 181501 bases at least 030
Consensus quality: 184005 bases at least 020
Insert size: 194000, agarose-fp
Ouality overage: 3.8 in 020 bases; suarose-fp
Quality overage: 3.9 in 020 bases; suarof-contigs
                                                                                                                                                                                                                                                                                                                             NOME: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
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------ Project Information
Center project name: L6361
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Center code: WIBR
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3529 59
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1352 3428:
                                                                                                                                            9 5941:
2 6041: gap
                   8391: contig of 2250 bp
8391: gap of 100 bp
11392: contig of 3001 bp
11492: gap of 100 bp
13568: contig of 2076 bp
13668: gap of
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3428: contig of 2077 h
19 gap of 100 bp
5941: contig of 2413 k
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16500 1652 gap or 1 gap of 2845 ...
16500 19204: contig of 2845 ...
19205 19304: gap of 100 bp
19205 29306: contig of 3732 bp in length
23037 23156: gap of 100 bp
23037 23156: gap of 100 bp
23037 23156: gap of 100 bp
23037 2316: gap of 100 bp
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27388 27488; gap of 27488 343238; Config of 4897 bp in length
32885 3432388; config of 6896 bp in length
32885 37570; Config of 5086 bp in length
37571 34701; Config of 6731 bp in length
37571 44401; Config of 6731 bp in length
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52876 60711: contig of 7836 bp in length
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                      /note-"assembly_fragment"
71845. 84379
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52876. .60711
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19305. .23036
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8392. .11392
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60812. .71744
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44502. .52775
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32485. .37570
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27488. .32384
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/db_xref="taxon:9606"
/clone="RP11-577C21"
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AUTHORS
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ORGANISM
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US-09-471-276-831_COPY_1_16 x AC022937/rev
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ORIGIN
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LOCUS ECJ224437
                                                                                                                                                                                                                                                                                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_ba:ECJ224437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AC022937 from: 1 to: 189679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
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Direct Submission R.A., Plant Biology,
Submitted (13-MAR-1998) Andersson R.A., Plant Biology,
50 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 (750 07 
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Ratio:
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Pectobacterium carotovorum subsp. carotovorum.
Pectobacterium carotovorum subsp. carotovorum.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia carotovora subsp. carotovora sigma factor RpoS (sigma s)
Mol. Plant Microbe Interact. 12 (7),
                                                                                                                                                                                                                                                                                                                                                                                     SWEDEN
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Andersson, R.A.
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98276. .112174
/note="assembly_fragment
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162371. .189679
/note="assembly_fragment"
136533 c 36141 g 55883 t
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143638. .162270
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126439. .143537
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112275. .126338
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                                                                                                                                                              344. .1264
                                                                                                                                                                                                                                                                    /organism="Pectobacterium
/strain="SCC3193"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .2797
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                                                    /note="rssA homologue"
                                                                           /gene-"expL"
                                                                                                     /gene-"expL"
353. .1264
                                                                                                                                                                                 /gene-"expL"
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                      codon_start=]
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Gaps:
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gene

RBS

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alignment_block:
US-09-471-276-831_COPY_1_16 x
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LOCUS AL136379 1
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Percent Similarity:
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      HTG;
                                                  AL136379.18 GI:14970781
                                                                                              SEQUENCING IN PROGRESS ***, 6 unordered pieces AL136379
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HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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VVNECJAAGINEILIVTHSS"
1 562 c 756 g 776 t
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/cransibtion-"modphackhilviddeavrsvlagyltsigasvreatngldal
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Slleryhedhifolnewhogslypdmetsqlneldqlmoddslngspeaitkllagi
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/protein_id-"CAA11942.1"
/db_xref-"GI:3319928"
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Lugaay akardan sarakgabargas akarda sarakas ak
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LLRTLFNGLLQEHLVDQQHRLPYLPTLLKQVNQLLRQASLDGRFPLLVGYYHRPLKQL
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2604. .>2797
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2593. .2797
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/transi_table~11
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1381. .2397
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1370. .2397
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1370. .1373
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Percent Identity:
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RBS

ORIGIN BASE COUNT

SOURCE KEYWORDS VERSION DEFINITION

ACCESSION

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BASE COUNT
ORIGIN
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chemistry: Dye-Lerminator Big Dye; 99% of reads
Chemistry: Dye-primer Big Dye; 09% of reads
Consensus quality; 190267 bases at least 040
Consensus quality; 140700 bases at least 020
Consensus quality; 141500 bases at least 020
Tasert size; 14028; 30% of contigs
Tasert size; 137842; 30% error; agarose-fp
Ouality coverage; 7.73x in 020 bases; agarose-fp
Coverage: 9.23x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBiO 15A, UK. E-mail enquiries: humqueryésanger.ac.uk Clone requests: clonerequestésanger.ac.uk
On Jul 19, 2001 this sequence version replaced gi:14529732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing
Chemistry:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142558)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XCAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266; contig of 2667 bp in length
2668 2767; agp of 100 bp
2768 2767; agp of 100 bp
5994; contig of 297 bp in length
5995; 5994; agp of 100 bp
7986; contig of 2195 bp in length
7988 8087; agp of 100 bp
7888 8087; agp of 100 bp
135904; contig of 127816 bp in length
135904; contig of 3277 bp in length
139340; agp of 100 bp
139341; 139340; agp of 3218 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                          33414 a
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5795. .
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alignment_block:
US-09-471-276-831_COPY_1_16 x AL136379/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Mar 16, 2000 this sequence version replaced g1:6721264 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, p. (1996-1997)
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-222B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                     Sequencing vector: M13. M77815, 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.960731 Consensus quality: 14737 bases at least Q40 Consensus quality: 148358 bases at least Q30 Consensus quality: 148358 bases quality: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L5191
Center clone name: 222_B_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
Insert size: 151522; sum-of-contigs
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Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Institute/ MIT Center for Genome Research
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ENCE, 15
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NOTE: This is a 'working
                                                     Quality coverage: 4.8 in Q20 bases; agarose-fp Quality coverage: 4.8 in Q20 bases; sum-of-contigs
draft' sequence
It currently
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The true order of the pieces

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence be preserved. as soon as it is available and the accession number will 2652 2751: 1023 1122: 2651: 1022: contig of 1022 bp in length of. contig of 1529 bp in length of 100 bp of 2690 100 þ þ

83835 103507: contig of 19673 bp 103508 103607: gap of 100 bp 103508 129866: contig of 26259 bp 129867 129966: gap of 65245 65344: gap of 100 bp 65345 83734: contig of 18390 bp 83735 83834: gap of 100 bp 83735 83834: gap of 100 bp 34533 34632; gap of 100 bp 34633 44164: contig of 9532 bp in length 44165 4264 gap of 100 bp 44265 65244; contig of 20980 bp in length 5442 5541: 5542 76 Location/Qualifiers 20324: gap of 100 bp 27472: concig of 7148 bp in length 27572: gap of 100 bp 34532: contig of 6960 bp in length 7726: gap of 100 bp 12283: contig of 4557 bp in length 12383: gap of 100 bp 16229: contig of 3846 bp 16329: gap of 100 bp 20224: contig of 3895 bp 152922: contig of 22956 bp 5441: 7626: 441: contig gap of contig of 2085 bp in length of 100 bp 100 bp gg in length in length

/organism-"Homo sapiens" .152922

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/note=" /clone_ lib-"RPCI-11 Human Male BAC"

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alignment_block:
US-09-471-276-831_COPV_1_16 x AC021458/rev
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LOCUS AC092729 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTATAAAAATTGTTTTTATCACACTCTGGGGACTGTGGTGGGGT 15227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ayele, K., Beckstrom-Sternberg, S. M., Benjamin, B., Blakesley, R. W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Ho, S.-L., Idol, J. R., Karlins, E., Lec-Lin, S.-O., Legaspi, R., Lim, M., Maduro, O. L., Maduro, V. B., Mastello, C., Mastrian, S. D., McCloskey, J. C., McDowel, J. J., Pearson, R., Prasad, A., Shavchenko, Y., Snyder, B., Stantipop, S., Thomas, J. W., Lang, J. C., H., and Green, E.D., Woth, J. L., Walker, M. A., Wetherby, K. D., Zhang, L. H., and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-JUL-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Canis familiaris clone RPB1-60B6, WORKING DRAFT SEQUENCE, 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49092 a
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                                                                                                       conter project name: 0.019
Center close name: 0.01966s
Sequencing vector: plasmid: n/a: 1.00% of reads
Sequencing vector: plasmid: n/a: 1.00% of reads
Chomistry: pye-terminator BJ pye: 100% of reads
Assembly program: Phray, version 0.990319
Consensus quality: 16,0809 bases at least 0.30
Consensus quality: 11,11490 bases at least 0.30
Consensus quality: 11,11490 bases at least 0.30
Consensus quality: 11,11490 bases at least 0.30
Insert size: 152000; agarose-fp
Insert size: 16377; sum-of-contigs
Quality coverage: 11.00x in 020 bases; sum-of-contigs
Quality coverage: 10.24x in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                               Contact: nisc_mouse@nhgrl.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: NIH Intramural Sequencing
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103608. 129865_fragment
/note "assembly_fragment
clone_end:sp6
vector_sde:right"
129967. 152922
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29431 c 28272 g 44723
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Gaps: 0
Percent Identity: 53.333
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alignment_scores:
Quality:
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                 seq_documentation_block:
LOCUS AL357115 1
                                                                     seq_name: gb_pr:AL357115
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                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                     Align seg 1/1 to: AC092729
                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                             31963 TYGACAGTGACAAGACTATTATGGGGAATTACATGGGGC
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                                                                                                                                               4 LeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
AL357115 164012 bp DNA PRI 02-FE Human DNA sequence from clone RP11-102P23 on chromosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                               39995
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108581. .163977
/note·*assembly_fragment*
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71773. 108480
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clone_end:SP6
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/note-"assembly_fragment
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3205. .7098
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/db_xref⊷"taxon:9615"
/clone~"RP81-60B6"
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4 spp of unknown length
8 contig of 8894 bp in length
8 spp of unknown length
5 contig of 7797 bp in length
5 spp of unknown length
3 cantig of 10228 bp in length
5 spp of unknown length
5 contig of 10722 bp in length
5 contig of 10772 bp in length
                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length
contig of 55397 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of unknown length
contig of 28427 bp in
gap of unknown length
contig of 36708 bp in
                                                                                                                32001
                                                                                                                                                                                                                                                                                                                                                                                                               708 others
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                 02-FEB-2001
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DEFINITION

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DEFINITION
                                                                                                                      seq_documentation_block:
                                                                                                                                                                                              seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AL357115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-471-276-831_COPY_1_16 x AL357115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                      3282 GTTTACCTTTTACTTTGGGGTATTTGGTGGGGG 3314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                         6 ValPheLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                         gb_htg:AL512502
AL512502 177263 bp DNA HTG
Homo sapiens chromosome X clone RP11-807E6,
PROGRESS ***, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amoutated repeat sequence elements. Where the sequence is ambiguous, there is a monotation using the funsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Dan., BMBL, Sw., SMISSPROT, Tr., TREMBL, Mp., WORMPEP, Information on the WORMPEP database can be found at the MORMPEP database can be found at the MORMPEP database can be found at the MORMPEP of the MORMPEP database can be found at the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known such as compressions and repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: pBACe3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RP11-102P23 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      was generated from part of bacterial clone contigs of human chromosome X. constructed by the Sanger Centre Chromosome X Mapping Group, Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On Feb 5, 2001 this sequence version replaced gi:12329354. 
During sequence assembly data is compared from overlapping clones. 
Where differences are found these are annotated as variations 
together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wray, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
1 (bases 1 to 164012)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL357115.24 GI:12666259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xq13.3-21.1, complete sequence. AL357115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGP/Chrx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48623 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence is the entire insert of clone RP11-102P23 The true end of clone RP11-346E8 is at 115722 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-11.1"
29015 c 31474 g 54900 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-102P23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="q13.3-21.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .16401
                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 164012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 11
Gaps: 0
Percent Identity: 72.727
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                                                   * * *
                                                                                  10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                         misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL512502.4 GI:14456353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heath, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 177263)
                                                                                                                                                                                                                                                                 fragment_chain:
69141. .108593
                                                                                                                                                                                                                                                                                                                                                                                  8440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                          108694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
     /note-"assembly_fragment:01412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-807E6"
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                                                                                                                                                          .113120
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Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 17509 bases at least 040
Consensus quality: 175106 bases at least 020
Consensus quality: 175106 bases at least 020
Insert size: 176763; sum-of-contigs
Insert size: 174694; 7.7% error; adarose-fp
ounlity covarage; 7.0x, in 020 bases; sum-of-contigs Ouality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 15, 2001 this sequence version replaced gi:13092346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBiO 15A, UK. E.mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    830 8439; gap of 100 bp in length

8440 69040; contig of 60060 bp in length

69041 69140; sontig of 60061 bp in length

69041 108593; contig of 19453 bp in length

108594 108693; gap of 19453 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113121 113220: gap of 100 bp
113221 14881: contig of 3591 bp in length
148812 149911; gap of 100 bp
148912 177263: contig of 28352 bp in length
/note="assembly_fragment:00292
fragment_chain:1"
113221. .148811
                                                                                                                                        /note-"assembly_fragment:03321
fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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US-09-471-276-831_COPY_1_16 x AL512502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                          consensus quality: 172503 bases at least 040 consensus quality: 17766 bases at least 020 consensus quality: 17767 bases at least 020 setimated insert size: 187007. agarose-fp estimation guality coverage: 7.91 in 020 bases; agarose-fp estimation quality coverage: 7.91 in 020 bases; agarose-fp estimation quality coverage: 7.93 in 020 bases; agarose-ft currently estimation.

*NOTE: This is a "working draft" sequence. It currently consists of 16 contigs. The true order of the pieces.

* is not known and their order in this sequence record is * arbitrary, Gaps between the contigs are represented as * runs of M, but the casct sizes of the gaps are unknown.

* This record will be updated with the finished sequence as second sizes are the sequence.
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                                                                                                                                                                                                                                                                                                                    Summary Statistics
                                                                                                                                                                                                                                                                                                                                                 Center clone name: RPCI-23_449F12
                                                                                                                                                                                                                                                                                                                                                                 Center Project Name:
                                                                                                                                                                                                                                                                                                                                                                                 Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 185839)
DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing of Mouse
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Mammalla; Eutherla; Rodenti
1 (bases 1 to 185839)
DOE Joint Genome Institute,
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                 as soon as it is available and be preserved.
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fragment_chain:1"
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1081: contig of 1081 t
1181: gap of unknown 1
4298: contig of 3117 t
4398: gap of unknown 1
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Gaps: 0
Percent Identity: 72.727
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RP23-449F12, WORKING DRAFT SEQUENCE, 16
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Rodentia;
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Sclurognathi; Muridae; Murinae; Mus
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                                 JOURNAL
                                                                 AUTHORS
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             Submitted (28-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                               Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186882)
                                                                                                                                                                                                                              Human DNA sequence from clone RP3-38088 on chromosome 6p24.1.25.3 Contains a gene encoding the protein Neuritin, which is involved in promotion of neuritic outgrowth, a Pyruvate kinase (PKM) pseudogene, a novel mRNA, 4 CpG islands, ESTs, STSs and GSSs,
                                                 Direct Submission
                                                                 Brown, J.
                                                                                                                                 Homo sapiens
                                                                                                                                                                HTG; CpG island; Neuritin; PKM2
                                                                                                                                                                                  AL136307.12 GI:8574124
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91.667
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4 43498 c 42466 g 49655 t 1501 others
  clonerequest@sanger.ac.uk
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/clone."RP23-449F12"
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185839: contig of 35466 bp in
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150273:
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Gaps: 0
Percent Identity: 66.667
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contig of 18324 bp in
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of 3819
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of 4794
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of 10510 bp in
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence is the entire insert of clone RP3-380B8 The true left end of clone RP1-525021 is at 141303 in this sequence. The true right end of clone RP1-182016 is at 57138 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.asonger.ac.uk/HGP/Chr6
RP3-98088 is from the library RPGT-3 constructed at the Roswell
Park Cancer institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
ECTOR: PCTPG:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanggr.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of batterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: SW:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jun 20, 2000 this sequence version replaced gi:8573783.
During sequence assembly data is compared from overlapping clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Further information can be found at
                                                               7357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR repeat: matches 77. .145 of con
MIR repeat: matches 77. .145 of consensus"
2540. .3786
/note-*MIR repeat: matches 71.
8007. .8093
                                                                                                                                                         /note-"MLTID repeat: matches 308 ... 505
                                                                                                                                                                                                                                  6987.
                                                                                                                                                                                                                                                                                                                                              /note="MLT1D repeat: matches 14. .283 of consensus MLT1D repeat: matches 14. .283 of consensus" 6031 6005
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="L1MA9 repeat: matches 4632. .6308 of consensus L1MA9 repeat: matches 4632. .6308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSx repeat: matches 1..300 of consensus
AluSx repeat: matches 1..300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4034 ..4653
/note="L1M9 repeat: matches 4022 ..4632 of consensus L1M89 repeat: matches 4022 ..4632 of consensus" 4654 ..4953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2542. .3786 /note="LIPA5 repeat: matches 4900. .6143 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MIR repeat: matches 16.
MIR repeat: matches 16. .236 o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                             MER67A repeat: matches 374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="L1MB3 repeat: matches 5281. .6174 of consensus
L1MB3 repeat: matches 5281. .6174 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP3-380B8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="p24.1-25.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1PA2 repeat: matches 4900. .6146 of consensus"
                                                                                              'note="MIR repeat: matches 71. .262 of consensus"
                                                                                                                                                                                                                                                                                            'note="MER67A repeat: matches 374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hes 16. .236 of consensus
.236 of consensus"
                                                                                                                                                                                                                                                             .543 of consensus"
                                                                                                                                                                                             308.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .145 of consensus
                               .177 of consensus
                                                                                                                                                              of consensus"
                                                                                                                                                                                         .505 of consensus
                                                                                                                                                                                                                                                                                            .543 of consensus
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/note-"MER5A repeat: matches 43.
MER5A repeat: matches 43. .189 o
14785. .14859
20482...20806
/note="1/TR16C repeat: matches 56...387 of con: LTR16C repeat: matches 56...387 of consensus"
                                                                                                                                                                                                                                                                                                                                                                  /note-"MLTIC repeat: matches 1. .193 of con:
MLTIC repeat: matches 1. .193 of consensus"
join(<19542. .19799,20379. .>20477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MLT1C repeat: matches 193, .466 of con
MLT1C repeat: matches 193, .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note**MIR repeat: matches 78. .133 of consensus MIR repeat: matches 78. .133 of consensus* 18611. .18904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2664.
complement(16038..16616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="liki3A repeat: matches 5525. .5777 of consensus
LIME repeat: matches 5525. .5777 of consensus*
15317. .15774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MIR repeat: matches 15. .262 of consensus MIR repeat: matches 15. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"LIMAIO repeat: matches 5479. .6315 of consensus LIMAIO repeat: matches 5479. .6315 of consensus" 1299, .1326 repeat: matches 9. .290 of consensus /note-"AluSx repeat: matches 9. .290 of consensus AluSx repeat: matches 9. .290 of consensus" 13548. .13778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"MIR repeat: matches 134. .252 of consensus" 12145. .12963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLT1G repeat: matches 65. .512 of con
MLT1G repeat: matches 65. .512 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER33 repeat: matches 192. .324 of con
MER33 repeat: matches 192. .324 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="THE1B repeat: matches 1. .364 of consensus THE1C repeat: matches 1. .371 of consensus" octo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9200
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LlM4 repeat: matches 5688. .5772 of consensus"
8094. .8229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluSg repeat: matches 1..310 of con
AluSg repeat: matches 1..310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L1ME3A repeat: matches 5785, .5859 of consensus
L1ME repeat: matches 5785, .5859 of consensus"
15550, .15303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="LIMB8 repeat: matches 6029. .6173 of consensus
LIMB8 repeat: matches 6029. .6173 of consensus"
                                                                                                                                                                                                                                     /evidence=not_experimental
/product="dJ380B8.3 (a novel mRNA)"
join(19542. 19799,20379. .20477)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="L1 repeat: matches 3951. .4433 of consensus"
15943. .16022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1M4 repeat: matches 3951. .4454 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10364. .
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                                                                                                     /note="15 copies 2 mer ac 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="match:
                                                                                                                                                       note-"match:
                                                                                                                                                                               /gene="dJ380B8.3"
19669. .20180
                                                                                                                                                                                                                                                                                                                           note="match: ESTs: Em:R79825"
                                                                                                                                                                                                                                                                                                                                                      /gene="dJ380B8.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .15774
                                                                                                                                20184
                                                                                                                                                       GSS:
                                                                                                                                                       Em: AQ401011"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Em: AQ541664"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        .193 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .310 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .512 of consensus
                                          .387 of consensus
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US-09-471-276-831_COPY_1_16 x
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                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_htg:AC012285
                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                              ACCESSION
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Percent Similarity:
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
Bifren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, M., Beckerly, R., Boguel awkly, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocoko, P., DeAcellano, K., Dewar, K., Domino, M., Douclan, L., Doyle, M., Ferreira, P., Fitchugh, M., Forrest, C., Funke, R., Gage, D.,
                                                                                                                                Birren, B., Linton, L., Nusbaum, C.
Homo sapiens, clone 3_F_23
                                                                                                                                                                                                                                                                                         unordered pieces.
AC012285
AC012285.1 GI:6094585
                                                                                                                                                                                                                                                                                                                                           ACU12285 283388 bp DNA HTG 22-OCT-1.
HOMO Saplens clone 3_F_23, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 283388)
                                                                                                                 Unpublished
                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                   AC012285
                                                                                                 (bases 1 to 283388)
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/note-MIR repeat: matches 65. .196 of consensus*
MIR repeat: matches 65. .196 of consensus*
27177. 27238

/note-La repeat: matches 2644. .2709 of consensus*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"HERVI6 repeat: matches 882. .1164 of con
HERVI6 repeat: matches 882. .1164 of consensus"
25788. .26094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLAM_A repeat: matches 10. .99 of consensus 21469. .21856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26354. .26477
/note-*LIME repeat: matches 458.
26716. .26792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.00
4.909
84.615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L2 repeat: matches 27243. .27405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L2 repeat: matches 2666. .2741 of consensus complement(26932. .27550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"AluY repeat: matches 1. .307 of consensus AluY repeat: matches 1. .307 of consensus"
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HERVL repeat: matches 2992. .4228 of consensus"
23429. .24388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note:"HERVL repeat: matches 4345.
22192, ,23403
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Galbagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Lohozard, J.C., Johnson, R., Jones, C., Kann, I., Kardtas, A., Klein, J., Lahozard, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Klein, J., McCanghiln, J., Mardrim, J., McCardyn, J., Maylor, J., Norman, C.H., O'Connor, T., O'Connell, P., Peterson, K., Pollara, V., Rilcy, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teafaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A., and Zody, M.

Submitted (22-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMsker: Smit, A.F.A. & Green, P. (1996-1997)

NOTE: This is a "working draft' sequence, it currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is a rishitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

2094: contig of 2094 bp In length

74966: 58925: 55793: 50111: 45512: 42512: 35590: 31970: 29547: 26404: 23922: 21641: 18762: 16645: 14198: 2094: contig gap of 4249: contig gap of 38764: 12051: 6744: 9597: gap of gap of gap of gap of contig gap of contig gap of gap of contig gap of gap of contig gap of gap of contiq gap of contly gap of contig contig gap of gap of contig contig gap of contig contig gap of contig gap of contig contig gap of unknown of 4954 unknown of 3132 unknown of 5682 unknown of 4599 unknown of 3748 of 3174 unknown of 3620 unknown of 2423 unknown of 3143 unknown of 2482 unknown of 2281 of 2879 unknown of 2117 unknown of 2454 unknown of 2853 of 2155 unknown of 3063 of 2447 of 2376 of 3000 of 2147 of 2495 of 2571 of 3077 unknown unknown unknown unknown unknown unknown bp in l length bp in l length bp in l length bp in l length bp in 1 length bp in l length length bp in l length bp in l bp in l фþ length bp in 1 þ g g gd ф length bp in length bp in Length ф bp in length þ g length ij in = in length length length length Jength length length Length length length length

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BASE COUNT
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alignment_block:
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                      Percent Similarity:
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Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C.,
Levis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulsegod, H., Lozador, R., Lu, L., Lucier, A., Lucier, R., Luna, R.,
Kartindale, A., Martinez, E., Wassey, E., Wahnlary, E., RoLeod, M.P.,
Mandor, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G.,
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Mendor, M., Mei, G., Merscher, S., Metzker, M., Miller, A., Miner, G.,
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                                                                                                                       Direct Submission
Submitted (13-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Whashington,C., Watlington,S., Woley,K., Wu,C., Wu,Y., Wu,Y., R., Zhou,J., Zorrilla,S., Kucherlapati,R. and Gibbs,R.
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Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 111121)
3 (bases 1 to 111131)
Worley, K.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC046131.35 GI:14669932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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COMMENT

Direct Submission

TITLE JOURNAL

Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of MoLecular and Human Genetics, Baylor Collige of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2011 this sequence version replaced gi:12656690.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this cione. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and

local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green

unpublished.) for Human and Mouse Sequences.
Genes and Region of Sequence similarity are identified by BIAST (Nuc. Acids Res. 25:388-3402) similarity (expect < 10-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum of standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguittes or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguittes. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

OUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards estimated error rate less than 1 per 10,000 bases.

Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrites can be found at URL: http://gc.bom.tmc.cdu/808/quality.info/genbank.annotation

QUALSTAT - REPORT - - - - - - -

Number of consensus changing edits: Number of N's in consensus :	Fraction of Phrap values less than 40 :	Average error rate (BCM-Phrap estimate):	Phrap values in estimate:	Contig length:	Summary Statistics
0 52	0.0102396	1.53449e-05	110454	111131	

35164	35126	35039	35004	35002	34999	24292	24289	24247	21493	20451	19617	17387	11107	11098	11091	5038	Position	
gtatttttag(n)agagatgggg	caactacagg(n)gcacaccacc	tggattgcag(n)ggtgctatct	ttttnaana(n)ggagtctcac	ttttttnaa(n)anggagtctc	tttttttt(n)aananggagt	gggcaggnca(n)ggcaggggag	gaagggcagg(n)canggcaggg	gggcagggca(n)ggcagggcag	tttctcactt(n)tttattagct	ctgtggtaac(n)atagtttgca	tgttctctaa(n)tttttaaat	cctgggcaac(n)cggtgaaacc	cntggtotgg(n)tttttttt	gccntaggcc(n)tggtctggnt	ttattaggcc(n)taggccntgg	ctgagattgc(n)ccattgcact	Original+Context	Consensus changing edits
gtattttag(t)agagatgggg	caactacagg(t)gcacaccacc	tggattgcag(g)ggtgctatct	tttttaaga(t)ggagtctcac	tttttttaa(g)atggagtctc	ttttttt(t)aagatggagt	gggcagggca(g)gqcaggggag	gaagggcagg(g)cagggcaggg	gggcagggca(g)ggcagggcag	tttctcactt(c)tttattagct	ctgtggtaac(a)atagtttgca	tgttctctaa(t)tttttaaat	cctgggcaac(a)cggtgaaacc	cttggtctgg(t)tttttttt	gccttaggcc(t)tggtctggtt	ttattaggcc(t)taggccttgg	ctgagattgc(a)ccattgcact	Edited+Context	ts

cccaggagag(c)tgataagtgg	cccaggagag(n)tgataagtgg	86864
aaaaacaagc(a)atggggaaag	aayc(79337
clgatctttg(a)caaacctga	ctganctttg(n)caaacctgag	79316
aactatotga(t)otttgacaaa	nactatctga(n)ctttgncaaa	79310
gcatatotac(a)actatotgat	-	79300
6	tgcatatcta(n)nactatctga	79299
ô	_	79277
	Ξ	79276
aaacagagat(a)tagatcaatg	aaacagagat(n)tagatcaatg	79249
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cagctaagag(a)actagaaggg	cagctannnn(n)nctagaaggg	69187
acagctaaga(g)aactagaagg	acagctannn(n)nnctagaagg	69186
aacagctaag(a)gaactagaag	aacagctann(n)nnnctagaag	69185
gaacagctaa(g)agaactagaa		69184
tgaacagcta(a)gagaactaga	tgaacagcta(n)nnnnnctaga	69183
tgggtggaat(t)tttacctctt	tgggtggaat(n)tttacctctt	60057
agtaaaacac(a)caatttcccc	Ξ	57233
9	Ξ	57224
cactcatttt(c)taaggtgcat		57135
gtatttggga(c)tatttttac	gtatttggga(n)tatttttac	56998
caagagatag(a)caaatatagc	caagagatag(n)caaatatagc	56972
tittatitic(a)caastaaatt	ttttattttc(n)caaataaatt	56941
3	tntctgngca(n)ttatatttta	56925
tcagtttctg(t)gcatttatat		56921
ttatttcagt(t)tctgtgcatt	(n)tctgng	56916
ttttagtgta(t)ggttatttca	(n)ggttatt	56903
	tctcnnttag(n)gtanggttat	56899
taagatotot(t)ttagtgtatg	taagatctcn(n)ttagngtang	56894
	_	56893
caccactcat(t)aaccacaac	_	56868
ggaaaaaaca(a)tgtgcaaat	n)tgtgcaaat	47731
tatacctasa(a)gasagasast	tatacctaan(n)gaaagaaaat	47109
atatacctaa(a)agaaagaaaa	atatacctaa(n)ngaaagaaaa	47108

----- Distribution of Quality < 40 Bases

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bases
              1000
900
800
700
600
500
400
300
200
100
100
     ហ
     10
Phrap Value Range
     30
     35
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US-09-471-276-831_COPY_1_16 x AC046131/rev
                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                  source
                                                                                                                                       repeat_region
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                                                              53.00
4.417
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/db_xref:"taxon:9606"
/chromosome:"12"
                                                                                                                                                                                                                               Location/Qualifiers
                                               80.000
                                         Gaps: 0
Percent Identity: 53.333
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
REFERENCE
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                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                     misc_feature
                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemistry: Dye-terminator Hig Dye: 56% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 142341 bases at least 040
Consensus quality: 142713 bases at least 030
Consensus quality: 142713 bases at least 020
Consensus quality: 142710 bases; agarose-fp
Cuality coverage: 8.97 in 020 bases; sum-of-contigs
Cuality coverage: 8.97 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (04-MAY-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA On Aug 9, 2001 this sequence version replaced gi:14626398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 143219)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC068600 143219 bp DNA HTG 09-AUG-2001 HOMO Sapiens chromosome 2 clone RP11-567N20, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H_NH0567N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 143219)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-primer ET; 44% of reads Chemistry: Dye-terminator Big Dye; 56%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: plasmid; 56%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 44%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                 142009
                                                                                                                                                                                                                                                                                                                                                                                       141909
/note="assembly_name:Contigl1
clone_end:SP6
                                                                           1. .141908
                                                                                                                                                /organism~"Homo sapiens"
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/chromosome="2"
                                                                                                                                                                                                                                                                            1. .143219
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                     /clone-"RP11-567N20"
                                                                                                                                                                                                                                                                                                                                       141908: contig of 141908 bp in length 142008: gap of unknown length 143219: contig of 1211 bp in length.
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dodgé,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,R., Gage,D., Galdyna,S., Ginde,S., Goyette,M., Girahm,J., Gardyna,S., Ginde,S., Goyette,M., Grahm,J., Gardyna,S., Ginde,S., Goyette,M., Grahm,J., Gardyna,S., Gardyna,S., Heaford,A., Horton,L., Howand,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Hein,J., LaRocque,K., Lanaeres,R., Landers,T., Lehoczky,J., Levine,R., Liew,C., Liu,G., Locke,K., Haddmald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McRernan,K., McPheeters,R., McCarthy,M., McDewn,P., McGurk,A., McRernan,K., McPheeters,R., McCarthy,M., McDewn,P., McCarthy,M., McDewn,P., McCarthy,M., McDewn,P., McCarthy,M., McCarthy,
                                                                                                                                                                                                                                                      Submitted (07-JUL-2000) Whitchead Institute/AIT center for Genome Research, 320 Charles Street, Cambridge, MA 02141, US On Aug 12, 2000 this sequence version seplaced gi:8954162.
All repeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                          Contact: sequence_submissions@genome.wi.mit.edu
                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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Genome Center

Project Information

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seq_documentation_block:
LOCUS AC073948 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22755 GTGCTCTTGCAATTTCTAAGTCTTTGGGGTGTTCTTTGGGGG 22796
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Boguslavkiy.L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                    2 (Lases 1 to 143850)
Birren.B., Linton.L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,Y., Beda,F.,
                                                                                                                                                                                1 (bases 1 to 145856)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-21G15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACO73948 145856 bp DNA HTG
Homo sapiens chromosome 18 clone RP11-21G15
                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                     Homo sapiens
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142009. .143219
/note="assembly_name:Contig5"
28074 c 28420 g 42168 t
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4.818
78.571
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Percent Identity: 64.286
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misc_feature
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                                                                                                                                                                                                                                                                                    95030 109604: contry 0. 100 bp
109605 109708: gap of 10704 bp in length
109705 122428: contig of 12724 bp in length
122429 12528: gap of 100 bp
122529 129527: contig of 16999 bp in length
139528 139627: gap of 100 bp
139528 145855: contig of 6229 bp in length
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Sequencing vector: M13, M77815; 100% of reads
Chemistry: Dye-terminator H10 Dye, 100% of reads
Assembly program: Phrap, version 0, 560731
Consensis quality; 113967 bases at least 040
Consensis quality; 113967 bases at least 040
Consensis quality; 113967 bases at least 040
Consensis quality; 112846 bases at least 020
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Insert size: 144056; sum-of-contigs
Quality coverage: 3.1 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 bases; sum-of-contigs
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Center clone name: 21_G_15
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94989 95088: gap of 100 bp
95089 109604: contra of 14516 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53821 5920; gap of 100 bp
53921 58914; contig of 4994 bp in length
58915 59014; gap of 100 bp
59915 89355; contig of 26341 bp in length
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85456 94988: contig of 9533 bp in length
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19789 21805; contig of 2017 bp in length
21906 21905; gap of 100 bp
21906 23993; contig of 2088 bp in length
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15452 168
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24094 27304: contig of 3211 bp in length
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16929 17939: contig of 1011 bp in length
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      /note: "assembly_fragment"
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                                                                                         /note…*assembly_fragment
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                                                                                                                                                                                                                                                     /organism·"Homo sapiens"
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.63: gap of 5957 bp in length
.53820: contig of 5957 bp in length
.700 bp
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43108: contig of 5791 bp in length
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32590: contig of 5186 bp in length
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                        JOURNAL
REFERENCE
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ORIGIN
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                                                                                                                 REFERENCE
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                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                        ACCESSION
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                                                                                                                                                                                                                                                     /ERSION
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                                                                   AUTHORS
TITLE
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                                                                                                                                                                               ORGANISM
      AUTHORS
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11||1||1||:::|||1||1||:::||
14470 TCAATGCTGTATATCTTTCTTCTAGTTTGGAGAAGCCAGTGGGGT 14514
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2 (bases 1 to 155804)
Birren, B., Linton, L., Nusbaum, C.,
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 155804)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                        pieces.
AC019241
                                                                                                                                                                                                                                                                                                                   AC019241 155804 bp DNA HTG 10-NOV-2000 HOMO sapiens clone RP11-45120, WORKING DRAFT SEQUENCE, 6 unordered
                                           Unpublished
                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-45I20
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                  AC019241.5 GI:11136802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41606 a
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59015. .85355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note
37318.
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30265 c 28947 g 43233 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note--"assembly_fragment"
139628. .145856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"assembly_fragment"
122529. .139527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /noter assembly_fragment 109705. .122428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note "assembly_fragment" 47864. .53820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note...*asscmbly_fragment*
32691. .37217
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27405. .32590
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21906. .23993
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19789. 21805
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/note-"assembly_fragment"
18040. .19688
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4.818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note-"assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 27304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Gaps:
   Lander, E., Abraham, H., Allen, N.,
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                                                                                                                                                                                                                                                                                                               source
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Sequencing vector: Plasmid; n/a; 53% of reads
Sequencing vector: Plasmid; n/a; 53% of reads
Chemistry: Dye-terminator B19 Dye: 100% of reads
Assembly program: Phrup; version: 960731
Consensus quality: 154752 bases at least 040
Consensus quality: 154752 bases at least 020
Consensus quality: 154765 bases at least 020
Consensus quality: 15500B bases at least 020
Trisert size: 135000. agarose: fp
Quality: coverage: 111. Th 020 bases; agarose: fp
Quality: coverage: 111. Th 020 bases; agarose: fp
Quality: coverage: 117. Th 020 bases; agarose: fp
Quality: coverage: 117. Th 020 bases; agarose: fp
Louisits of contigs: The true order of the pieces
18. DOLKNown and their order in this sequence are conditions.

**Into Grad will be water stream of the grads are unknown.
**Into Ford will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (31 DEC-1999) whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, M. 02141, USA on Nov 10, 2000 this sequence version replaced 91:8056820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gardyna.S., Grant.G., Hagos.B., Heaford.A., Horton.L.,
Howland J.C., Johnson, R., Jones C., Kann.L., Karatas A., Klein, J.,
Landers T., Lehoczky, J., Levine.R., Lieu, C., Liu, G., Locke, K.,
Macdonald P., Marquis N., McEwans, P., McGura, A., McKernan, K.,
McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., MyLor, J.,
McRan, C. H., O'Connor, T., O'Donnell, P., Ollvar, J., M., Pecerson, K.,
Lerre, N., Plaani, C., Dellara, V., Raymond, C., Rley, R., Rothman, D.,
Lerre, N., Plaani, C., Dellara, V., Raymond, C., Rley, R., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boguslawkly, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Cole, M., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, S., Baldwin, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41730 47544: contig of 5825 bp in length 47645 47644: gap of 100 bp 47645 5935: contin of 500 bp 59337 favor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                             117656 117755: gap of 100 bp
117756 155804: contig of 38049 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               47845 47644: gap of 100 bp in length 47645 59936: contig of 1229 bp in length 59937 60036: gap of 100 bp 60037 83181: contig of 23145 bp in length 83182 83281: gap of 100 bp 83282 117655: contig of 34374 bp in length 10364
vector_side:left"
                                              /note="assembly_fragment
clone_end:SP6
                                                                                                                                                          /clone="RP11-45I20"
/clone_lib="RPCI-11 Human Male
                                                                                                                                                                                                                                       /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                .41619
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                                                                                                                                                               BAC*
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                                                                             COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35549 ATGATGGTGTTTTTGTTCTTTTGTGGGGACTGAGGTGG 35511
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Boguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Canpopiano, A., Costie, A., Choepel, Y., Cohangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Donino, M., Doyle, M., Ferreira, P., Fitzhigh, M., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, M., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Grand-Pierre, M., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Klein, J., LaBorque, K., Lamazares, R., Landers, T., Leboczky, J.,
Klein, J., LaBorque, K., Lamazares, R., Landers, T., Leboczky, J.,
Levine, R., Lieu, C., Lilu, G., Locke, K., Macdonald, P., Marquis, N.,
Levine, R., Lieu, C., Lilu, G., Locke, K., Macdonald, P., Marquis, N.,
Levine, R., Lieu, C., Lilu, G., Locke, K., Macdonald, P., Marquis, N.,
Levine, R., Lieu, C., Lilu, G., Locke, K., Macdonald, P., Marquis, N.,
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Levine, R., Lieu, C., Lilu, G., Locke, R., Macdonald, P., Marquis, N.,
Levine, R., Lieu, C., Lilu, G., Locke, R., Macdonald, P., Marquis, N.,
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Levine, R., Lieu, C., Lilu, G., Locke, R., Macdonald, P., Marquis, M.,
Levine, R., Lieu, C., Lilu, G., Locke, R., Macdonald, P., Marquis, M.,
Levine, R., Lilu, G., Locke, R., Macdonald, P., Lander, M.,
Levine, R., Lilu, G., Locke, R., Marquis, M.,
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Levine, R.,
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Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 14, 2000 this sequence version replaced gi:11181821.
All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                        Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tiglino, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Tiglino, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Mu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                             roung, G.,
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117756. .155804
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47645. .59936
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clone_end:T7
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                                                                                                                                                                                                                                                                                                                    Zainoun, J., Zimmer, A. and Zody, M.
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Percent Identity: 61.538
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BASE COUNT
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Center clone name: 22_F_15

Sequencing vector: M13; M78113; 3% of reads
Sequencing vector: Plasmid: n/a; 97% of reads
Consensus quality: 157651 bases at least 040
Consensus quality: 158950 bases at least 040
Consensus quality: 158950 bases at least 020
Consensus quality: 159930 bases at least 040
Consens
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http://ftp.genome.washington.edu/RM/RepcatMasker.html
                               49637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11466 11565; gap of 100 bp
11566 22290; contig of 11355 bp in length
22921 23020; gap of 100 bp
22921 23020; gap of 100 bp in length
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85808 160294: contig of 74487
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43186 85707: contig of 43522 bp in length
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29398 c 29387 g 51172 t
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85808. .160294
                                                                                                                                                                                                                                                                                                                                                                    5890
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43186. .85707
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23021. .43085
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11566, ,22920
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /note··"assembly_fragment"
2277. .5789
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clone_end:SP6
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/db_xref="taxon:9606"
/clone="RP11-29E15"
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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alignment_block:
US-09-471-276-831_COPY_1_16 x AC025621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_htg:AC073872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 53.00
Ratio: 5.300
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AC025621 from: 1 to: 160294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66325 CTTTTTCTAATTCTGTGGGGAATTACATGG 66354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValPheLeuLeuTrpGlyValThrTrp
                                                                                                                   Submitted (30-JUN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC073872 162080 bp DNA HTG 15-JUL-20 HOMO sapiens chromosome 12 clone RP11-546D23, WORKING DRAFT
Center code: WUGSC
                    Center: Washington University Genome Sequencing Center
                                                                                                 MO 63108, USA
                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                Waterston, R.H.
                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                         The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                          1 (bases 1 to 162080)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC073872
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC073872.1 GI:8844170
                                                                                                                                                                                                                           (bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162080 bp
                                                                                                                                                                                                                        to 162080)
                                         Genome Center -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                          Louis
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Chemistry bye-primer ET; 100% of reads
Chemistry bye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0,900319
Consensus quality: 15231 bases at least 040
Consensus quality: 15231 bases at least 030
Consensus quality: 15107 bases at least 030
Consensus quality: 15107 bases at least 030
Insert size: 160680; sun-of-contigs
Ouality coverage: 4.54 in 020 bases; sun-of-contigs
Quality coverage: 4.54 in 020 bases; sun-of-contigs Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0% Center project name: H_NH0546D23 Web site:http://genome.wustl.edu/gsc/index.shtml consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will NOTE: This is a 'working draft' sequence. It currently be preserved 1867 1967 3660 3760 5684 5784 3659: 3759: Project Information gap of unknown contig of 1924 is gap of unknown contig of 2525 is contig of 1866; gap of unknown contig of 1693 length bp in length bp in length bp in length bp in length length

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FEATURES
alignment_block:
US-09-471-276-831_COPY_1_16 x AC073872
                                                                           alignment_scores:
Quality:
                                                                                                                                       BASE COUNT
ORIGIN
                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                      53242
                                                                Ratio:
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105579
120821
120921
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8409
12810
12910
12910
22138
22238
21507
31607
40675
40775
51623
51723
51723
61564
61664
61664
61664
61664
61664
77410
91452
91552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="massembly_name:Contig6"
8409, .12809
                                                                                                                                                                                                                                              /note="assembly_name:Contig14" 91552. .105478
                                                                                                                                                                                                                                                                                                                                                                     clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                  vector_side:left*
40775. .51622
                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                               31607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig8"
22238. .31506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig7"
12910, .22137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig4"
3760. 5683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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                                              53.00
4.417
80.000
                                                                                                                                                    /note="assembly_name:Contig17"
28804 c 27772 g 50759 t
                                                                                                                                                                                   /note="assembly_name:Contig16"
120921. .162080
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77510. .91451
                                                                                                                                                                                                                                                                                                           61664
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1967. 3659
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51622 counting of 10848 bp in length
51722 gap of unknown length
61633 counting of 9841 bp in length
61633 gap of unknown length
61633 gap of unknown length
77409 counting of 13746 bp in length
77509; gap of unknown length
91451: counting of 13942 bp in length
91451: counting of 13942 bp in length
91551: gap of unknown length
105478; counting of 13947 bp in length
105478; counting of 15242 bp in length
120920; gap of unknown length
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22237
31506
31606
40674
40774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               .40674
                                                                                                                                                                                                                                                                                                         .77409
                                       Length: 15
Gaps: 0
Percent Identity: 53.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
of 9068
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unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 4401
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seq_documentation_block:
ID AC011936 standard
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Birren B., Linto
"Homo sapiens, o
"Hopublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren B., Linton L., Nusbaum C., Lander E., Allen N., Anderson M.,
Baldwin J., Barran N., Beckerly R., Boguslawky L., Boukhgalter B.,
Brown A., Castle A., Colangelo M., Collins S., Collymore A., Cooke P.,
DeArellano K., Dewar K., Domino M., Donelan L., Doyle M., Ferreira P.,
Eltzhugh W., Forrest C., Funke R., Gage D., Galgan J., Gardyna S.,
Grant G., Hagos B., Heaford A., Horton L., Howland J.C., Johnson R.,
Jones C., Kann L., Kartatas A., Klein J., Leboczky J., Lieu C., Locke K.,
Macdonald P., Marquis N., McEbwan P., McGurk A., McKernan K., McLaughlin J.
Meddrin J., Morrow J., Naylor J., Norman C.H., O'Connor T., O'Donnell P.,
Tirrell A., Wassiliev H., Vo A., Wheeler J., Wu X., Wyman D., Ye W.J.,
Tirrell A., Wassiliev H., Vo A., Wheeler J., Wu X., Wyman D., Ye W.J.,
Assembly program: Phrap: version 0.960731
Consensus quality: 13371 bases at least Q30
Consensus quality: 152498 bases at least Q30
Consensus quality: 15555 bases at least Q20
Insert size: 170000; agarose-fp
                                                                                                                                                                                                                                                                                                            On Feb 28, 2000 this sequence version replaced g1:6479009 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-OCT-1999) to the Whitehead Institute/MIT Center Cambridge, MA 02141, USA
                                                                                        Sequencing vector: M13; M77815; 100
Chemistry: Dye-terminator Big Dye;
                                                                                                                                             Center project name: L3520
Center clone name: 16_D_24
                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                 Center code: WIBR
Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens clone RP11-16D24, WORKING DRAFT SEQUENCE, 19 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-1999 (Rel. 61, Created)
03-MAR-2000 (Rel. 62, Last updated, Version 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC011936.4
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                                                                                                                                                                                ----- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_htg_hum:AC011936
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ens, clone RP11-16D24";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; HTG; 165689 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebra
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases. for Genome Research, 320 Charles Street.
                                                                                     100% of reads
ye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 162080
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                                                                                                                                                                                                                                                          tor Genome Research
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J.,

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Insert size: 163889; sum-of-contigs
Ouality coverage: 3.8 in Q20 bases; agarose-fp
Ouality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                              misc_feature
         misc_teature
                               misc_feature
                                                 misc_feature
                                                                      misc_teature
                                                                                         misc_feature
                                                                                                                                                     misc_teature
                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 19 conties the true order of the pieces is not known and their order in this sequence record is arbitrary daps between the conties are represented as runs of N. but the exact sizes of the paps are unknown. This record will be updated with the finished conknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                        40126 48025; gai

40126 48125; gai

48126 57772; gai

57673 8675;

6773 8675;

6773 8675;

6774 8635; gai

6774 8284;

6774 8284;

6775 9685;

9675;

96857 118840;

118841 118940;
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12786
12886
16978
17078
17078
22034
22134
26598
31120
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                                                                                                                                                                                                                                                                                                                                                                                                   40026
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                                                                                                                                                                                                                                                                                                                                                              96856: gap of 100 bp
118840: contig of 21984 bp
                                                                                                                                                                                                                                                                                                                         68863: gap of 100 bp
82748: contig of 13885 bp
                                                                                                                                                                                                                                                                                                                                              57772: gap of 100 bp
68763: contig of 10991 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12885: gap of 100 pl
16977: contig of 4092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9988: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                         31219:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 26697: gap of 100 bp
31119: contly of 4422 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17077: gap of
                                                                                                                                                                                                                                                        142301: cr
                                                                                                                                                                                                                                           165689: contig of 23288
                                                                                                                                                                                                                                                                                                       96756: contig of 13908 bp
                                                                                                                                                                                                                                                                                                                                                                                                                             35831: contly of 4612 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26597:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22033: contig of 4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8: gap of 100 bp
12785: contig of 2797 bp
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9989 .12785
                                                                                         /note-"assembly_fragment"
6350. .9888
                                                                                                                                /note-
1459.
           /note: "assembly_fragment"
22134. .26597
                             /noter assembly_fragment 17078. . 22033
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/note…"assembly_fragment~clone_end:T7~vector_side:right"
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12886. .16977
                                                                                                                                                               /clone_lib~"RPCI-11 Human Male
                                                                                                                                                                         /organism∽"Homo sapiens"
/clone∴"RP11-16D24"
                                                                                                                                                                                             /db_xref·"taxon:9606"
                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                            contig of 23361 b
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                                                                                                                                          assembly_fragment"
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Direct Submission
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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AC013707.2 GI:7212036
HTG; HTGS_PHASE1; HTGS_DRAFT
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142402. .165689
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48126. .57672
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40126. .48025
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RP11-22L6, WORKING DRAFT
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Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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                                                                51366
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Assembly program: Phrap; version 0 960731
Consensus quality: 16375 bases at least 040
Consensus quality: 164944 bases at least 020
Consensus quality: 164950 bases at least 0
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Center clone name: 22_L_6
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Insert size: 165749; sum-of-contigs
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79157 166349: contig of 87193
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1215 2270: contig of 1056 bp
2271 2370: gap of 100 bp
                                             79157. .166349
/note="assembly_fragment"
a 31182 c .30388 g 52813
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clone_end:SP6
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2371. ,3468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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US-09-471-276-831_COPY_1_16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boukhgalter, B., Brown, A., Burkett, G., Campopiaño, A., Câstle, A., Chepelly, Collangelo, M. Collins, S., Collymore, A., Cooke, P., Chepelly, Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArtellano, K., Diazz, J. S., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Geror, P., Fitzhylh, W., Forrest, C., Gage, D., Callen, J., Gardyna, S., Ginde, S., Goyette, M., Garbam, L., Grand-Pletre, M., Grand, G., Horton, L., Grand-Pletre, M., Grand, G., Horton, L., Grand-Pletre, M., Grand, G., Horton, J., Lauge, L., Lauge, L., Lauge, C., Kann, L., Kartes, A., Klein, J., Lauge, C., Liu, G., Locke, K., Macdonald, P., Margus, M., Mareneus, J., Lauge, T., Milbora, T., Milanda, C., Milora, M., Milanda, C., Milora, M., Milanda, C., Milanda, C., Milora, M., Milanda, C., Milora, M., Milanda, C., Milanda, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Jun 11, 2001 this sequence version replaced gi:12583848 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, M., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Stevery, P., Spencer, B., Stange-Thomann, M., Stojanovic, N., Storamanian, A., Talamas, J., Tesfayo, S., Theodore, J., Tirroll, A., Travers, M., Triglilo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 168208)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-272P15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                Center project name: L5830
Center clone name: 272_P_1
                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Research
Sequencing vector:
                                                                                                                                                                                          ------ Project Information
      ------ Summary Statistics equencing vector: M13; M77815; 5% of reads
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                                                                                                      272_P_15
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70.000
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Sequencing vector: Plasmid; n/a; 95% of reads

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alignment_block:
US-09-471-276-831_COPY_1_16 x AC024359
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                                                                                                                     seq_documentation_block:
LOCUS AC023569 1
                                                                                                                                                                                                                                                      seq_name: gb_htg:AC023569
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                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ValPhcLcuLeuLeuTrpGlyValThrTrp 15
HTG 06-APR-2000 HOMO sapiens chromosome 18 clone RP11-513M1 map 18, WORKING DRAFT SEQUENCE, 17 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 168000; agarose-fp
Insert size: 168000; agarose-fp
Oublity coverage: 5,7 in 020 bases; agarose-fp
Oublity coverage: 7,7 in 020 bases; agarose-fp
Oublity 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8590 8899; cantig of 85799 bp in length 85800 8899; gap of 100 bp p in length 98590 9674; cantig of 10715 bp in length 96715 96714; cantig of 10715 bp in length 116317 116416; gap of 100 bp in length 116317 116416; gap of 100 bp 11 length 116316 11845; gap of 100 bp in length 141846 118429; gap of 100 bp in length 141846 118429; cantig of 26365 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
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96715. .116316
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31238 c 30497 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Claries Street, Cambridge, Mr. 02141, US. 00, Apr 6, 2000 this sequence version replaced g1:6978265.
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Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 513_M_1
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1001 1130; gap of 100 hp in length 1131 2617; contig of 1487 bp in length 2618 2717; gap of 100 hp 2718 2750; contig of 2392 bp in length 5110 5209; gap of 100 hp
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7360 88118: gap of 100 bp
88115 10366; contig of 1527 bp in length
10362 103761; gap of 100 bp
10362 103761; gap of 100 bp
103762 134075; contig of 30314 bp in length
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134076 134175: gap of
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1335 13494: gap of
1345 17701: contig of 4207 bp in length
17702 17801: gap of
17802 22017: contig of 4216 bp in length
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44883 58944: contig of 14062 bp in length
58945 59045 gap of 100 bp
59945 73159: contig of 14115 bp in length
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34370 44782: contig of 10413 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="18"
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13394: contig of 2280 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8324: contig of 3115 bp in length
8424: gap of 100 bp
11014: contig of 2590 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25803: contig of 3686 bp in length
903: gap of 100 bp
34269: contig of 8366 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 8324
                                                                                                                                                                                                                                                                                                       .44782
                                                                                                                                                                                                                                                                                                                                              .34269
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ORIGIN
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KEYWORDS
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LOCUS AC092580 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                     Sequencing vector: plasmid: 63%
Chemistry: Dye-primer EF: 2% of reads
Chemistry: Dye-terminator Big Dye; 900319
Consensus quality: J1107 bases at least 040
Consensus quality: J1167 bases at least 030
Consensus quality: J11757 bases at least 030
Consensus quality: J1777 bases at least 030
Consensus quality: J1777 bases at least 030
Timert size: 185000: agarose-fp
Owality coverage: 9.86 in 020 bases: narrose-fp
Owality coverage: 9.86 in 020 bases: sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
Mo 63108, USA
On Jul 19, 2001 this sequence version replaced gi:7107944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                      * arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13: 37%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0016D24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                             * NOTE: This is a 'working draft' sequence. It currently 
* consists of 5 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
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as soon as it is available and the accession number will be preserved.
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4.818
73.333
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Genome Center ---

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US-09-471-276-831_COPY_1_16 x AC023569
                                                                                                                                                                                                                                                                                                                                                            166598 TCAATGCTGTATATCTTTCTTAGTTTGGAGAAGCCAGTGGGGT 166642
                                                                                                                                                                                                                                                                                                                                                                                           2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172005)
                                                                                                                                                                                      AC092580 AC011936
                                                                                                                                                                                                                               Homo sapiens chromosome
The sequence of Homo sapiens clone
                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                           unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32780 c
                                                                                                                                                                                                                                                172005 bp
                                                                                                                                                                  GI:14916165
                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 169607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33552 g
                                                                                                                                                                                                                               DNA HTG
2 clone RP11-16D24,
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0
60.000
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VERSION
KEYWORDS
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US-09-471-276-#31_COPY_1_16 x AC092580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS AC016080 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39818 GTGCTCTTGCAATTTCTAAGTCTTTGGGGGTGTTCTTTGGGGG 39859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly
Baldwin, J., Barna, M., Beckerly, R., Bogusiavky, L., Boukhgaller, B., Allen, M., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Bogusiavky, L., Boukhgaller, B., Brown, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., Dearlellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrett, P., FitzHugh, M., Forrest, C., Bunke, R., Gege, D., Horton, L., Galdagn, J., Gardyna, S., Grant, G., Heos, B., Hestorda, A., Horton, L., Hobland, J., Candyna, R., Jones, G., Kann, L., Karatas, A., Klein, J., Kebana, P., McGurk, A., McKennan, K., McLanghin, J., McHarler, C., Locke, R., McConnor, T., Obonell, J., McGurko, J., Norman, C. H., O'Connor, T., O'Donnell, J., McGurson, K., Bollara, V., Klaylor, Santos, R., Severy, P., Severy, P.
                                                                                                                                                                                                                                                                 1 (bases 1 to 176921)
Birren, B., Linton, L., Nusbaum, (
Homo sapiens, clone RP11-23N14
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC016080 176921 bp DNA PRI HOMO Saplens, clone RP11-23N14, complete sequence
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC016080.5 GI:14017515
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1554
2881
2981
7451
7551
67266
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67366. .172005
/note, "assembly_name:Cont1g24"
1 34632 c 35587 g 50224 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"assembly_name:Contig22
clone_end:T7
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4.818
78.571
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7551. .67265
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2981. .7450
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/db_xref."taxon:9606"
/chromosome."2"
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67265: contig of 59715 bp in length
67365: gap of unknown length
172005: contig of 104640 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2980: gap of unknown length
7450: contig of 4470 bp in length
7550: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 172005
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Gaps: 0
Percent Identity: 64.286
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                                                                                                                                                                                                                                                                                                                 Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L4401
Center clone name: 23_N_14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Whitehead Institute/ MIT Center for Genome Research
                                               /rpt_family~"(TA)n"
4084. .4214
                                                                                                                                                                                                                                                                                                                                                          /rpt_family~"MIR" complement(1027. .
                                                                                            /rpt_family~"L1MC1"
3742. .3821
                                                                                                                                         complement (2756.
                                                                                                                                                                                /rpt_family-"MLT2B1" complement(2440. .27
                                                                                                                                                                                                                             complement(1594.
                                                                                                                                                                                                                                                                                                                                                                                                       complement(703
                       /rpt_family-"L2"
                                                                                                                                                           /rpt_family…"AluJb"
                                                                                                                                                                                                                                               /rpt_family="(CA)n"
                                                                                                                                                                                                                                                                       /rpt_family="MLT-int"
1551. .1591
                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family-"AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib. "RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone-"RP11-23N14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref…"taxon:9606"
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Barra N. Bastich, V. Boguslavky L. Boukhgilter B. Brown A.

Commercia J. Compopiano A. Changy J. Choopel Y. Colangelo M.

Collins S. Collymore A. Cooke P. DeArelland P. Colangelo M.

Collins S. Collymore A. Cooke P. DeArelland R.

Disz J. S. Dodge S. Paro S. Perreira P. Pittelligh M. Gage D.

Galagan J. Gardyna S. Ginde S. Gogette M. Groban H.

Grad Pitter N. Hagos B. Haford A. Horton L. Hilme M.

Illoy J. Johnson R. Johnson S. C. Kratas A. Lacince, Liu G.

Haczares R. Landers T. Tebocky J. Levince, R. Liu G.

Haczares R. Landers T. Tebocky J. Hedirim J. Heneus L.

Hechan P. McKernan K. Hophseters R. Hedirim J. Heneus L.

Hibora T. McKernan K. Hophseters R. Hedirim J. Heneus L.

Hibora C. H. O'Gon T. D'Oonell P. Colly D. Golver J.

Hetta R. Heback, R. Biley, R. Rise C. Rogov P. Romen J.

Peterson K. Heback M. Riley, R. Rise C. Rogov P. Romen J.

Peterson K. Heback M. Struss B. Stohaut S. Schupback R. Seaman S.

Stolaylor J. Sounce C. Spence B. Stange Thoman J. Teafaye S.

Stolaylor J. Rowser B. W. Stone Thoman J. Teafaye S.

Precond J. J. Wilson B. Hu X. Hymen D. Ye M. J. Young G.

Zanbak I. J. Zambak J. J. Limer A. and Zody M. Ye M. J. Young G.

Stolaylor J. J. Wilson B. Hu X. Balling M. Ye M. J. Young G.

Zanbak J. J. J. Limer A. and Zody M. Ye M. J. Young G.
Submitted (30-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02114, USA (100 May 10, 2001 this sequence version ceplaced gi:13357421.
All repeats were identified ssing RepeatMasker:
smit, A.F.A. & Green, P. (1936-1937)
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/rpt_family=""."
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/rpt_family="L2"
16941. 16964
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complement(12516. .13835)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="<30 qual SNGL region"
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                                                                                                                                                                                                                                                                                                                                            rpt_family-"AT_rich"
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2, .16017
                                                                                                                                                          _ramily="AluSx"
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                                                                    _family="L1ME3"
|ement/2020;
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US-09-471-276-831_COPY_1_16 x AC016080
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                                             Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromasomes 3. 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thai/this fragment has an overlap with ATCHRIV39 at the 5' end and an overlap with ATCHRIV39 at the 5' end.
                                                                                                                                      Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 1Ba, D-82152 Martinsried, FRG, E-mail: Lencke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                Arabidopsis thaliana Arabidopsis thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. | (beses 1 to 19746) | (beses 1 to 19746) | EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCHRIV40 197405 bp DNA PLN 16-MAR-2) Arabidopsis thaliana DNA chromosome 4, contig fragment No. ALIG1540
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22737. . 22790
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               Location/Qualifiers
1. .197405
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22875. .22905
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Gaps: 0
Percent Identity: 70.000
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exon	intron	exon	Intron	exon	intron	exon	intron	exon	Intron	exon	intron	exon	intron		exon	intron										Coo	Cpe	e e		gene	exon		
complement(1028610349) /gene.*MY4g14790* /number-9	complement(1016310285) /number·8	complement(988310162) /gener*Kr4g14790*	/number-7 /number-7	complement(96189739) /gene "AT4g14790"	complement(95409617) /number-6	complement(9299539) /gener.AT4g14790* /number.A		complement(91269246) /gene-*A74914790* /numbers	complement(90079125)	Complement(88849006) /gene-*MY4914790*	/ number: 3 complement (86998883)	complement(86218698) /gener*A14914790"		4	complement(83638531)	complement(82818362)	LPPETRAQATRRUDETNOFOULASDAIGNOGLINGINST LIFTURKTORIDET VS LPPETRAQATRRUDETNOFOULASDAIGNOGLINGINST LIFTURKTORSETROLTV SEIKQIAGRAGREQSKFPIGEVTCLHKEDLPLLHSSLKSPSPILEANIAH*	PERULAMBEMAN KINNAN WELDILI TOGENDIA BEGITTIKAN YI PENGUYI SYI DILAI IDEI QASILARIMILKKSTRTFCIGFAFTRALIGIANDELHLIGODPA VVPLVEDILIKUTGODVE VHYVEHI SELVELIKUTGODVE	TGTTSKFOFTDLTCPHTWY DARKKRKVILHVGARTUSKALKHLEGGATTGTT BI BI AMEDIATE HIVANIVEGTA TTGGFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	/protein_id-"CAB78521.1"	/codon_start 1	Contains ATP/GTP-binding site motif A (P-loop) AA136-143;EF-hand culcium-binding domain AA383-395"	/note: "similarity to probable RNA helicase SUV3, ATP-dependent, yeast (Saccharomyces cerevisiae)	1028610349)) /gene-"AT4g14790"	8884. 9006,9126. 9246,9299. 9539,9618. 9739,9883. 10162,	9290 9262 9521 9621	6884. 9006,9126. 9246,9299. 9539,9618. 9739,9883. 10162, 10286. 10346,9126. 10346,9299. 10386. 10386. 103883. 10382,	/gene."A714g14790"	/number:1 815010349	complement(81508280) /gcnc:"AM4g14790"	/db_xref."taxon:3702" /chromosome."4"	/organism·"Arabidopsis thaliana" /varicty·"Columbia"
exon	intron	exon	intron		PKO	intron	exon	intron	reneat region					CDS	Action	2000	exon	exon		intron	600		intron								CDS	exon	gene
/number-4 15348 15365 /gene · AT4914810*	/gene-"AT4q14810"	15165. 15253 /gene-^AP4914810* /number-4	1370315164 /genew.RT4g14810" /number:-3	7.5	/gumber=2 /number=2 13550 13700	/number-2 13502 .13558	/gene	13043 13393 /gene-"AT4914810"	DGGGSQLG INVNETQALALPKACHVETPPASRCHSK INSLSMH** 13001 13024	/ VICTORS 14 TO 1.7 MOVE 2007 / VICTORS 14 TO 100 VICTOR WHIT VICTOR VIC	/product~"Nypothetical protein" /protein_id~"CAB78523.1" /ab voct."rr.7589337"	contains EST gb:AA042489, AI998638.1, T88290* /codon_start~1		join(1292813042,1339413501,1355913702,1516515253, 1534815365,1584615983)	/qene-"AT4q14810"	/number-1	/number-5 12928 13042 /dene-7/T4014810*	/geneAT4g14800"	.7.2	/number-z 11291. 12260 /non-s-mart/14800*	/gene=AT4g14800"	/number-1	1107611166 /genec-"AT4g14800"	MAGYDKEAGASLYYIDYIATLHKYDKGAFGYGSYFSLSTMDRHYRSDMSVEEAIELVD KCILEIRSRLVIAPPNFVIKIVDKDGAREYGWRISTADA*	/translation~"MECVFGLVGNGFAIVAADTSAVHSILLHKNKEDKIMTLDSHKLV AASGEPGDRVQFTEYVQKNVSLYQFRNGIPLSTAAAANFTRGELATALRKNPYSVNIL	/protein_id="CAB/8522.1" /db_xref="GI:7268226"	/product. Protessome chain protein*	CONTAINS EST 9D:A1933/3:1, 109359, R65485, T2212/, F13874"		ng similarity to proteasome o	/number··1 join(1091811075,1116711290,1226112578)	1091B11075 /gene-"AT4g14800"	10918 12578 /gene^Ar4g14800"

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REFERENCE
AUTHORS
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US-09-471-276-831_COPY_1_16 x ATCHRIV40
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ORGANISM
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LOCUS ATFCA2 2
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                                                                                                                                                                               AUTHORS
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                     schuelleemips blochem.mgg.de,mayer@mips.blochem.mgg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 70J Worwich, UK,
                                                                                Direct Submission
Direct Submission
Submitted (25-UN-1999) MIPS, at the Max-Planck-Institut fuer
Submitted (25-UN-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                                                                                                                                                                                                                                                  Bevan, M., Stiekema, M., Murphy, G., Wambutt, R., Pohl, T., Teryn, Kreis, M., Kavanach, T., Entian, K.D., Rieger, M., James, P., Phildomenech, P., Hatzopoulos, P., Obermaier, B., Duesterhöft, A., Jones, J., Palme, K., Masorqe, W., Delseny, M., Bancroft, I., Meees, H. W., Schueller, C. and Chalwatzis, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATFCA2 202860 bp [Arabidopsis thaliana DNA
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachephyta;
Spermatophyta; Hagnotlophyta; eudicotyledons; core eudicots
Spermatophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis,
   E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                        EU Arabidopsis sequencing, project.
                                                                                                                                                                                                                             Unpublished
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attachment site AA252-582: Prokaryotic membrane lipoprotein
lipid attachment site AA344-354: Prokaryotic membrane
lipoprotein lipid attachment site AA513-523
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Gaps: 0
Percent Identity: 63.636
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COmplement(joln(1563), 1584),16271,16328,16682,1631

16815,17057,17098,17157,17295,17739,18223,18333,
                                                                                                                                                                                                                                                                                                                                                 PENROJLLSKYEDEEEEEPISKYLOGGÖDEDYGLYKGNPFSFAGSEYSQAWIDRILS
TAATEG TYATAGSKYUGHELDEEEEEPISKYLOGGÖDEDYGLYKGNPFSFAGSEYSQAWIDRILS
TAATEG TYATAGSKYUGHELDEEEKKEEFFRAHNOJHAAUSLUKUANANANA
TAASSOGGIDEDAMATUDANASAATIJAAOCUFSAAFINGAESTLASVYSSAAVANIKS
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SOGJUFTITAGAATDINSGIDLGIGSKLELYEBITTIKGVOTILAAKHEEWILASVITH
SOKLITSTGSSNINKUSSASSSSISGELVOOENFILOTGSBALAACGULATRIKKOO
SKLITSTGSSNINKUSSASSSSSISGELVOOENFILOTGSBALAACGULATRIKKOO
SKLITSTGSSNINKUSSASSSSSISGELVOOENFILOTGSBALAACGULATRIKKOO
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glutamate-binding chain, rat"
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                                          complement(16732.
                                                                         /number=3
                                                                                              /gene-"dl3410c"
                                                                                                                                                                     complement(16329.
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/varlety="Columbia"
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                                                                                                                                                                                                                             'gene="d13410c"
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36297. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MCKTSKWFRSLLTGKKERTKEHIIQSECVFTSSIPGTPKEKRRW
SFRRSSATGPPPDACLITLKUSPPPPPPPPPPPPPPVEIVONEDSGIKNYSAES
IEEPAALKIQOV;PSHELBNEBLK V ZEMDOSKMWSAPSPASLTEMSPBAKSSIPEDCON
SFNTAQSSPQCFSRFKEYYNGDTLSSYDYPLFPNYMANTQSSKAKARSQSAPKQRPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"d13415w"
/note-"weak similarity to actin-depolymerizing protein
N_WASP, brain, bovinc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"45bp AT tandem repeat" 34748. .34771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(17098.
/gene-"dl3410c"
/number-5
                                                                                          /note:"similarity to centromere protein E (kinesin-related
protein CENP-E) - human"
                                                                                                                          /genen d13420w"
join(41035, .45039,45135, .46160)
/genen d13420w"
                                                                                                                                                                                                                                41035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /producto"hypothetical protein"
/protein_id "CAB10254.1"
/db_xrefn"GI:2244832"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="24bp CA tandem repeat"
35515. .36969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gener"dl3410c"
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/number-4
                                             /product."centromere protein
/protein_id."CAB10255.1"
                                                                                                                                                                                                                                                                                36943
                                                                                                                                                                                                                                                                                                                              36858
                                                                                                                                                                                                                                                                                                                                                                                                                             35872
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IYEKOMSGRRRSSMEAPRNNGVPRAVRMORSSSOLGSNTAKESQQHHHHQYYPWMAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="dl3415w"
35515. .35871
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/translation-"MDSKVKTMIKLIEADADSFARRADMYFKKRPELMKLVEELYRAY
             db_xref-"SPTREMBL:023332"
                             /db_xref- "GI: 2244833"
                                                                               /codon_starto
                                                                                                                                                                                              /number
                                                                                                                                                                                                            /gene--"d13420w"
                                                                                                                                                                                                                                            number 3
                                                                                                                                                                                                                                                            /gene-"d13415w"
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                                                                                                                                                                                                                                                                                                           /gene~"d13415w"
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                                                                                                                                                                                                                                                                                                                                                                                                           /gene" d13415w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number-5
                                                                                                                                                                                 .46160
                                                                                                                                                                                                                                                                                .36969
                                                                                                                                                                                                                                                                                                                              .36942
                                                                                                                                                                                                                                .45039
                                                                                                                                                                                                                                                                                                                                                                                .36857
                                                                                                                                                                                                                                                                                                                                                                                                                             36296
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RALLER PEDHAC STEEL KANDER PROJESTEM LEGGORDE STATULKE RESURS SESSE PREADTRALAGON EN AGRESSES TO STANDAY CALLES WERE STATULKED TO STANDAY CALLES AGRESSES AG
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JOURNAL
REFERENCE
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ORGANISM
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LOCUS AC090737 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-471-276-831_COPY_1_16 x ATFCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 53.00
Ratio: 4.818
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ValValPheLeuLeuTrpGlyValThrTrp 15
Dodgé, S., Faro, S., Porreira, P., FitzHugh, M., Cago, D., Callagan, J.,
Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N.,
Hagos, B., Heaford, A., Hotton, L., Hulme, W., Illev, I., Johnson, R.,
Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T.,
Labozzky, J., Lavine, R., Liu, C., Hecken, C., Macdonald, P.,
Marquis, N., Hatthews, C., McCerrhy, M., McBenan, McKernan, K.,
McCheeters, R., Meddin, J., Manuas, L., Milova, T., Mlands, V.,
McCheeters, R., Meddin, J., Manuas, L., Milova, T., Mlands, V.,
                                                                                                                                                                                                                               2 (bases i to 214/46)
Birran B, Linton L. Nasbaum, C., Lander, E., Allen, N., Anderson, S.,
Barna N., Bastien, V., Boguslavkiy, L., Boukhpaller, B., Broom A.,
Cambasta J., Campopiano A., Choepel V., Collangelo, M., Collins S.,
Collymore, A., Cooke, P., peare llano, K., Dewar, K., Disz, J.S.,
Collymore, A., Cooke, P., peare llano, K., Dewar, K., Disz, J.S.,
Collymore, A., Cooke, P., peare llano, K., Dewar, K., Disz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi; Mammalia; Eutheria; Primartes; Catarrhin; Hominidae; Homo.
1 (bases 1 to 214146)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone CTD-2542M11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC090737.2 GI:14210585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214146 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 11
Gaps: 0
Percent Identity: 63,636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WORKING DRAFT
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Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Pete

Peterson, K.,

COMMENT

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FEATURES
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misc_feature
                                                           misc_feature
                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                   source
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Strauss.N., Subramanian,A., Talahas.J., Tesdaye,S., Theodore,J.,
Travers.M., Travis.N., Trigillo,J., Vassillev,H., Viel,R., Vo.A.,
Milson,B., Nu,X., Wyman,D., Ye,M.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer.A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 7 contides The ture order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      All repeats were identified using RepeatMasker:
Smlt, A.F.A. & Green, P. (1966-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Roy, A., Santos, R., Schauer, S., Schupback, R., Seama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phunkhang, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1433 1582; gap of 100 bp
1583 11395; contig of 9813 bp in length
11396 11495; gap of 100 bp bp in length
11496 24222; contig of 12797 bp in length
24293 2232; gap of 100 bp
24393 24392; gap of 100 bp
45184 45283; gap of 100 bp
45184 45283; gap of 100 bp
45284 96515; contig of 1732 bp in length
95616 244446; contig of 117531 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 210000; agarose-fp Insert size: 213546; sum-of-contigs Outlity coverage: 7.5 in 020 bases; Quality coverage: 7.4 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap: version 0.660731 Consensus quality: 210578 bases at least 040 Consensus quality: 212578 bases at least 020 consensus quality: 313256 bases at teast 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       687 786: gap of
   /note="assembly_fragment"
24393. .45183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (09-MAR-2001) whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA, 2001 this sequence version replaced gi:13259456.
                                                                                   /note="assembly_fragment"
                                                                                                                   /note="assembly_fragment"
1583. .11395
                                                                                                                                                                                               /note-"assembly_fragment"
                                                                                                                                                                                                                                                           /clone_lib="CITD Human BAC"
                                                                                                                                                                                                                                                                                           /clone="CTD-2542N11"
                                                                                                                                                                                                                                                                                                                                               /chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism≖"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pierre, N., Pollara, V., Raymond, C., Retta, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1482: contig of 696 bp in length
                                                                                                                                                                               . 1482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               686: contig of 686 bp in length
                                                           . 24292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosetti, M.,
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
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Bilren, B. Lilton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, M., S., Belren, N., Calsman, N., Deckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cocke, F., Dearelland, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, N., Cardyna, S., Gardyna, S., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Hotton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karetas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McRernan, K., McRernan, K., McReylan, P., McGurk, A., McKernan, K., McLaughlin, J., McHarlan, J., McMernan, R., Santos, R., Savery, P., Stabge-Thoman, N., Stojanovic, N., Submanian, A., Talamas, J., Wesfaye, S., Tirrell, A., Vassilie, H., Vo, A., Wheeler, J., Wu, X., Weller, J., Wu, X., McKernan, K., Dring, R., Roy, A., Santos, R., Savery, P., Stabge-Thoman, N., Stojanovic, N., Submanian, A., Talamas, J., Willian, M., Wassilie, H., Vo, A., Wheeler, J., Wu, X., Weller, J., Wu, X., Williand, M., Wassilie, H., Vo, A., Wheeler, J., Wu, X., Weller, J., Wu, X., Well
Illiev.I., Johnson.R., Jones, C., Karatas, A., LaRocque, K.,
Lamazaros, R., Landers, T., Lehocky, J., Levine, R., Lilu, G.,
Mcclean, C., Mecdonnid, P., Marquis, N., Methers, C., McCarthy, M.,
McElan, P., McKernan, K., McPheetters, R., Mellerim, J., Meneus, L.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyon, C.; Norbu, C.,
Mihova, T., Mienga, V., Murphy, T., Naylor, J., Waynond, C.,
McEarson, K., Phunkhang, P., Pletre, N., Pollara, V., Raymond, C.,
Peterson, K., Phunkhang, P., Pletre, N., Pollara, V., Raymond, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, R., Allen, M., Anderson, Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Canapopiano, A., Chang, J., Choepel, Y., Colangelo, M., Colliyance, A., Cooke, P., Dearellano, K., Dewar, K., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Collymore, A., Cooke, P., Pitzhugh, M., Gage, D., Calagan, J., Gardynn, S., Gilde, S., Colyette, M., Graham, L., Graham, L., Cooke, C., Calagan, J., Gardynn, S., Gilde, S., Colyette, M., Graham, L., Cooke, C., Calagan, J., Calagan, B., Heaford, A., Botton, L., Hulme, M., Crand, Plate, M., Magos, B., Heaford, A., Botton, L., Hulme, M., Candard, P., Calagan, M., Candard, A., Botton, L., Hulme, M., Candard, A., Botton, L., Hulme, M., Candard, A., Botton, L., Hulme, M., Candard, M., Candard, A., Botton, L., Hulme, M., Candard, M., Candard, A., Botton, M., Candard, M., Candard, A., Botton, M., Candard, M., Can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (27-OCT-1999) Whitehead Institute/NIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 220715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-354A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome
AC012410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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96616. .214146
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45284. .96515
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1 39699 c 39585 g 66718 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220715 bp
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Percent Identity: 70.000
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                                                                                                                                      Norbu,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson, S.
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Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J.,

repeat_region compiement(1210012179)	/rpt_familyo"AluSp	repeat_region complement(11439, .11760)	repeat_region complement(1073910815)	rcpcat_region complement(9451, .9583)			repeat region 8632. 8847	repeat_region complement() 7777)	repeat_region complement(66046888)	repeac_region oitoo399	/rpt_	/rpt_family:"L2"	repeat_region complement(36884201)	repeat_region complement(36133685)	repeat_region complementy: A1rep	repeat_region 3124 .3162	repeat_region 22902316 /rpt_family.~"(GGAAA)n"	repear_region 20042007 /rpt_family~"(TG)n"	7rp	/note. "<30 qual SNGL region" repeat region 1671 . 1701	unsure 902915	unsure 826, 878	ale clone	repeac_region complemenc(709//9) /rpt_family."Lipa4"			/map"8" /clone."RP11-354A3"	/db_xret="taxon:9606" /chromosome=="8"	organism."Homo sapiens"	loc	Center clone name: 354_A_3	Center project Information	Contact: sequence_submissions@genome.wi.mit.edu		Center: Whitehead Institute/ MIT Center for Genome Research	Smit, A.F.A. & Green, P. (1996–1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	All repeats were identified using RepeatMasker:		TITLE Direct Submission JOURNAL Submitted (29-MAY-2001) Whitehead Institute/MIT Center for Genome		Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,	Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Strotanovic, N., Strenger, N., Schramonian, A., Talamar, I., Tesfave, S., Strotanovic, N., Strotanovic, N
	repeat_region	repeat_region		repeat region	repeat_region	repeat_region	repeac_region	rebear_regrou		repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	iòr 6a i Trada i		repeat region	repeat_region	repeat_region	repeat_region	repeat_region	100000000000000000000000000000000000000	repeat region	repeat_region	repeat_region	repeat_region	repeat_region	unsure	repeat_region		repeat region	repeat region	repeat_region	repeat_region	repeat_region	repeat_region	t abear_t ad ton	100000	repeat_region	repeat_region	repeat_region	repeat_region
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KEYWORDS
SOURCE
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LOCUS CET27E9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Mar 30, 1997 this sequence version replaced gi:156020. Coding sequences below are predicted from computer analysis, usi predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome sequence of the nematode C. elegans: a platform for luvestigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998) 99069613
                                                                                                                                     sequence AL032665.
The true right end of clone T27E9 is at 16930 in sequence 292813.
The start of this sequence (1. .104) overlaps with the end
                                                                                                                                                                                                                                                                                                                                dye primer and dye-terminator reaction, from distinct subclones. 
Exceptions are indicated by an explicit note. 
IMPORTANT: This sequence is not the entire insert of clone T27E9
                                                                                                                                                                                                                                                                                                                                                                                                      sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Current sequence finishing criteria for the C. elegans genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-MQV-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. B-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis
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name-T27E9
                For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/acc/clegans/scq/sequence?
                                                                  sequence 292813.
                                                                                          The end of this sequence (22142.
                                                                                                          sequence AL032665
                                                                                                                                                                                                                                      neighbouring submissions.
The true left end of clone T27E9 is at 19189 in
                                                                                                                                                                                                                                                                                 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                     once,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lloyd, C.R.
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(bases 1 to 22245)
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/rpt_family-"THE18"
34573. .34845
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36413. .36768
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                                                                                      .22245) overlaps with the start
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FEATURES

Location/Qualifiers

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EMBL:M99114 comes from this gene; cDNA EST EMBL:Z14645 comes from this gene cDNA EST yebb.5 comes from this gene; cDNA EST EMBL:T00728 comes from this gene; cDNA EST CEMSE14F comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity to bowine ADP/ATP carrier protein (SW:P32007), contains similarity to Pfam domain: PF00133 (Mitochondrial Carrier proteins), Score=382.1, E-value=1.88=111, N-1 CDNA EST EMBL:214700 comes from this gene: cDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /casslation="MSSHKEEPLEADVPQLTQYRERCADHVTEFKSILDECNDRVNSR
SNTEETCHOEMADYWHLLDHCAMRAFASIK"
join(1298. _ 1355,1464. _ 1528,1574. _ 1794,1848. _ 2406)
                                                                                                                                                                                                                                                                                                                                      from this gene cDNA EST yk62h6.: cDNA EST yk62h6.: comes from this gene; cDNA EST yk64g12.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA EST CEMSG56F comes from this gene; cDNA EST yk62e3.3 comes from this gene; cDNA EST yk67e1.7 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMA EST CEMSAAGF comes from this gene; cDNA EST CEMSB32FB comes from this gene; cDNA EST CEMSB59F comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comes from this gene; cDNA EST EMBL: 214655 comes from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA EST yk268b2.5 comes from this gene"
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cDNA EST yk96e10.5 comes from this gene;
                                                        cDNA EST yk84d7.5 comes from this gene; cDNA EST yk89b8 comes from this gene; cDNA EST yk90c1.5 comes from this
                                                                                                                                                   cDNA EST yk75e5.5 comes from this gene; comes from this gene; cDNA EST yk82f9.5
                                                                                                                                                                                                                                               CDNA EST yk67e1.5 comes from this gene; cDNA EST yk67f9.5 comes from this gene; cDNA EST yk75d7.5 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA EST yk96e10.3 comes from this gene; cDNA EST yk60b7.5 comes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA EST yk67f9.3 comes from this gene; cDNA EST yk75e5.3 comes from this gene; cDNA EST yk77g11.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comes from this gene; cDNA EST CEMSE14R comes from this
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/gene=*T27E9.1"
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/db_xref="GI:3880275"
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/chromosome="III"
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                                                                                                                                                                                  cDNA EST yk75e7.5
                                                                                                                                                   comes from this
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obN. EST yk201f4.3 comes from this gene; oby yk201f4.5 comes from this gene; obNA EST yk from this gene; obNA EST yk somes from this gene; obNA EST yk851b5.3 comes from this gene; obNA EST yk871b2.3 comes from this gene; cDNA EST yk864Bh4.5 comes from this gene; cDNA EST yk8666f2.3 comes from this gene; cDNA EST yk8666f2.3 comes from this gene; cDNA EST yk8
(Eukaryotic protein kinase domain). Score:279.8,
E-value:1.1e=80, N:-1
CDNA EST yk101f9, 3 comes from this gene
CDNA EST yk101f9.5 comes from this gene
CDNA EST yk171d8.3 comes from this gene
CDNA EST yk171d8.3 comes from this gene
CDNA EST yk171d8.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA EST yk291c7.5 comes from this gene; yk231e9.3 comes from this gene; cDNA EST from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA EST yk150b7.5 comes from this gene: cDNA EST yk150b7.3 comes from this gene: cDNA EST yk453h1.3 from this gene
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cDNA EST yk172c2.5 comes from this gene;
yk172g6.5 comes from this gene; cDNA EST
from this gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from this geno
CfA EST yK111[3.5 comes from this gene: CDNA EST
yK115g5.5 comes from this gene; cDNA EST yK56[6.3 comes
from this gene
CDNA EST yK94b5.3 comes from this gene; cDNA EST
yK100h10.3 comes from this gene; cDNA EST
                                                                                                                                                                 /gene.wrg2789.3"
//gene.wrg2789.3"
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                                                                                                                                                                                                                                    complement(join(2885. .2971,3024. .3104,3505. 3691. .4144,4190. .4278,4326. .4362))
                                                                                                                                                                                                                                                                                     /gene-"T27E9.3"
                                                                                                                                                                                                                                                                                                        complement(join(2885. .2971,30
3691. .4144,4190. .4278,4326.
                                                                                                                                                                                                                                                                                                                                                        GIAQVVTVGSGILSYPWDTVRRRMMQSGRKDILYKNTLDCAKKIIQNEGMSAMFKGA
LSNVERGTGGALVLAIYDEIQKFL"
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FLEGLDKKKDEWKE FAGNLASGGAAGATSLCFYYKDJBARTRLAADIGKANDREEKGL
ADCLIKTYKSDGPTGLYRGFFYSVGGTTYRAAYFGMFDTAKNVFASDGGKLMFFAAM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id…"CAB04874.1"
/db_xref~"GI:3880276"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation~"MSKEKSFDTKKFLIDLASGGTAAAVSKTAVAPIERVKLLLQVQD
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78,4326..4362))
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yk175a4.5
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yk231e9.5 comes
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1 (bases 1 to 9559)
1 (bases 1 to 9559)
Washington University Genome Sequencing
The C. briggsee Genome Sequencina Profes
                                                                                                                                                                                          Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 6:
Submitted by:
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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HTG.
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4.333
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                                                                                                                                                                                                                                                                                                                                                        /organism·"Caenorhabditis
/strain-"GujArat G16"
/db_xref~"taxon:6238"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e-mail: jspieth@watson.wustl.edu
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LST yk38bll.3 comes from this gene
LST yk38bll.3 comes from this gene
LST yk349a.3 comes from this gene
LST yk379e6.5 comes from this gene
EST yk38bll.5 comes from this gene
EST yk38bll.5 comes from this gene
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Center Caenorhabditis

University,

63108,

USA

complete

04-NOV-2000 sequence.

CDS gene

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alignment_scores:
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                                                        Align seg 1/1
                                                                                                         US-09-471-276-831_COPY_1_16 x HS191E19/rev
                                                                                                                                                                                            Percent Similarity:
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MetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
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                                                                                                                                                                                                                   Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Dm., EMBL; Sw., SWISSPROT; Tr., TREMAL INFORMAT; This sequence is not the entire insert of clone 191219. It may be shorter because we only sequence overlapping sections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on Aug 3, 1999 this sequence version replaced gi:556490.
During sequence assembly data is compared from overlapping clones
where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cancer Institute by the group of Picter de Jong. For further details see http://baspac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence was generated from part of bacterial clone contigs 
human chromosome 6, constructed by the Sanger Centre Chromosome 
Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            neighbouring submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191E19 is from the library RPCI-1 constructed at the Roswell Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             feature key.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          requests:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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4.333
85.714
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/clone="RP1-191E19"
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/db_xref="taxon:9606"
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clonerequest@sanger.ac.uk
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105067 TTGATGGTACTCTTTACTCTTTGGGTGGGGGTGGTGTGGGGA 105026
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seq_documentation_block: gb_pr:AC067945

KEYWORDS SOURCE VERSION DEFINITION ACCESSION AC067945.4 GI:13786486 Homo sapiens BAC clone RP11-629B4 from 2, complete sequence aC067945 162471 dq 09-AUG-2001

REFERENCE ORGANISM AUTHORS Mammalia; Eutheria; Primates; 1 (bases 1 to 162471) Sulston, J.E. and Waterston, R. Homo sapiens Eukaryota; Metazoa; Chordata; Primates; Catarrhini; Hominidae; Homo Craniata; Vertebrata; Euteleostomi;

REFERENCE MEDLINE JOURNAL TITLE The sequence of Homo sapiens Toward a complete human genome sequence Genome research. 8 (11), 1097-1108 (1998) Isak, A., Elliott, G., 99063792 (bases 1 to 162471) Doebber, A., Abbott, A., Hawki sapiens BAC clone RP11-62984

REFERENCE AUTHORS TITLE AUTHORS JOURNAL Unpublished 3 (bases 1 (bases 1 to 162471) Hawkins, M. and Falk, A.

REFERENCE JOURNAL MO 63108, USA 4 (bases 1 to Waterston, R.H. Waterston,R.H. Direct Submission Submitted (27-APR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. to 162471) St. Louis,

REFERENCE TITLE JOURNAL AUTHORS Direct Submission
Submitted (25-APR-2001) Genome
University School of Medicine, Waterston, R 2 8 63108, (bases I USA to 162471) Sequencing Center, Washing 4444 Forest Park Parkway, Washington St. Louis,

Submitted (09-AUG-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Apr 25, 2001 this sequence version replaced gi:13518285. Direct Submission USA

COMMENT

TITLE

AUTHORS

JOURNAL

Center: Washington University Genome Sequencing Center Center code: WUGSC

clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. NOTICE: This sequence may not represent the entire insert of this

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. John D. MAPPING INFORMATION: Department of Genetics, Washington University, St. Louis dditional information about the map position of this

SOURCE INFORMATION:
The RFGI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E Frengen, E.

sequence, McPherson,

For additional information about the map nce, see http://genome.wustl.edu/gsc

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FEATURES
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The clone sequenced to the left is RP11-45219, 200 bp overlap; the clone sequenced to the left is RP11-31739. Actual start of this clone sequenced to the right is RP11-31739. Actual end is at base cost the right is RP11-62984; actual end is at base position 195 of RP11-62984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takemo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genotics. Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6
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5997. .61
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5617. .59
                                                           /rpt_family."MER1_type"
18139. .18209
                                                                                                                                                                                  /rpt_fami
16030. .1
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6135. .6178
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18210. .18521
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12472. .1
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9226. .9268
    /rpt_family~"Alu"
18522. .18865
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17221 . .17290
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12297. . 12325
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10528. .10562
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1887. .2071
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/db_xref-"taxon:9606"
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1. .162471
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209. .3257
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14747
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US-09-471-276-831_COPY_1_16 x AC067945
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41942
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48861. .48888
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4.333
92.308
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48269. .48422
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48201. .48248
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42719. .42746
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42641. .427
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42371, .42439
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25927. .26475
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36502. .36816
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21523. .21828
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21212. .21327
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20271. .20291
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26898. .27113
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19330. .19710
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_family~"L2"
                                                                                                                                                                                                                                                                                                                                                                                        family "(CA)n"
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'. .47789
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                                                                                                                     Percent Identity:
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                                                                                                                                 Gaps:
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61.538

101072 CTTTTAATTCTGTTTCTTTTACTGTGGAGAGTTGCATGG 101110

This record will be updated with the finished sequence

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REFERENCE
AUTHORS
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Birren,B., Linton,L., Nusbaum,C. and Lander,E
Homo sapiens chromosome 2, clone RP11-310D24
NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Smit, A.F.A. & Green, F. (1230-227)
http://ftp.genome.washington.edu/RW/RepeatWasker.html
http://ftp.genome.center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (29-APR-2000) Whitehead Institute/AIT Center for Genome Research, 320 Charlus Street, Cambridge, MA 02141, USA On Jun 4, 2000 this sequence version replaced gi:7670145.
All repeats were identified using RepeatMasker:
smit, A.F.A. & Green, P. (1996-1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13, M7815; 100% of reads Sequencing vector: M13, M7815; 100% of reddechemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phtap, version 0,960731 Consensus quality: 117725 bases at least Q40 consensus quality: 187810 bases at least Q30 consensus quality: 18810 bases at least Q30 consensus quality: M8811 bases at least Q30 consensus quality: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project Information
Center project name: L10091
Center clone name: 310_D_24
                                                                                                                                                                                                                                                                Quality coverage: 4.9 in Q20 bases; agarose-fp Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                     Insert size: 187000; agarose-fp Insert size: 185099; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nusbaum, C., Lander, E., Abraham, H., Allen, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA HTG (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of reads
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135149 187399: contig of 52251 bp in length
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19395
21705
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73021 81047; contig of 8027 bp
81048 81147; gap of 100 bp
81148 88415; contig of 7268 bp
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66233 729
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40295 4576
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34195 4019
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1110 1209: gap
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2434 5417:
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5518. .
                                                                                                /note="assembly_fragment"
9350, .12316
                                                                                                                                                                                                                                                                           clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
                            /note="assembly_fragment"
12417. .14957
                                                                                                                                                                                           6302.
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2434. 5417
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1210 .2333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21804: gap of 100 bp
25038: contig of 3234 bp
25138: gap of 100 bp
29374: contig of 4236 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19394:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12416: gap of
14957: con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9349:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6301:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5517:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55863:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50873:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29474:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .187399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jap of 40194:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515: gap of 100 bp in length 99641; contig of 11126 bp in length 741; gap of 100 bp in length 135048; contig of 35307 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              080: gap of 100 bp
66132: contig of 4052 bp
232: gap of 100 bp
77920: contig of 6688 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363: gap of 100 bp 61980: contig of 6117 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373; gap of 100 bp
55763; contig of 4890 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368: gap of 100 bp
50773: contig of 4905 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194: gap of 100 bp
45768: contig of 5474 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94: gap of 100 bp
21704: contig of 2310 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57: gap of 100 bp
19294: contig of 4237 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12316:
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contig of 6000 bp in length
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contig of 2541 bp
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of 100 km
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88516. 99641
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99742. .135048
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62081. .66132
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50874. .55763
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40295. .45768
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34195. .40194
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15058. 19294
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135149. .187399
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73021. .81047
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19395. .21704
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 14
Caps: 0
Percent Identity: 57.143
                                                                                                                                                                                                     16 clone RP11-557E6,
                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                              to: 187399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2303 others
                                                                                                                                                                                                     LOW-PASS SEQUENCE
                                                                                                                                                                                                                      26-JAN-2000
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Dirive, Walnut Creek, CA 94598, USA on Jan 26, 2000 this sequence version replaced gi:5885929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generated and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be appeared.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
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                                                 14984
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                                          gap of unknown length
gap of unknown length
locality of 173 bp in length
locality of 182 bp in length
locality of 182 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
locality of 1146 bp in length
locality of 1846 bp in length
locality of 187 bp in length
locality of 187 bp in length
locality of 189 bp in length
gap of
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g of 486 bp in length
if unknown length
g of 703 bp in length
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g of 605 bp in le
f unknown length
unknown length
of 926 bp in length
unknown length
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unknown length
of 745 bp in length
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of 648 bp in length
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unknown length
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unknown length
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of 258 bp in length
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35667 36541: contig of 875 by in length 36542 37859: contig of 138 by in length 36542 37859: contig of 1318 by in length 37860 38724: contig of 825 by in length 38725 40403: contig of 825 by in length 38725 40403: contig of 1879 by in length 40404 41689: contig of 1286 by in length 40590 42617: contig of 1286 by in length 41690 42617: contig of 3286 by in length 42618 43987: contig of 1370 by in length 42618 43987: contig of 1772 by in length 42730 47312: contig of 1553 bp in length 43988 45759: contig of 1753 bp in length 43980 47312: contig of 1553 bp in length	31239 32178: contig of 940 bp in length 31239 32178: contig of 940 bp in length 32179 32246: contig of 660 bp in length 32247 33821: contig of 660 bp in length 32247 33821: contig of 1575 bp in length 392 of unknown length 393 of unknown length 395 of unknown length 397 of unknown length 398 of unknown length 398 of unknown length	19637: contrig 19845: contrig 20057: gap of 20057: gap of 20057: gap of 20057: gap of 20057: gap of 221514: contrig 221514: contrig 221519: gap of 221619: gap of 2217: gap of 2317: gap of 25572: gap of 25573: gap of 25573: gap of 25573: gap of 25573: gap of 25573: gap of 25573: gap of	15969 16759; contig of 791 bp in length pap of unknown length 16760 16909; contig of 150 bp in length 16760 17075; contig of 150 bp in length 16910 17075; contig of 156 bp in length 16910 17075; contig of 156 bp in length 17076 17651; contig of 576 bp in length 17076 17651; contig of 575 bp in length 17076 18442; contig of 571 bp in length 17652 18442; contig of 7919 bp in length 18443 19359; contig of 917 bp in length
seq_documentation_block: AC023766 227611 bp DNA HTG 10-MAY-2000 DEFINITION Homo spitens chromosome 5 clone RP11-459A22 map 5, WORKING DRAFT SEQUENCE. 62 unordered pieces. ACCESSION AC023766. 2 G1:7767814 VERSION AC023766. 2 G1:7767814 KEYWORDS HTG: HTG: HTG: HTG: HTG: HTG: HTG: HTG:	alignment_block: US-09-471-276-831_COPY_1_16 x AC009146/rev Align seg 1/1 to reverse of: AC009146 from: 1 to: 188249 Align seg 1/1 to reverse of: AC009146 from: 1 to: 188249 3 MetteuvalvalPheteuLeuTrpGlyvalThrTrpGly 16	3.337 5.6wn 6.6wn 4.56 6.002 b 1.002 b 1.0	48547: contig of 11235 50263: contig of 1276 50263: contig of 1776 9ap of unknown 51618: contig of 1355 9ap of unknown 53315: contig of 1897 9ap of unknown 53515: contig of 1897 9ap of unknown 55107: contig of 1992 9ap of unknown 55007: contig of 1992 9ap of unknown

5

length

JOURNAL Grand-Pierre, N. Grant, G. Hagos B. Heaford, A. Hotton, L. Howland, J.C., Illev I. Johnson, R. Jones, C. Kann, L., Kartas, A. Kieln, J., Landers, T., Largocque, K., Loboczky, J., Levine, R. Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McBean, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McBensus, L., Milova, T., Mitanda, C., Mienga, Y., Morrow, J., Maylor, J., Nemman, C. H., O'Connor, T., O'Connell, P., O'Hell, D., Ollvar, T. M., Peterson, K., Plerre, N., Disani, C., Pollista, Y., Raymond, C., Rilby R., Rogor, P., Rottman, D., Roy, A., Sancos, R., Schuer, S., Sewery, P., Spencer, D., Stance, Thoman, M., Sancos, M., Sichuer, S., Submannian, A., Talmas, J., Tesfiye, S., Theodore, J., Tirrell, A., Wu, X., Wilson, B., Stance, N., Vo, M., Wilson, M., Wilson, M., Tayman, D., Yes, M., Vo, M., Wilson, Submitted (17-FBB-2000) Whitehead Institute/AIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 0140, Boukhyalter, B., Brown, A., Burkett, G., Campopiano, A., Ca:
Chospel, Y., Colangelo, M., Collins, S., Coljmore, A., Cool
Chospel, Y., Colangelo, M., Collins, S., Coljmore, M., Doylo, M.,
DoArrollano, K., Dewar, K., Dodge, S., Donino, M., Doylo, M.,
Fenestor, J., Gerrelra, F., Itzätleh, M., Forrest, C., Gago Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Greham, J.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Greham, J., http://ftp.genome.washington.edu/RM/RepeatMasker.html Direct Submission Zody, M. Anderson, S., Baldwin, J., Barna, N., Consensus quality interest significant of the second of th NOTE: This is a 'working draft' sequence. It currently consists of 62 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. Sequencing vector: M13; M77815; 100% of reads Center project name: L6351 Center clone name: 459_A_22 Project Information Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu Center code: WIBR Center: Whitehead Institute/ MIT Center for Genome Research 1 1178: contig of 1178 bp in length 1179 1278: gap of 100 bp 1279 2325: contig of 1047 bp in length 3504: contig of 1079 bp 55 3604: 9pp of 100 bp 55 3604: 9pp of 100 bp 55 3604: contig of 1208 bp 114912: 9pp of 10124 bp 176436: supp of 11424 bp 17666: contig of 1170 bp 17706: 9pp of 1170 bp 17706: 9pp of 1514 bp 17706 1 9320: gap of 100 1 10404: contig of 1 15 10504: gap of 10 15 1787: contig of 1 18 11887: gap of 10 / 7706: 9c; 9220: / 1278: gap of 100 bp 2325: contig of 1047 bp in length 2425: gap of 100 bp 100 bp 100 bp 1283 Goyette, M., Graham, L., Beda, F., Boguslavkiy, L., dq ф g bp in ф ni dq ín 'n 'n 'n 'n agarose-fp sum-of-contigs length length length length length of reads Gage, D., Cooke, P., Castle, A., 101703 101603 39295 39395 17985 18085 19858 15926 16026 16428 56722 50924 51023: 24 51023 contrig of 2021 bp 11
24 51023 gap of 100 bp 12
24 51023 gap of 2024 bp 11
25 5327; contrig of 2024 bp 11
25 5327; contrig of 3394 bp 11
25 56721; contrig of 3394 bp 11
25 58718; contrig of 1897 bp 11
25 58818; gap of 100 bp 11
26 58818; gap of 100 bp 11
26 58818; gap of 100 bp 11 2955: contig of 1129 bp in 1
56 26055: gap of 100 bp
56 27976: contig of 1921 bp in 1
7 28076: gap of 100 bp
7 2974: contig of 1798 bp in le
5 29974: gap of 100 kp
1 31504: ~ 100 kp 78765: C.... 78865: gap of 100 bp 3783: contig of 4918 bp j 718R3: gap of 100 bp 718R3: gap of 4671 bp 5 18084: gap 5 19857: 45488: contig of 2052 bp 45588: gap of 100 bp 47902: contig of 2314 bp 48002: gap of 100 bp 29974: gap or 31504: contig of 1530 bp 31604: gap of 100 bp 92987: gap of 100 bp 97174: contig of 4187 bp 97274: gap of 100 bp 101602: contig of 4328 bp 88654: gap 92887: c 101702: gap of 107534: cont 92987: gap of 100 bp 69576: 64999: 62016: 43436: 41464: gap of 43336: con 39394: 35754: 33076; gap of 34237; cont 19957: 14624: gap of 15925: con 13496: gap 16527: 100 bp
64899; contig of 2883 bp 1.
5499; gap of 100 bp
69476; contig of 4477 bp ir
74433 - 100 bp 37531; contig of 100 bp 37531; contig of 1877 bp in 7731; gap of 100 bp 39294; contig of 1563 bp in 1394; gap of 100 hr 00 bp 016: contig of 3098 bp 016: gap of 100 km 64899: con* 100 bp 100 dp 436: gap of 1872 bp 45488: confir 100 hr J83: gap or 88554: contig of 4671 654: gap of 100 b 23157: cont unt 16427: 100 bp 100 bp 100 bp 133: contig of 4857 bp 133: gap of 100 bp 18765: conti 34237: contig of 1161 bp 137: gap of 100 bp 35654: contig of 1317 bp 14524: contig of 1028 bp in 13396: contig of 1509 bp 96: gap of 100 bp 24526: contig of 1269 bp 21461: contig of 1504 bp 16427: contig of 402 bp 1 27: gap of 100 bp 17984: contig of 1457 bp 1364: contig of 1970 bp gap of gap of gap of contig of 1 contig of 1773 bp contig of 1301 bp in contig of 5832 100 bp 100 bp of 2204 bp 100 bp dq 001 .596 bp bp in length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                     AUTHORS
                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                              LeuLeuTrpGlyValThrTrpGly 16
Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bhby, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.
                                               Muzny, D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., All
Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barb
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.
                                                                                                                                                                                                                                      Homo sapiens chromosome 12 clone RP11-793H13, SEQUENCE, 5 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                               Elikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Nammalia; Eutheria; Primates; Catarrhni; Homunidue; Homo.
1 (bases 1 to 173188)
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                       AC023509.31 GI:14861644
                                                                                                                                                                                                                                                                          AC023509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
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141226 (141325; qap of 1
141326 (141325; contig of 6
141327 (14326; gap of 1
14327 (14326; gap of 1
14327 (14326; gap of 1
154102 (14326; gap of 1
154102 (14326; gap of 1
154102 (14326; gap of 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124947 129670; contig of 4
129671 129770; gap of 1
129771 134148; contig of 4
134149 134248; gap of 1
134249 141225; contig of 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213218 213317: gap of 100 bp
213318 227611: contig of 14294 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200239 200338: gap of 100 bp
200339 213217: contig of 12879 bp
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179771 189052: contig of
189053 189152: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160593 160692: gap of
160693 170151: contig of
170152 170251: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121061 121160: gap of 121161 124846: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112108 112207: gap of
112208 117172: cont
117173.117272: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107535 107634: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/map="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.00
5.778
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                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 9
Gaps: 0
Percent Identity: 88.889
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6391 bp in length
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100 bp
778 bp in
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100 bp
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6901 bp
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5775 bp in length
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                                                                                                                                                                                                                                                         WORKING DRAFT
                                                                  Barbaria, J.,
                                                                                   Allen,C.
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Foster P. Prints, P. Gablis J., Gao J., Gardin A. Garrer T.
Garan M. Gill, R. Gorrei J. H. Gosvara M. Gunaratne P. Hale S.
Hamilton K., Harris C. Harris X. Hart M. Haylak P.; Hawan A.,
Hernandez J., Harris C., Briss X. Hart M. Haylak P.; Hawan A.,
Hernandez J., Harris C., Hodgson A., Houses M., Holloway C.,
Hellins B. Hons L. F. Howard, S. Huber J. Hilly K. S. Hume J.
J. Harris C., Krachson E., Kally S., Khan U. King J. Korrah J.,
Kovar, C., Kratovic, J., Kureshi A., Landry N., Leal B. Lewis L.C.,
Lewis L. L. J. L. L. Liz Littarge, O., Lieu C., Liu J., Liu N.,
Lewis L. L. Li J. L. L. Liz Littarge, O., Lieu C., Liu J., Liu N.,
Lewis L. L. Li J. L. L. Liz Littarge, O., Lieu C., Liu J., Liu N.,
Louiseged, H., Lozado, R. J., Liu X., Lucler A., Lucler A., Hucler A.,
Martinez E., Hassey E., Maner J., Michell T., Mohabbat K.,
Morgan, M., Moyris, S., Moser M., Neal, D., Newtson, J., Newtson, N.,
Myyen, A., Myyen, N., Moysen, N., Nicketson, E., Moyenko, S.,
Myyuyan, A., Morris, S., Moser M., Nedel, D., Newtson, J., Newtson, N.,
Myyuyan, N., Myyen, N., Nicketson, E., Moyenko, S.,
Myyuyan, N., Moyen, N., Nicketson, E., Moyenko, S.,
Myuyan, N., Peters L., Pickens, R., Primus, E., Pu, L.,
Duiles M., Ren, Y., Rives M., Rojas A., Rojbookan, I., Rojfe, M.,
Ruiz, S., Savery G., Scheter S., Scott, G., Shen, H., Shooshtari, N.,
Stone H., Stoton A., Vander J., Wellon, P., Tamerisa, A., Taberisa, K.
Frand, H., Tansey, J., Taylor, C., Taylor, T., Telfrod B., Vincen, B.
                                                                                                                                                                                                                                                                                                                                                                                   Thomas.S., Ugmanik.K., Vasquez.L., Vera, V., Villaion, D., Vinson, R., Wall, R., Mang, S., Ward-Moore, S., Warren, R., Washington, C., Wallilams, G., Williamson, A., Wileczyk, R., Wooden, S., Worley, K., Wil, C., Wu, Y., Wil, F., Zhou, J., Zorrilla, S., Nelson, D., Wellstock, G., Gu, G., Wu, Y., Wil, S., Williams, G., Will
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Coyle,M.D., Dathornes,S., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delaper,H.,
Denn,A.L., Ding,Y., Dinh H.H., Douthwaite,K.J., Draper,H.,
Denn,A.L., Ding,Y., Dinh H.H., Davitwaite,K.J., Draper,H.,
Denn,A.L., Davitwaite,H.H., Davitwaite,H., Davitwaite,H.,
Denn,A.L., Davitwaite,H., Davitw
                   Unpublished
2 (bases 1
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                                                                                                                                                                                                                                                                                                     Direct Submission
(bases 1 to 173188)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nelson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vinson, R.,
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JOURNAL REFERENCE AUTHORS TITLE JOURNAL

TITLE

Submitted (15-FBB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 18, 2001 this sequence version replaced gi:146 Worley, K.C. Direct Submission

COMMENT

----- Genome Center

Contact: hgsc-help@bcm.tmc.edu Center project name: HAGA Center clone name: RP11-793H13 Web site: Center: Baylor College of Medicine Center code: BCM http://www.hgsc.bcm.tmc.edu/

Sequencing vector: plasmid; M77789 Sequencing vector: M13; L08821 ----- Summary Statistics

Chémistry: Dye-primer Bodisy: 4% of reads
Chemistry: Dye-primer Bodisy: 4% of reads
Chemistry: Dye-cerminator Big Dye- 96% of reads
Assembly program. Phrap: version 0.990339
Consensus quality: 17263 bases at least 0.40
Consensus quality: 171067 bases at least 0.20
Consensus quality: 17131 bases at least 0.20
Consensus quality: 17224 sum of contigs estimation
quality coverage: 0.0x in 0.20 bases; suprof-contigs estimation
quality coverage: 0.0x in 0.20 bases; suprof-contigs estimation

NOTE: Estimated insert size may differ from sequence Length (see http://www.hgsc.tom.tor.edu/docs/Genhank_draft_data.html) NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the piece consists of 5 contigs. The true order in this sequence record is

arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

as soon as it is available and the accession number will be preserved.

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BASE COUNT
ORIGIN
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US-09-471-276-831_COPY_1_16 x AC023509/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_htg:AC068889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AC023509 from: 1 to: 173188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51803 GTTTCCTTTTTACTACTTTGGGGGGATAACTGGGTGGGGG 51765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
Millon, C., Addonso, C., Addo-Odiolb, B., Ali-Osman, F.R., Alicon, C., Alsbrooks, S.L., Amarstunge, M.C., Are, J.R., Barks, T., Barbaria, J., Bowin, B., Brown, M., Bryant, N.P., Carcon, T.F., Carcia, J., Burkett, C., Burrell, K.L., Bartia, C., Chen, R., Chen, R., Checko, J., Chacko, J., Chacko, J., Charles, D., Cox, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., Coyle, M.D., Darhorne, S. R., David, R., David, M.L., Davis, C., C., Dayer, D., Edward, C., Denne, T., D., Edward, C., Denne, J., Edward, M., Carcia, A., Garrer, T., Coster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garrer, T., Garcia, M., Gularathe, P., Hawes, A., Hernandez, J., Hernandez, J., Hodges, M., Holloway, C., Hella, S., Homst, F., Howard, S., Huber, J., Hull, K., J., Howard, S., Huber, J., Hull, K., J., Lin, K., Hartis, S., Homst, T., Howard, S., Huber, J., Hull, K., J., Lin, K., Hartis, J., Lin, K., Hartis, J., Lin, K., Hartis, J., Lin, K., Lind, C., Lind, J., Lin, M., Louise, R., Luna, R., Martindle, A., Mort, M., Mort, M., Mort, M., Mort, M., Nockson, N., Nockson, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValValPhcLeuLeuLeuTrpGlyValThr...TrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC6889 182930 bp DNA 14TG 26-JUN-2001
HOMO SAPItens chromosome 12 clone RP11-774122, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Memmalia; Eutheria; Primates; 1 (bases 1 to 182930)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC068889
AC068889.27 GI:14547453
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57678
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/db_xrefo"taxon:9606*
/chromosome-"12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.682
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57877 app of unknown length
12590 contig of 67713 bp in length
12590 app of unknown length
145187 contig of 16670 bp in length
145187 app of unknown length
165077 contig of 21630 bp in length
167077 app of unknown length
173188 contig of 6171 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182930 bp
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SOURCE

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On Jun 25, 2001 this sequence version replaced g1:13605936.
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Direct Submission
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sequencing vector: M13, L08921
sequencing vector M13, L08921
sequencing vector M13, L08921
sequencing vector M13, L0892
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Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: RP11-774122
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_datm.html). NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces
as soon as it is available and the accession number will be preserved.
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165524 165624 172846 172946 177160

gap of

of 4214 unknown unknown of 7222 unknown unknown length of 12615 bp in of 10644 bp in of 18368 bp in unknown length unknown length

ni dq nı da length length

165623: 172845: 152908: 165523: 142064: 142164:

gap of contig gap of contig

152809 142065 123597 105916

42165 23697 105816

10581 82649 59469: 59569: 82549:

contig of 21950 bp in 1
gap of unknown length
contig of 22980 bp in 1
gap of unknown length
contig of 23166 bp in 1
gap of unknown length
contig of 17681 bp in 1

123696: 105915

gap of contig

37420 37520 59470

37519 37419:

gap of unknown length

59570

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KEYWORDS
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LOCUS RNO302031
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US-09-471-276-831_COPY_1_16 x AC068889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-DEC-2000) Gardmo C., Department of Medical Nutrition, Karolinska Institutet, Novum F60, Huddinge, S-14186, SMEDEN Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deoxyribonucleic acid with homology to the human
alphalB-glycoprotein, characterizing a new protein family
Endocrinology 142 (6), 2695-2701 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardmo,C., Persson,B. and Mode,A.
Cloning of a novel growth hormone-regulated rat complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha 1B-glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gardmo, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
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180099
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/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-774122"
a 43236 c 42404 g 47843
                                                              /product-*putative alpha 18-glycoprotein*
/protein_id-*CRC19029_1*
/protein_id-*CRC19029_1*
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/db_xref-*CI:11877349*
/db_xref-*CI:11877349*
/db_xref-*SI:#SILTFVLIAGEFLGPGNALMINSGSEPELRAEPOSILEPWAN
/translation-*HSILTFVLIAGEFLGPFUSYRESJOTISNSGYPERGRGVEP
PUDIOLALISKMYNESUNLEYTEKEPLPFSKANADEVSHTPSKASCOLEVYLNGRAVANGOV
TYLLAKEGYDOGTOK PDVOHKGTAGFLTYKFONYSGSYLTHAGGEPSEBSA LVTYKKASC
TYLLAKEGYDOGTOK PDVOHKGTAGFLTYKFONYSGSYLTHAGGEPSEBSA LVTYKGNYSGSYLTHAGGEPSEBSA LVTYKKASC
TYLLAKEGYDOGTOK PDVOHKGTAGFLTYKFONYSGSYLTHAGGEPSEBSA LVTYKGNYSGSYLTHAGGEPSEBSA LVTYKGNYSGSTAGFLTYKGNYSGSYLTHAGGEPSEBSA LVTYKGNYSGSYLTHAGGEPSEBSA LVTYKGNYSGSYLTHAGGEPSEBSA LVTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGSTAGFLTYKGNYSGTAGFLTYKGNYSGTAGFLTYKGNYSGTAGFLTYKGNYGTAGFLTYKGNYSGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAGFLTYKGNYGTAG
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84.615
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TQLPPSLCLMGSYLTIYPQKTHETLACKAPRNAAEFQLRQGERVLNIQGFSPTRDATI
YYVNLKELDNQSPFTCRYRMHKYMHVWSEDSKPVELMWSDEKLPAPVLTAEPSSHNLE
                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sprague Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
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180198: gap of unknown length
182930: contig of 2732 bp in length
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Mus musculus bromodomain-containing FSH-like protein FSRG2 (Fsrg2)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalia; Eutheria;
1 (bases 1 to 2933)
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/protein_id: AAF78072.1"
/db_xref: GI:8575733"
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4.636
84.615
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1, .2933
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/db_xrefo"taxon:10090"
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Sciurognathi; Muridae; Murinae; Mus
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69.231
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AUTHORS
TITLE
    COMMENT
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LOCUS AC019542
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US-09-471-276-831_COPY_1_16 x HSCANPX/rev
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Ratio: 6.375
Similarity: 100.000
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        Direct Submission
Submitted (30-DEC-1999) Celera Genomics,
Rockville, MD, USA

**Achtified as CDM:10210
                                                                                                                                                 Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha: Ephydroidea: Drosophilidae: Drosophila. [1] (bases 1 to 45605)
                                                                                                                                                                                                                                                                             Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                             HTG: HTGS_PHASE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster,
This sequence was identified as CDM:10210130 by the submitter
                                                                                                                       Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                   fruit fly
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Percent Identity:

100.

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Length: Caps:

from:

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to: 3628

DNA

*** SEQUENCING

IN PROGRESS ***, in ordered

03-JAN-2000

45 West Gude Drive,

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Belsito, A., Piluso, G. and Nigro, V. A novel X-linked calpain-like protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 3628)
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                                                            QGHISEKVISSDDLTEL"
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/product-"calpain-11ke protease, CANPX"
/protein_id-"CAA04051.1"
/db_xref-"G1:2274962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation~"MGPPLKLFKNQKYQELKQECIKDSRLFCDPTFLPENDSLFYFRL
LPGKVVWKRPQDICDDPHLIVGNISNHQLTQGRLGHKPMVSAFSCLAVQESHWTKTIP
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US-09-471-276-831_COPY_1_16 x AC019542/rev
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TITLE
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Ratio:
                                                                                                                                                                                                                                                                                                                                       corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence is the entire insert of clone 512B11. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           requests: clonerequestésanger.ac.uk
On Aug 5, 1998 this sequence version replaced gi:3355573.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                           This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-OCT-1998) Sanger Centre, Hinxton, Cambridgeshire CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; Desmoplakin I; DPI
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                                                                                                               Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                       512B11 is from the library RPCI3 constructed at the Roswell Park
                                                                                                                                                                                               http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                   feature key
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This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14162
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/db_xref="taxon:7227"
, 9337 c 8941 g 13165 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                               Location/Qualifiers
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QATSREIMMINDCEEEELLYDWSDKNINIAQKQEAFSIRMSQLEVKEKELNKLKQESD QLVLNQHPASDKIEAYMDTLQTQWSWILQITKCIDVHLKENAAYFQFFEEAQSTEAYL

RGVITDONSDGYCOTGTMSRHONONTIQELLONCSDCLMRAELIVOPELKYGDGIQLT RSRELDECFAQANDOMEILDSLIREMROMGOPCDAYOKRLLQLQEQMRALYKAISVPR

RNPDYRSNKPIILRALCDYKQDQKIVHKGDECILKDNNERSKWYVTGPGGVDMLVPSV

KGLQDSIRKKYPCDKNMPLQHLLEQIKELEKEREKILEYKRQVQNLVNKSKKIVQLKP NSHRGIHNSIGDYRWQLDKIKADLREKSAIYQLEEEYENLLKASFERMDHLRQLQNTI VRRASSKGGGGYTCQSGSGWDEFTKHVTSECLGWMRQQRAEMDMVAWGVDLASVEQHI /db_xref="SPTREMBL:075993" /translation="MSCNGGSHPRINTLGRMIRAESGPDLRYEVTSGGGGTSRMYYSR

/product-*dJ512B11.1 (Desmoplakin I (DPI))*
/protein_id-*CAA19927.1*
/db_xref-*G1:3702136*

/evidence-not_experimental /codon_start-1

proteins Q14189 P15924 Q03001 P97395 P97396

SOURCE

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700Ce-PickLive CpG island*
700Ce-PickLive CpG is
6976. 51913

/genne-di527811.1*

/genne-di527811.1*

/genne-di527811.1*

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/gene-di527811.2*

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/note-*MIR repeat: matches 238. .119 of consensus*
3977, .4014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6625
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complement(5087. .5168)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4480.
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/note="19 copies 2 mer tg 90% conserved"
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1606. .1722
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/clone="RP3-512B11"
/clone_lib="RPCI-3"
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                                                             /note:"2
19422. .1
                                                                                                  complement(1838). 10461). Out of Consensus folice. 11403 repeat: matches 2486. 2405 of consensus complement(1876. 1859). Out of Consensus folice. FLAN_C repeat: matches 131. .11 of consensus 1942. 19429.
                                                                                                                                                                                                                                  /note-"match: GSSs B92850 AQ085909"
17617. .17920
                                                                                                                                                                                                                                                                                             /note: "AluSx repeat: matches 1. 17480. .17689
                                                                                                                                                                                                                                                                                                                                                                              /note- "AluSp repeat: matches 297. complement(15382. .15693)
                                                                                                                                                                                                                                                                                                                                                                                                                    /noter*AluSg repeat: matches 2. .300 of consensus* complement(13702. .1333)
/noter*MIR repeat: matches 192. .60 of consensus* complement(14492. .14786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"MIR repeat: matches 146. .48 of consensus" complement(12765. .13075)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noten 18 copies 2 mer tt 81% conserved complement(11838, 11934)
                    complement(19996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9808.
                                        /note…"22 copies 2 mer ac 100% conserved"
                                                                                                                                                                                                                                                                                                                                        16684
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                                                                                                                                                                                                        /note-- "AluSx repeat: matches 5. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                          /noter AluJb repeat: matches 295. .1 of consensus
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13328. .13625
                                                             '2 copies 24 mer 96% conserved".19465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9843
                                                                                                                                                                                                                                                                                                                                     16980
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repeat:
                    . 20293)
matches 288.
                                                                                                                                                                                                                                                                                                                 .294 of
.1 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                               .2 of consensus
                                                                                                                                                               .2405 of consensus"
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COMMENT

requests: clonerequest@sanger.ac.uk
On Jun 12, 2001 this sequence version replaced gi:13443552

---- Genome Center

Submitted (10-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,

UK. E-mail enquiries: humquery@sanger.ac.uk Clone

REFERENCE

AUTHORS TITLE

Direct Smith, M.

Submission

JOURNAL

CB10 1SA,

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VERSION
KEYWORDS
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us-09-471-276-831_COPY_1_16 x HS512B11
                                                                                 SOURCE
                                                                                                                                          ACCESSION
                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                    seq_name: gb_htg:AL590044
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                                                                                                                                                                                                                                                                                            GTGATTTTCCTATTGGGCTGGGGTGTGACTTATGGC
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 71990)
                                                                                                                                                  Homo sapiens chromosome 6 clone PROGRESS ***, in ordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                           Homo sapiens
                                                                                              HTG; HTGS_PHASE2; HTGS_CANCELLED
                                                                                                                    AL590044.3 GI:14348513
                                                                                                                                                                                                AL590044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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/note-"MER42c repeat: matches 1323. .1538 of consensus" complement(22529. .22700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note--"L1MD1 repeat: matches 971. .805 of consensus" 22737. .23037
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20526. .20795
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6 clone RP5-875120,
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Gaps:
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FEATURES
                                                              source
                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LOB752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality; 71614 bases at least Q40
Consensus quality; 71615 bases at least Q30
Consensus quality; 71883 bases at least Q30
Consensus quality; 71883 bases at least Q30
Insert size: 71909; sum-of-contigs
Insert size: 79291; 16.0% error: agarose-fp
Quality coverage: 6.78x in Q20 bases; sum-of-contigs Quality
coverage: 6.16x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: This is a 'working draft'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Sanger Centre
                                                                                                                 by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                    This sequence will be replaced
/organism~"Homo sapiens"
/db_xref~"taxon:9606"
                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ···· Project
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/chromosome="6" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_110" /cloe_100 /cloe_110" /cloe_100 /cloe_100" /cloe_10
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US-09-471-276-831_COPY_1_16 x AL590044 ...
Align seg 1/1 to: AL590044 from: 1 to: 71990

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Sequence

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AZIDSZ/gogdatz/geneseq/geneseqn/MA2091.DM7. AA408299 H
/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA408299 H
/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA408299 H
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/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA607259 H
/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA607299 H
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/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA60749 H
/STDSZ/gogdatz/geneseq/geneseqn/MA2001.DM7. AA60740 H
/STDSZ/gogdatz/geneseq/geneseqn/MA2001.D
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Sequence
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Database sequences: 930621
Database length: 428663619
Search time (sec): 93.320000
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-O-/G902_J(1976_Spool_U959471176_Frunat_07012002_142445_19912/app_query.fasta_1.274
-De+N_Geneseq_1101 -OFFF-6astap -SUPFIX=ring -GAPOP=12.000
-GAPOP=4.000 -HINMATCH-0.100 -LOOPE1-0.000 -LOOPEXT-0.000
-GAPOP=4.000 -GAPEXT-0.030 -XAAPOP=10.000 -XAAPEXT-0.500
-FRAPOP=6.000 -GAPEXT-7.000 -YAAPOP=10.000 -XAAPEXT-0.500
-ERAPOP=6.000 -EGAPEXT-7.000 -STAPT-1 -MARKX-10sum62
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-TRANS-10man40.cd1 -LIST-100 -DOCALIGN-200 -TRAS-CORE-DGU
-TRAS-TUMBAN40.cd1 -LIST-100 -DOCALIGN-200 -TRAS-CORE-DGU
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               EXEXTX8X
                                                                                                                                                                                      seq_documentation_block:
ID AAV88297 standard;
                                                                                                                                                                                                                                                      seq_name:
               Expressed sequence tag; secreted protein; haematopolesis regulator;
                                                      EST clone GD177
                                                                                                    12-FEB-1999
                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV88297
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                                                                                                    entry)
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allgnment_block:
US-09-471-276-831_COPY_1_16 x AAV88297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 87.00
Ratio: 5.438
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAVBB297
                                                                                                                                                                                                                               _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful blood(ea. activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities in all animals of the suppression activity, animals stimulating or suppressing activity, activin/inhibit activity, chemosatic/chemokinetic activity, haemosatic activity, and the suppression activity, and the suppression activity, and the suppression activity, the suppression activity, the suppression activity, and the suppression activity, the suppression activity.
Human: 5' EST; expressed sequence tag: secreted protein; diagnosis; gene therapy; chromosome mapping; upstream regulatory sequence; forensic; location; development; protein synthesis; stability;
                                         Human; 5' EST;
                                                                              Human 5' EST isolated from a cDNA library SEQ ID NO:43
                                                                                                                             01-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 348-349; 641pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070078/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; heemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                        AAZ42284 standard; cDNA; 412 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                             37
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                                                                                                                                                                                                                                                                                                             ATGTCCATGCTCGTGGTCTTTCTTTGCTGGGGGTGTCACCTGGGGC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J, Jacobs K,
Spaulding V,
                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 A; 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lavallie ER, McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 T; 0 other;
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us-09-471-276-831_COPY_1_16 x AAZ42284
                                                                                                                                                                                                                                       seq_documentation_block:
                                                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC8725
                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAZ42284
                                                                                                                                                                                Percent Similarity: 100.000
                09-MAR-2001 (first entry)
                                                   AAC87257 standard; cDNA; 1908
                                                                                                                                                                                                                                                               treating a variety of human conditions. Secreted proteins have therapeutic value, and the identification of new secreted proteins is valuable. AAX42249 to AAX42264 and AAX64644 to AAX64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 195; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic, forensic, gene therapy, and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                      Sequence 412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel secreted protein 5' expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulation; identification; ss.
                                                                                                                                                                                                                                                        sequences used in the exemplification of the present
                                                                                                35
                                                                                               2000-038446/03
                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                          Ratio:
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98US-0069047
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5.438
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                                                                                                                                     from: 1 to: 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence tag sequences
                                                                                                                                                                                                                                      80 T; 3 other;
                                                                                                                                                                                          Gaps:
                                                                                                                                                                                 100.000
                                                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in
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Mouse liver growth hormone-induced cDNA clone 5,

SEQ ID NO:7

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involves correlating the level of expression of certain specific genes with the level of GH activity in the liver, or with an expected change at the condition of the liver as the result of GH activity. Excessive GH artivity in the liver as the result of GH activity. Excessive GH art the condition of the liver as the result of GH activity. Excessive GH art the condition of the liver as the result of GH activity. Excessive GH art the condition of the liver size as a a consequence of both hyperplasia and the paccoyte hypertrophy, and hepatocollular lesions which progress with age. Studies in transgenic mice which express high levels of bovine growth hormone identified a number of genes whose expression in the capture of the liver is altered by high GH levels. The genes which are upregulated are those encoding alpha-fetoprotein, corticosteroid binding globulin, corticosteroid binding globuling growth hormone corticosteroid binding globuling growth hormone corticosteroid binding globuling growth hormone growth hormone processor, cone 5 (AAG9725) and clone 45 (AAG97258) are also upregulated corticosteroid binding globuling growth hormone growth binding growt
                                                                                                                                                                                                                                                                                                                                                                                                     comprising administering the drug to the transgenic animal; and preventing or treating a liver pathology in a patient comprising administering a drug which inhibits the expression of a GH-induced gene. The method of the invention is used for diagnosing abnormal levels of the activity in the liver or predicting a chape in the condition of the liver or predicting a chape in the condition of the liver of predicting a chape in the condition of the liver in response to abnormal levels of GH activity. The GH-regulatable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isomerase appears to be downregulated. The invention also relates to transgenic nonhuman mammals comprising a GH-induced transgene which exhibit or have a propensity to develop a liver pathology; an assay for drugs which inhibit the development of, or which treat a liver pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of diagnosing abnormal levels of growth hormone (GH) activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 51-52; 65pp; English
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P-PSDB; ADB48724, ABB48725, AAB48726, AAB48727, AAB48728, AAB48739, AAB48731, AAB48732, AAB48733, AAB48733, AAB48733, AAB48733, AAB48737, AAB48735, AAB48737, AAB48737, AAB48738, AAB48739.
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                                                                                                                              liver genes and proteins are useful as diagnostic markers of liver pathology. Assays for the expression of these genes is useful for the diagnosis of liver pathologies associated with gigantism or acromegally with diabetes, as other causative agents may act directly or indirectly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             markers
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                                                                    upon the same genes. The present sequence represents the novel mouse
cDNA clone 5, expression of which is upregulated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of liver pathology
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Sequence 1908
 BP;
A; 475 C; 477
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431 T; 0 other
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alignment_scores

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seq_documentation_block:
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US-09-471-276-831_COPY_1_16 x AAC87257
                                               alignment_scores:
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  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-NOV-1998;
28-NOV-1997;
17-DEC-1997;
                                                                                                                                                                                                             The present sequence represents the complete genome of :ilamydia trachomatis open reading frames (ORES) of the genome encode polypeptides ANY50754-Y3794) The polypeptides can be used as warcines against Chlamydia trachomatis. Antisense and riboxyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendefact trachoma, paratrachoma, and inclusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; eye disease; conventional trachoma; nonendemic trachoma; nonendemic trachoma; nonendemic trachoma; nonendemic trachoma; nonendemic trachoma; noculation condjunctivitis; certicitis; salpingitis; certicitis; salpingitis; certicitis; salpingitis; harpholocitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of Chlamydia trachomatis
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                                                                                                                                             epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use
                                                                                                                                                                                           conjunctivitis; genital diseases such as nongonococcal uretritis,
                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 373-656; 1755pp; English
                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-371125/31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ01425 standard; DNA;
                                                                                                Sequence 1038602 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTCTCTGCTGCTACTGTACTGCTGCTCTGGGGGGTTCACTCTGGGC 58
                                 Quality:
                                                                                                                                these diseases.
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97FR-0015041.
97FR-0016034.
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80.000
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                                                                                                   305001 T; 432 other;
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seq_name:
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US-09-471-276-831_COPY_1_16 x AAA07999/rev
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Percent Similarity:
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                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                    The present sequence may be used to identify the geographic origin or plant. Plants may be genetically marked for identification by introducing a DNA sequence into the plant genome. The DNA sequence is at least 100 base pairs, is unique in the genome, and does not contain a sequence that alters transcription or encodes a functional protein. The sequence is readily describing and retrievable. The method is useful for tracking or identifying the distribution of
                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 11pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetically marking a plant or plant cell for tracking or identifying plants, especially the distribution of propriety plants, comprises introducing a DAM sequence having specific information content into a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DISC-)
                                                                                                                                                                                                                                              Sequence 56 BP; 38 A; 12 C; 3 G;
                                                                                                                                                                                                                                                                          propriety plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                    plant genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kao C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1999;
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                              TTTTTTTACTTTGGGGTTTACTTTGGGGT 25
                                                        PhoLeuLeuTrpGlyValThrTrpGly 16
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/SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF32085
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                                                                                      to reverse of: AAA07999 from:
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seq_documentation_block:
ID AAV88355 standard;
                                                                                                                                                                              alignment_block:
us-09-471-276-831_COPY_1_16 x AAF32085
                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                  Align seg 1/1 to: AAF32085
                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                   central and peripheral nervous system disorders, pain, stroke, chronic obstructive pulmonary disease, hypercholesterolatemia, hyperlipidaemia pyperlipoproteinemia, thereselerosis, arteriosclerosis and coronary artery disease. The present sequence is the open reading frame for humanitory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relation relates to novel human coding sequences and proteins designated M010 (ARF32082 and AM56884), M019 (ARF32084 and AM568895), M019 (ARF32084 and AM56895), M010, M019 and M024 proteins and compounds which modulate their activity or which bind M010, M019 and M070 m074 are useful for prevention and treatment of a variety of disorders including cancer, obesity, diabetes, osteoporosis, astima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New gene encoding proteins designated M010, M019, M024, useful for diagnosis, prophylaxis and treatment of cancer, obesity, diabetes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nervous system disorder; pain; stroke; hypercholesterolaemia; atherosclerosis; chronic obstructive pulmonary disease; hyperlipidaemia; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 98pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osteoporosis, asthma, atherosclerosis and pulmonary disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPT; 2001-112434/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000WO-US18097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200100644-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperlipoproteinemia; arteriosclerosis; coronary artery disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; M010: M019; M024; cancer; obesity; diabetes; osteoporosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human M019 open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF32085 standard; cDNA; 255 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                 34
                                                                                                                 6
                                                                                 GTCTTTTTACTTCTCTGGGCCTTTATCTGGGGA
                                                                                                                 ValPheLeuLeuTrpGlyValThrTrpGly
                                              /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV88355
                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB66893,
standard; cDNA; 339 BP
                                                                                                                                                                                                                                                                                                                                       255
                                                                                                                                                                                                                                                                                                                                     BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0345293.
99US-0345680.
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5.333
81.818
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                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                  from: 1 to:
                                                                                                                                                                                                                          Length: 11
Gaps: 0
Percent Identity: 72.727
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seq_documentation_block:
ID AAF32084 standard;
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US-09-471-276-831_COPY_1_16 x AAV88355/rev
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                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF32084
                                                                                                                                                                             Alian seg 1/1
                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an expressed sequence tag (EST), and is a polynucleotide of the invention are all secreted so the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predeted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities animals although no supporting data is given. Suggested activity, hazamatopolesis regulating activity, the mane stimulating or suppressing activity, activity, this cativity, chemoactic/themokinetic activity, hazamatory activity, cadherin/tumour invesion suppression activity, antimour inhibition activity, activity, activity, activity. Segmences are also stated to be useful for gone activity. The EST sequences are also stated to be useful for gone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pituitary, retina and colon cDWA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09845437-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed sequence tag; secreted protein; haematopolesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemotinesis; haemostasis; ene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
 12-APR-2001
                                                                                                                                                                                                                                                                                                                               Sequence 339 BP; 90 A; 74 C; 47 G; 128 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 368; 641pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST clone GP56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1999
                                                                                                                       74
                                                                                                                                                  SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
                                                                                                                       AGTATAAAAATTGTTTTTATCACACTCTGGGGACTGTGGTGG 33
                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                             to reverse of: AAV88355
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Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
(first entry)
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                                                                                                                                                                                                                                               48.00
4.364
78.571
                                                     cDNA; 1202
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Treacy M;
                                                                                                                                                                                                                                          Length: 14
Gaps: 0
Percent Identity: 50.000
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 ZXEXEXXXX
                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                             364
                        H. pylori GHPO 1365 gene
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1202 BP; 406 A; 226 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB66893, AAB66894, AAB66895
                                                                                                            AAX13948
                                                                                                                                                                             GTCTTTTTACTTCTCTGGGCCTTTATCTGGGGA
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Human; M010; M019; M024; cancer; obesity; diabetes; osteoporosis; asthma; nervous system disorder; pain; stroke; hypercholesterolemia; chronic obstructive pulmonary disease; hyperlipidemia; atherosclerosis; hyperlipoproteinemia; arteriosclerosis; coronary artery disease; ss.
WO200100644-A1
                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         Human M019 coding sequence
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WPI; 2001-112434/12.
                                                                                                                                                                         04-JAN-2001
                              Khodadoust M;
                                                             (MILL-) MILLENNIUM PHARM INC
                                                                                            30-JUN-1999;
                                                                                                                                          30-JUN-2000; 2000WO-US18097
                                                                                            99US-0345293.
99US-0345680.
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New gene encoding proteins designated M010, M019, M024, useful for the diagnosis, prophylaxis and treatment of cancer, obesity, diabetes, osteoporosis, asthma, atherosclerosis and pulmonary disorders

Claim 1; Fig 2; 98pp; English.

The present invention relation relates to novel human coding sequences and proceins designated MOIO (AAF32082 and AA666881), MOI9 (AAF32084 and AA666895), MOI9 (AAF32084 and AA666895), MOI0 (AAF32086 and AA666895), MOI0 (MOI) and MOI4 (Proceins and compounds which modulate their activity or which bind MOI0, MOI9 and MOI4 proceins and compounds which modulate their activity or which bind MOI0, MOI9 and/Or MOI4 are useful for prevention and treatment of a variety of disorders including concer, obesity, disbetes, osteoporosis, astima, only the second of the s central and peripheral nervous system disorders, pain, stroke, chronic obstructive pulmonary disease, hypercholesterolæemia, hyperiphdæmmia, hyperiphdæmia, byperiphoproteinemia, atheroscierosis, arterioscierosis and coronary artery disease. The present sequence is the coding sequence for human

309 G; 261 T; 0 other;

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alignment_block:
US-09-471-276-831_COPY_1_16 x AAF32084
                                                                                                                                                      alignment_scores
                                Align seg 1/1 to: AAF32084
                                                                                                         Percent Similarity:
ValPheLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                       Quality:
                                                                                                                          Ratio:
                                                                                                         48.00
5.333
81.818
                                from: 1 to:
                                                                                                     Gaps: 0
Percent Identity: 72.727
                                1202
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAX13948

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31-MAR-1999
                                            standard;
(first entry)
                                            DNA;
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GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;

inflammation; ischaemic shock; Alzheimer's disease;

restenosis;

AIDS:

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alignment_block:
US-09-471-276-831_COPY_1_16 x AAX13948
                                                                                                                            seq_documentation_block:
                                                                                                                                               scq_name:
                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                            Align seg 1/1
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Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; Lissue; cancer; tumour; neurodegenerative disorder; leukaenia; developmental abnormality; foetal deliciency; blood; allergy; erenà; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
                                                    Human secreted protein gene
                                                                                                                                                                                                                                                                                                                                                         Isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, Including acute, chronic, and atrophic gastritis, and applic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Helloobacter polynucleotides - used to develop products for the diagnosis, provention and treatment of Hellcobacter infections and gastrointestinal diseases
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01-APR-1997;
                                                                         30-SEP-1999
                                                                                              AAZ06220
                                                                                                                  AAZ06220 standard; DNA; 2062 BP
                                                                                                                                                                                                                                                                                                                             Sequence 1425 BP;
                                                                                                                                                                                                                                                                                                                                                  detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a polynucleotide of the invention. It was
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 166-168; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Al-Garawi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INMR ) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacter
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                                                                                                                                                                                 4 LeuValValPheLeuLeuTrpGlyValThrTrpGly
                                                                                                                                                                   CTAGAAATAGTGCTTTTGCGTTTTTTTTTGGGGG
                                                                                                                                                                                                                                                               Similarity:
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                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ06220
                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                              to: AAX13948
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                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kleanthous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0902615.
97US-0833457.
97US-0881227.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
97..1374
                                                                                                                                                                                                                                                               48.00
5.333
69.231
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                                                                                                                                                                                                                                                                                                                             415 A;
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                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 61.538
                                                    No.
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 XSXEXEX
                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                   seq_documentation_block
                                                                                                     seq_name: /SIDS2/gcydata/yeneseq/geneseqn/NA1999.DAT:AAV71763
                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                     US-09-471-276-831_COPY_1_16 x AAZ06220
                                                                                                                           1854
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09-MAR-1999 (first entry)

pneumoniae DNA probe KP-85-43

AAV71763 standard; DNA; 1747 BP

ATGTGTTTGTAATTTGTACTATTGTGGGGGGTATACTTGG

1892 15

MetLeuValValPheLeuLeuLeuTrpGlyValThrTrp

to: AAZ06220

from: 1 to: 2062

Similarity:

Quality:

Ratio:

4.800 76.923 48.00

Length: 13
Gaps: 0
Percent Identity: 61.538

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07-JAN-1998;
07-JAN-1998;
07-JAN-1998;
07-JAN-1998;
                                                            This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the generate a human immunoglobulin FC portion (e.g., AAZGGZI), for increasing the stability of the fused protein as compared to the human protein only. The invention relates to 36 novel genes and their fragments (Anglez) which are useful for preventing, treating our aneitorous the second conditions e.g. by protein or gone therapy. Also, pathological conditions e.g. by protein or gone therapy. Also, pathological conditions e.g. by protein or gone therapy. Also, pathological conditions can be dispussed by determining the amount of the new polymortlectides. Specific uses are described for each of the 16 polymortlectides, hased on which tissues they are most highly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cognitive disorder; schizophrenia; prostate: obesity, osteoclast; thymus; osteoporosis; arthritis; leastis, lung; thyroiditis; thyroid; dispestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsen
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human genes and the secreted polypeptides they encode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY38387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brewer LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JAN-1999;
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                                                 (see AAZ06219 for described uses).
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2062 BP;
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Rosen CA,
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98US-0070657.
98US-0070658.
98US-0070692.
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666 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                227pp;
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265 C;
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335 G;
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788
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8
other;
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ID AAA74241 standard;
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                                                                                                                                                                                                                                                                                       1392 ATGG 1389
                                                                                                                                                                                                                                                                                                                                                1442 GTGACAATATTGATATTATTCCTGCTGGTTGCAATGACCTGGGGAACCAC 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is a DMA probe used for the diagnosis of infection with Klabsiella pneumoniae. The detection method involves isolating genomic DNA from this bacterium, digesting it with Hindill restriction enzyme, and identifying clones capable of bloding to the bacterium then isolating and sequencing the Hindill fragments involved. The probes have sequences KP-77-45 KMP-80-27 KMP-98-33 and KMP-110-32. The probes allowing involved the probes allowed the supply and highly specific detection of Klebsiella pneumoniae in
                                                      Lobiolity pine; Simple Sequence Repeat; SSR; microsatelite DNA repeat; genetic marker; mapping; inheritance study; population genetics study; plant breeding programme; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 17-18; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA probes for diagnosis of Klebsiella pneumoniae infections -
obtained by HindIII diagestion of genomic K. pneumoniae DNA and
selection of bacterial-binding fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09842843-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Detection; diagnosis; infection; KP-77-46; KP-85-43; KP-98-22; KP-98-33; KP-110-32; probe; ds.
                               Pinus taeda
                                                                                                                                                  29-NOV-2000
                                                                                                                                                                                                          AAA74241 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1747 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biological samples such as blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FUSO ) FUSO PHARM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-1997;
                                                                                                                  Loblolly pine SSR locus RIPPT185
                                                                                                                                                                                                                                                                                                                                                                           MetSerMetLeuValValPheLeuLeuLeu.....TrpGlyValTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keshi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                          ťο
                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          reverse of: AAV71763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0071082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-JP01286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.50
3.167
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matsuhisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 A;
                                                                                                                                                                                                            451 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           367 C; 403 G; 443 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV71763/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 44.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ueyama H;
                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                          to: 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18
CCCCXXTTTXXXXXX
                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC87258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-471-276-831_COPY_1_16 x AAA74241/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a lobiolly pine Simple Sequence Repeat (SSR) locus. SSRs are also known as microsatellite DNA repeats. The present sequence is useful as a genetic marker for genetic mapping, population genetics studies and inheritance studies in various plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polynucleotide having simple sequence repeat useful as markers in plants for genetic characterization e.g. genetic mapping study, an inheritance study of a commercially important trait in a plant breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ECHT/)
                                                                                                                                                            hepatocellular lesion; hyperplasia: altered expression level; clone 45; diagnostic marker; gigantism; acromegaly; diabetes; hepatotropic; transgenic animal; drug screening; drug discovery; mouse; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          165
                                                                                                                                                                                                                                       Mouse liver growth hormone-induced cDNA clone 45,
                                                                                                                                                                                                                                                                       09-MAR-2001
                                                                                                                                                                                                                                                                                                                               AAC87258 standard:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Pages 32-33; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-482836/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Echt CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NELS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JAN-1999;
19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JAN-2000;
                                                                                                                                                                                                          Mouse; growth hormone;
                                         05-MAY-2000; 2000WO-US12366
                                                                                                      W0200066787-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MetLeuValValPheLeuLeuLeuTrpGlyValThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                        TTATTATTGTTGTTGTTGTTGTTATGGGGCATTACATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) INT PAPER CO.
) ECHT C S.
) NELSON C D.
) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nelson CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: AAA74241 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP;
                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US00325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0232884
99US-0232785
              99US-0132663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.00
3.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                 CDNA; 1453 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.
                                                                                                                                                                                                          GH regulatable gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 13
Gaps: 0
Percent Identity: 53.846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122 T; 0 other;
                                                                                                                                                                                                          liver pathology; hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                       ID NO:9
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VIND (-HOAD)

XTXTXTXXXXX

XXXXX XXXX XXXX XXXX

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alignment_block:
US-09-471-276-831_COPY_1_16
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                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA00844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of diagnosing abnormal levels of condition activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method condition of the liver in response to abnormal GH activity. The method the condition of the liver in response to abnormal GH activity. The method of the condition of the liver as the pression of cortain specific genes with the level of GH activity in the liver as the result of GH activity. Excessive GH activity in the liver as the result of GH activity. Excessive GH activity in the liver as the pression to Health, coursing an increase in liver streams a consequence of both hyperplasia and conceptority and hepatocellular lesions which prograss with the prograss with the prograss with depatocyte hypertrophy, and hepatocyte lular lesions which prograss with depatocyte hypertrophy, and namber of genes whose expression in the color studies in transgenic mice which express high levels of bowling globulin, and conding a half-aftebrottein, corticosteroid binding globulin, continue decreased by high GH levels. The genes which are upregulated are those encoding alpha-feta-prottein, corticosteroid binding globulin, continue decreased by high GH levels. The genes which are also updated the complete to abnormally high GH levels. Conversely, expression of the commerce to abnormally high GH levels. Conversely, expression of the commerce of northwan means of a GH levels. Conversely appears to be downregulated. The invention also relates to
                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAC87258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rransgoric monhuman mammals comprising a GH-induced transgene which exhibit or have a propensity to develop a liver pathology; an assay for drugs which inhibit the development of, or which treat a liver pathology, comprising administering the drug to the transgenic animal; and preventing or treating a liver pathology in a patient comprising administering a drug which inhibits the expression of a GH induced gene. The method of the invention is used for diagnosing abnormal levels of GH activity in the liver or predicting a change in the condition of the liver in response to abnormal levels of GH activity. The GH-regulatable liver genes and proteins are useful as diagnostic markers of liver pathology. Assays for the expression of these genes is useful for the pathology. Assays for the expression of these genes is useful for the pathology. Assays for the expression of these genes is useful for the pathology. Assays for the expression of these genes is useful for the light of the pathology. The constitution of the light of the pathology is a solution of the constitution of the light of 
AAA00844 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with diabetes, as other causative agents may act directly or indirectly upon the same genes. The present sequence represents the novel mouse liver cDNA clone 45, expression of which is upregulated by abnormal GH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 55-56; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dlagnosing abnormal levels of growth hormone activity in liver comprising assaying growth transcriptional activity and protein expression level of homeone-regulatable liver genes, as diagnostic markers of liver pathology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 2001-007239/01.
P-PSDB; AAB48740, AAB48741, AAB48742, AAB48743, AAB48744, AAB48745.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1453 BP; 363 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB48746, AAB48747, AAB48748.
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                                                                                                                                                                                          20
                                                                                                                                                                                                                                                        MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThr 14
                                                                                                                                                                                     ATGTCTCTGCTGCTACTGTACTGCTGCTCTGGGGGTTTCACT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tlong
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3.917
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                        x AAC87258
                                                                                                                                                                                                                                                                                                                                           from: 1 to: 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 G; 346 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
0
64.286
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H

Align seg 1/1 to: AAA00844

2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16

from: 1

to: 300

US-09-471-276-831_COPY_1_16 x AAA00844

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alignment_block:
                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ilibraries constructed from human colon cancer call lines. The present invantion also describes a method of detacting differentially expressed gene correlated with a cancerous state of a mammalian cell, compilating detacting at least one differentially expressed gene product in a test of the coll from a cell suspected the beginning of the differentially expressed gene product is correlated with a concerous state of the cell from which the text of the cell from the
                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams LT,
Reinhard C,
Lamson G, Dr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe;
                                                                                                                                                                                                                                                                                                                                                       Sequence 300 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      negative breast cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 384; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09958675-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     breast cancer; oestrogen receptor positive breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human colon cancer cell line polynucleotide sequence SEQ ID NO:835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA00844;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-NOV-1999
                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon cancer; tumour; diagnosis; gene expression product; detection; cancerous state; metastasis; identification;
                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escobedo
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98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
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                                                                                                                              46.00
3.833
                                                                                                                                                                                                                                                                                                                                                       72 A;
                                                                                    80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Randazzo F, Kennedy GC, Pot D, Kass
Crkvenjakov R, Dickson M, Drmanac S,
Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                       46 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                      lung cancer, and colon cancer.
                                                                                    Percent Identity: 46
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                                                                                                                                                                                                                                                                                                                                                       96 G; 86 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kennedy GC, Pot D, Kassam
R, Dickson M, Drmanac S, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sudduth-Klinger J;
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78

206

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seq_name:
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US-09-471-276-831_COPY_1_16 x AAV89754/rev
                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
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                                                                                                                                                             Align seg 1/1 to reverse of: AAV89754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The polynucleotide may also be useful for gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity immune stimulating or suppressing activity, haematopoless regulating activity, issue growth activity, activity/imibbin activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human secreted proteins - de.g. human blood, kidney, foetal lung, placents, testes, ovary, pituitary, retina and colon cDNA libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST clone CS485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV89754 standard; cDNA; 361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 319; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-070077/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                     256 ATGAGTTTGATGGTGACCTGGAGGTGAAACTGTGACTTCATGATGTTCTG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence represents a human expressed sequence tag (EST) polynuclectide, which is a secreted EST, and the encoded protein predicted to have useful biological activities which would make
pGlyValThrTrpGly 16
                                                                                                           /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAV89754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 BP; 88 A; 112 C; 80 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spaulding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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paulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0838821
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                                                                                                                                                                                                                                                                                                    46.00
3.067
68.182
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Treacy M;
                                                                                                                                                                                                                                                                                                Percent Identity: 36.364
                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                           Length:
Gaps:
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X S X W X D X X C
                                                                                                                                                                       seq_documentation_block:
ID AAF93704 standard;
                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF93704
                                                                            CDNA encoding SRT protein
                                                                                                          21-MAY-2001 (first entry)
                                                                                                                                           AAF93704;
                                                                                                                                                                       AAF93704 standard; cDNA; 539 BP
                                             Human; SRT; gene therapy; gene mapping; tissue typing; ss
                                                                                                                                                                                                                                                     GAGGCTGACCTGGGGT 191
                                                                            isolated from testis tissue SEQ ID 525
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New isolated nucleic acid molecule encoding a SRT polypeptide for production of recombinant SRT polypeptides, gene mapping, diagnosing genetic disorders and for gene therapy. WPI; 2001-112729/12 Baker KP, 26-JUL-1999; 21-JUL-2000; 2000WO-US20006 01-FEB-2001 W0200107611-A2 Homo sapiens. (GETH) GENENTECH INC Goddard A, 99US-0145701 Wood WI is useful

Sequences ARP93180 · ARP93743 represent polynucleotide sequences encoding human SRT proteins. The cDNA sequences are isolated from various different human tissue cDNA libraries. The invention relates to a method Claim 2; Fig 525; 663pp; English.

for detecting cDNA encoding an SRT protein, a vector containing cDNA encoding SRT, a host cell transformed with the vector, an isolated SRT polypeptide, and an antibody which binds to SRT. The polyvucleotide sequence can be used in gene therapy and is useful in the recombinant production of SRT polypeptides, as a hybridisation probe to screen libraries to isolate cDNAs with sequence identity to SRT polypeptides, map the gene encoding the SRT polypeptides and analysing genetic disorders, tissue typing and disease tissue detection. The SRT polyperide can be used in polymerase chain reaction, acreening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for new therapeutic molecules and generation of antisease RNA screening for the screening for new threatening for the screening for the screeni RNA č

Sequence 539 BP; 159 A; 107 C; 135 G; 137 T; 1 other;

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alignment_block:
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seq_documentation_block:
                                                                                                                                              Align seg 1/1 to reverse of: AAF93704 from: 1
                                                                                                                                                                                  US-09-471-276-831_COPY_1_16 x AAF93704/rev
                                                                                                                                                                                                                                        Percent Similarity:
                                                                                          SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
                                                                        AGCACAAAACTTTTATTAGCGCTTCTCTGGGGAATCACTTGG 342
                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                      46.00
4.182
78.571
                                                                                                                                                                                                                                        Percent Identity: 50.000
                                                                                                                                                                                                                                                           Length:
Gaps:
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH53784

AAH53784 standard; DNA; 1218 BP

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alignment_block:
US-09-471-276-831_COPY_1_16 x AAH53784
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                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANIS2304 to ANIS3970 represent nucleic acids (I) encoding polypeptides (II), given in ANG81434 to ANG83120, from staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) (I) with the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to acids produce the subjects and the raise antibodies against the bacteria. The polypeptides and the raise antibodies against the bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of S. epidermidis infections, e.g. endocarditis, AMH33971 to AMH35090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AMH35091 to AMH35090 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEO ID NO:4454 so even though sequences are given in the disclosure for SEO ID NO:4465 to 4472, no sequences are given in the disclosure for SEO ID NO:4465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 774-775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-316495/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WC200134809-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus epidermidis vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1218 BP; 366 A; 179 C; 245 G; 428 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAY-2001
59 GTGACATTGCTCATCATCATATTGGTTCTATGGCAGGTTTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cpidermidis open reading frame nucleotide sequence SEQ ID NO:2961
                                                                MetSerMetLeuValValPheLeuLeuTepGlyValThrTrp 15
                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                               6
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                                                                                                                                               AAH53784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0164258
                                                                                                                                                                                                                                                                                                                        46.00
3.538
86.667
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                                                                                                                                          from: 1 to: 1218
                                                                                                                                                                                                                                                                                                                             Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                           Caps:
                                                                                                                                                                                                                                                                                                                        15
0
40.000
    103
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seq_name: /SIDS2/gcgdata/genescq/geneseqn/NA1999.DAT:AAX17775

alignment_scores Percent Similarity:

Quality: Ratio

46.00 4.182 78.571

Percent Identity: 57

Length

Sequence 1338 BP;

238 A;

495

C

373 G;

232 T;

0 other;

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seq_documentation_block:

XX AX17775;
XX AX17775;
XX I2-MAY-1999 (first & XX I2-MAY-1999) (first & XX I2-MAY-1998) (first
                                                                                                                                                                                                                                               (ARDS), Rheumatold arthritis, osteoarthritis inflammatory Boxal Disease (IBD), psoriasis, dermatitis, asthma, allergies, becterial, fungal, protozoan and viral infections, especially those caused by HV-1 or HIV-2; HIV-associated cachaxia and other immunodeficient disorders; septic shock; pain, injury; cancers; anorexta; builmia; Parkinson's disease; cardiovascular disease including restenosis, abressorias disease; cardiovascular disease inflating restenosis, bypertension; urinary retention; angina pectoris, ulcers; benign prostatic hypertrophy; urinary retention; angina pectoris, ulcers; benign prostatic hypertrophy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide (PTLAR3). Host cells transformed with an expression vector comprising the HTLAR3) nucleic acid are used for the recombinant production of the protein. PTLAR33 polymucleotides and polypeptides are useful for diagnosing susceptibility to diseases and for screening for antagonists, agonists. Phase can be used in treatment to enhance (agonist) or block (antagonist) PTLAR33 activity. Diseases diagnosed prevented or treated include: bone loss and inflammatory disorders including osteopprosis, Adult Respiratory Disease Syndrome
                                                                              and psychotic and neurological disorders, including schizophrenia, manic depression, anxiety; delirium, domentia, severe menual retardation and dyskinesias, such as Huntington's disease or Gilles de la Touretto's syndrome. HTLAR3 polypeptides are also useful for mapping openes to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides - useful as diagnostic reagents and for prevention
and treatment of bone loss, neurological and inflammatory disorders
and cancer, HIV infections and angina pectoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory disorder: osteoporosis; Adult Respiratory Disease Syndrome, arthritis, peoriasis, dermatitis, astima; a latery; infection; HIV-1 arthritis; cachesia; immunodeficient disorder; septic shock; pain, injury; cancer; ancrexia; bulinia; arkinspor's disease; caddovascular disease; neurological disorder; Huntington's disease; den therapy; gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX17775 standard; cDNA; 1338
                                                       chromosomes, allowing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a YAK-1 related serine-threonine protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 15–17; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New serine-threonine kinase (HTLAR33) polypeptides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilles de la Tourette's syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAK-1; serine-threonine protein kinase; HTLAR33; bone loss; ARDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTLAR33 encoding cDNA (EST derived sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-MAY-1999 (first entry)
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97US-0053924.
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                                                       gene inheritance to be studied through linkage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             БP
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alignment_block:
US-09-471-276-831_COPY_1_16 x AAX17775
                                                                                                  alignment_block:
US-09-471-276-831_COPY_1_16 x AAX83568
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                                                                            Align seg 1/1 to: AAX83568 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block
                                                                                                                                                                                                                                                      The invention relates to a method for monitoring oil contamination of sea water by detecting in the sea water, a microbe having the following properties; (1) it has no flagelium; (2) it is a Gram-negative batterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it cannot assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30 cm alkanes. This sequence tepresents a fragment of the 16S rDNA gene from the microbe of the inventors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  845
                          132
                                                                                                                                                                                                                        Sequence 1535 BP;
                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 7; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                  Monitoring of oll contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-564435/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria
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                                                                                                                                                                                                                                                                                                                                                                                         Proteobacteria, gamma subdivision, etc.z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monitoring; oil; contamination; sea water; detection; flagellum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16S rDNA gene fragment from marine bacterium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SerMetLeuValValPheLeuLeuTrpGlyValThrTrp
                                                   LeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCCCCCTCCTGATGACCCTGCCACTCTGGGGCCCTCACCTGG 886
                          TTGTGGGGGATAACTTGGGGA 152
                                                                                                                                                                    Quality:
                                                                                                                                                       Ratio:
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6
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                                                                                                                                         46.00
6.571
100.000
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                                                                                                                                                                                                                        376 A;
                                                                                                                                                                                                                      349 C; 494 G; 316 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                         Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 1338
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                                                                              1535
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85.714
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                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                seq_documentation_block;
                                                                                                                                                                    132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1998;
Probe; human; microarray; gene expression; cervical epithelial cell;
                     Probe #4735 for gene expression analysis in human cervical cell sample
                                                   12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                              Sequence 1535 BP;
                                                                                                                                                                                                                                                                                                                                                                                         isolate K3-3.
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                                                  (first entry)
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seq_documentation_blook:
ID AAX83569 standard; DNA; 1535 BP.
XX AAX83569;
XX 21-DBC-1999 (first entry)
XX XX 21-DBC-1999 (first entry)
                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI14802
                                                                                                                                                                                                                                                                                                                         US-09-471-276-831_COPY_1_16 x AAX83569
                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAX83569
                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for monitoring oil contamination of sea water by detecting in the sea water, a microbe having the following properties: (1) it has no flagelium; (2) it is a Gram-negative bacterium; (3) it belongs to Proteobacteria, gamma subdivision; (4) it efficiently assimilate glucose as a single carbon source; and (5) it efficiently assimilates at least one of 10-30C n-alkanes. This sequence represents a fragment of the 16s TDNA gene from the microbe of the inventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monitoring of oil contamination of sea water - where oil contamination is evaluated by detection of a microbe having properties from e.g. having no flagellum, being a Gram-negative bacterium, belonging to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 7-8; 15pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monitoring; oil; contamination; sea water; detection; flagellum;
AAI14802 standard; DNA; 1966 BP
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                                                                                                                                                                                     10 LeuTrpGlyValThrTrpGly 16
                                                                                                                                                TTGTGGGGGATAACTTGGGGA 152
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6.571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 T;
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85.714
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EXEXEXEXE
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US-09-471-276-831_COPY_1_16 x AAI14802
                                                                                                         seq_documentation_block:
                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI36160
                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                        1282
                                                                                                                                                           1332
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21-SEP-2000;
27-SEP-2000;
                     Probe #4846 used to measure gene expression in human placenta sample
                                                                                               AAI36160 standard; DNA; 1966
                                                                                                                                                                                                                                                                                                                                                                                                           specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid protes (SBNP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-OCT-2000;
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26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer;
Probe; microarray; human; placenta; antenatal diagnosis;
                                                17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1966 BP; 406 A; 402 C; 610 G; 548 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOLE-)
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                                                                                                                                                           GAGGCTGACCTGGGGT 1347
                                                                                                                                                                                pGlyValThrTrpGly 16
                                                                                                                                                                                                         ATGAGTTTGATGGTGACCTGGAGGTGAAACTGTGACTTCATGATGTTCTG
                                                                                                                                                                                                                                                                                                                                      Quality:
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2000US-0207456
2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
2000US-0024263
                                              (first entry)
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3.067
68.182
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Percent Identity: 36.364
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                                                                                                                                                                                                                                                        1966
 PX S X X X X E X T X A X
                                                                                                                                                      seq_documentation_block:
ID AAI04592 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-2001
                                                                                                                                  AAI04592;
WO200157270-A2
                       Homo sapiens
                                                          Probe; human; breast disease; breast cancer; development disorder; ss;
                                                                                Probe #4583 used to measure gene expression in human breast sample
                                              inflammatory disease;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                         The present invention relates to single exon nucleic acid probes in the present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying ge expression in samples derived from human placents. The probes are for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                   WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                04-0CT-2000;
Sequence 1966 BP; 406 A; 402 C;
                                                                                                                                                                                   Claim 25; SEQ ID No 4846; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                   SG,
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2000US-0236359
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2000US-0632366.
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610 G; 548 T; 0 other;
                                                                      are useful
                                                                                                                                      (SENP).
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alignment_block
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA104592
                                                                                                                                                                      Align seg 1/1 to: AAI36160
                                                                                                                                                                                                     US-09-471-276-831_COPY_1_16 x AAI36160
                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                      1282 ATGAGTTTGATGGTGACCTGGAGGTGAAACTGTGACTTCATGATGTTCTG 133:
                                   1332 GAGGCTGACCTGGGGT 1347
                                                                     11
                                                                                                                                     pGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                           Quality:
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68.182
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                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                          Percent Identity:
                                                                                                                                                                      to: 1966
                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                          36.364
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(first entry)

1966 BP

proliferative breast disease;

non-carcinoma tumour.

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seq_documentation_block:
ID_AAX17774 standard; cf
XX AAX17774;
AC AAX17774;
XX 12-MAY-1999 (first e
XX YAK-1 related serine,
XX YAK-1; serine-threon;
KW YAK-1; serine-threon;
KW YAK-1; sprine-threon;
KW arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX17774
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                                                                                                                                                                                                                                                                                        1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe The probes are useful for measuring human gene expression in a human breast sample, where the prol mybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, steaping, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the hreast fiberouries for the breast fiberouries and prognosing diseases.
YAK-1; serine-threonine protein kinasa; HTLAR3; bone loss; ARDS;
inflammatory disorder; osteoporosis; Adult Respiratory Disease Syndrome:
arthritis; psoriasis; dermatitis; asthma; allergy; infection; HIV-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                           AAX17774 standard; cDNA; 2394 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single exon nucleic acid probe used to measuring gene expression
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                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                          pGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                              ATGAGTTTGATGGTGACCTGGAGGTGAAACTGTGACTTCATGATGTTCTG 1331
                                                                                                                                                                                                                                                                                        GAGGCTGACCTGGGGT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; SEQ ID No 4583; 322pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000GB-0024263
                                                                           serine/threonine protein kinase-HTLAR33 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 C; 610 G; 548 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 36.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1966
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alignment_block: US-09-471-276-831_COPY_1_16 x AAX17774

Percent Similarity:

Percent Identity:

57.143

Ratio

Align seg 1/1 to: AAX17774

from: 1 to: 2394

1901

seq_name: /SIDS2/gcgdata/geneseg/geneseqn/NA2000.DAT:AAA16647

TCCCGCCTCCTGATGACCCTGCCACTCTGGGGGCCTCACCTGG 1942 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp

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alignment_scores
                                                                                                                                                                                                                                                                             protozon and viral infections especially those caused by HIV-1 or HIV-2 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide (HTLAR3), Host cells transformed with an expression vector comprising the HTLAR3) nucleic acid are used for the recombinant production of the protein. HTLAR3 polymucleotides and polypeptides are useful for are useful for diagnosing susceptibility to diseases and for screening for antagonists, agonists. These can be used in treatment to enhance (agonist) or block (antagonist) HTLAR33 activity. Diseases diagnosed, prevented or treated include: bone loss and inflammatory disorders including osteoporosis, Adult Respiratory Diseases Syndrome (ARDS), Rhumatoid arthrits, osteoarthritis, Inflammatory Bovel Disease (ARDS), Rhumatoid arthritis, asthma, altergies; bacterial, fungal, [199].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New serine-threonine kinase (HTLAR33) polypeptides and polynucleotides - useful as diagnostic reagents and for prevention and treatment of bone loss, neurological and inflammatory disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIY-2; cachexia: immunodeficient disorder; septic shock; pain: injury; cancer; anorexia; bullima: Parkinson's disease; cardousscular disease; neurological disorder; Huntington's disease; gene therapy; gene mapping;
                                                                                                                                                                                             Sequence 2394 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA encodes a YAK-1 related serine-threonine polypeptide (HTLAR33). Host cells transformed with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 13-15; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and cancer, HIV infections and angina pectoris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW94997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-108353/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bergsma DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP894863-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilles de la
                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0027064
97US-0053924
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46.00
4.182
78.571
                                                                                                                                                                                                  478 A;
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                                                                                                                                                                                                  676
                                                                                                                                                                                                  င္ပ
                                                                                                                                                                                                  439 T;
                                                                                                                                                                                                  0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein kinase
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diabetes mellitus, myasthenia gravis, grafi-versus-host-disease and autoimmune infiammatory eye disease. The proteins can also be used to treat allergic conditions, such astima. AAA1678 to AAA16774 represent probes for the human secreted proteins from the present invention.

represent

Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent

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_documentation_block:
AAA16647 standard; cDNA; 3191 BP
                                                                                                                                                               AA16618 to AAA1697 encode the human secreted proteins given in AAV94898 to AAV94980, isolated from human adult brain, adult thyroid, adult retina, feetal carcinoma, adult boods, adult neural, feetal kidney, adult placenta, adult testins, whole embryo, adult cartilage, kidney, foetal brain, adult thymms, feetal placenta, adult therus, adult thour and adult bladder, cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. The polynucleotides can be used as markers for tissues in which the protein is preferentially expressed, as molecular weight which the protein is preferentially expressed, as molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong GG,
                                                                       markers on Southern gels, and as chromosome markers or tags to identify chromosomes or to map gene positions. The proteins can be used in the trontmont of immune deficiencies and disorders, such as severe combined immunedeficiency (SCTD), as well as viral, bacterial, fungal and orther infections. These infections include human manunodeficiency virus (HTV),
erythematosis, rheumatoid arthritis, autoimmune pulmonary inflammation
                  as connective tissue disease, multiple sclerosis, systemic lupus
                                     hepatitis, herpesviruses, mycobacteria, Leismania spp., malaria and candidiasis. The proteins can be used to treat autoimmune disorders such
                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotides encoding secreted proteins, which may have e.g. nutritional, chemokine, immune stimulating or suppressing, hematopolesis regulating, tissue growth, activin/inhibin antiinflammatory or tumor inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
connective tissue disease; multiple sclerosis; erythematosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antithyroid; immune deficiency; severe combined immunedeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibactcrial; antifungal; cytostatic; antiinflammatory; dermatological;
antidlabetic; antiasthmatic; antiarthritic; antirheumatic; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-205979/18.
DB; AAY94927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D, Treacy M, Clark HF, I
                                                                                                                                                                                                                                                                                                                                                                                Page 530-531; 641pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pendent diabetes mellitus; graft-versus-host-disease; inflammatory eye disease; allergy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0120575
99US-0132020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein clone ck213_12 nucleotide sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0096622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99us-0119931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        980S-0099229
980S-0105368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Agostino MJ,
Fechtel K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steininger RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spaulding V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evans C;
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seq_documentation_block
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
            AMB52304 to AMB5370 represent nucleic acids (I) encoding polypeptides (II), given in AMB3170, from StapPylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used (II) can contain the nucleic acids (I) may be used to produce the secondaining them which are used to produce hosts calls which express the containing them which are used to produce hosts calls which express the cused to vacchate subjects and to raise antibodies against the bacteria. The polypeptides (II) (and/or nucleic acids) may then be used to vacchate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                   Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                            useful for vaccinating against infections, e.g. endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides from Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH54911 standard; DNA; 3427 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3191 BP; 998 A; 716 C;
in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 LeuValValPheLeuLeuLeuTrpGlyValThrTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTAGCTGTTTTTCTCATTTGTTGGTGTGTGGGGTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                Page 2004-2005; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic polynucleotide sequence SEQ ID NO:4275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.00
4.600
76.923
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Caps: 0
Percent Identity: 61.538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2878
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US-09-471-276-831_COPY_1_16 x
     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH54481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AAH54911 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                       AMB52304 to AAH53970 represent nuclaic acids (I) encoding polypeptides (II), given in AAG811454 to AAB831120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the s. epidermidis polypeptides (II) yia the production of vectors containing them which are used to produce hosts cells which express the polypeptides if the product of vaccinate subjects and to raise antibodies against the bacteria used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e. 9, endocarditis. AAH53971 to AAH55990 represent specifically claimed S. epidermidis infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The present invention specifically claims all the polymoclectide sequences given in the sequence listing of the present specification however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
polynucleotide sequences from the present invention. AAH55091 to
AAH55098 represent oligonucleotide sequences and primers which are used
in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3427 BP; 1167 A; 642 C; 478 G; 1140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 1487-1488; 2188pp; English
                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kimmerly WJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GLAX ) GLAXO GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH54481 standard; DNA; 3450 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGACATTGCTCATCATCATATTGGTTCTATGGCAGGTTTTATGG 1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic polynucleotide sequence SEQ ID NO:3845
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Gaps: 0
Percent Identity: 40.000
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88888×8
alignment_block:
US-09-471-276-831_COPY_1_16 x AAH54481/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AAH54481 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2470 GTGACATTGCTCATCATCATATTGGTTCTATGGCAGGTTTTATGG 2426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The present invention specifically claims all the polymocleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4454 to 4472, no sequences are present for SEQ ID NO:455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001 (first entry)
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                                                                                                                                                                                                                                                         WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. epidermidis genomic polynucleotide sequence SEQ ID NO:4003
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                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection; diagnosis;
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polyapptides The polyapptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polyapptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g., endocardits. AMH5391 to AMH55090 represent specifically claimed S. epidermidis genomic DNA polyappties esquences from the present invention. AMH55091 to AMH55098 represent oligonucleotide sequences and primers which are used AMH55098 represent oligonucleotide sequences.

in the exemplification of the present invention

in vaccination. The nucleic acids (1) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the AMB52304 to AAH53970 represent nucleic acids (1) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis (1) and (II) can have antibacterial activity and therefore can be used Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -

Claim 8; Page 1677-1678; 2188pp; English

999998**%**&

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seq-documentation_block:

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AC AAC76440 standard; cl
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AC AAC76440:

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BOB Human ORFX ORF1995 pa
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US-09-471-276-831_COPY_1_16 x AAH54639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic: gene therapy, cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteobarchritis; graft vs host disease; cardiovascular disease; diabetes melitius; hypothyroldsm; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; astima; allorgy; aplastic aneemia; nocturna, haemoglobinuria; burn; wound; allorgy; aplastic aneemia; nocturna, haemoglobinuria; burn; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; open reading frame: ORFX; detection: cytostatic: hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarchritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibactorial; antifungal; antibhoumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.B. The present invention specifically claims all the polymiclectide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEO ID NO:4454 so even though sequences are given in the disclosure for SEO ID NO:4455 to 4472, no sequences are present for SEO ID NO:4455 to 4464.
                                                                                  Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621
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                                                                                                                                                                                                                                                                                                                                                                                                           (CURA-) CURAGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cartilage damage; antiinflammatory disease; coagulation;
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                                                                                                                                                                                                                                                                                                                              Leach M;
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99US-0127636.
99US-0127728.
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Gaps: 0
Percent Identity: 40.000
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neurodegenerative disorders and cardiovascular disease

Tang YT,

Liu C,

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Chen 70

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alignment_block:
US-09-471-276-831_COPY_1_16 x AAC76440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3313 TTAGCTGTTTTTCTCATTTGTTGGTGTGGGGTGGGGG
                                                                              25-JAN-2000;
17-JUL-2000;
03-AUG-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathological conditions issociated with an ORPX associated disorder. The nucleic acids can be used to express ORPX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lipus erythematosus, severe combined immunodeficierory (SCID), AIDS, vital, batterial or fungal infection, malaria, autoimmne disorders, asthments and combined infection, malaria, autoimmne disorders, asthments.
                                                                                                                                                                                                                                                                                                                                                     tomato; monkey; dog; sea urchin; expressed sequence tag; Es
diagnostics; forensic test; gene mapping; genetic disorder;
biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     allergies, aplastic anaenia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis, and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunostimulant; cardiant; thrombolytic; coagulant; vascropic; antiidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirhematic; antihyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatoctopic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; osteopathic; anticonvulsant; antiarihitic; immunosuppressant; osteopathic; anticonvulsant; antiarihitic; immunosuppressant;
                                                                                                                                                                                                                                02-AUG-2001.
                                                                                                                                                                                                                                                                         WO200154477-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human EST-derived coding sequence SEQ ID NO: 910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH99053 standard; cDNA; 5345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4522 BP; 1294 A; 1006 C; 1144 G; 1076 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 3161-3164; 5507pp; English
                                     (HYSE-)
                                                                                                                                                                                     25-JAN-2001; 2001WO-US02687
                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                      sheep; pig;
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                                     HYSEQ INC
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                                                                              2000US-0617746.
2000US-0631451.
2000US-0663870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                            2000US-0491404
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76.923
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Gaps:
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seq_documentation_block:
ID AAZ34627 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ34627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-471-276-831_COPY_1_16 x AAH99053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAH99053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2397 ATGAGTTTGATGGTGACCTGGAGGTGAAACTGTGACTTCATGATGTTCTG 2446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2447 GAGGCTGACCTGGGGT 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, menkey, macaque, yeast, bacteria, fruit; yeas urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess boodiversity, and for nutritional purposes. The present sequence is a cDNA boodiversity, and for nutritional purposes.
                                                                                                                                                                                                                                                                                                                                                                                           Clock; mouse; transcription factor; circadian rhythm;
jet lag; sleep disorder; depression; seasonal affective disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 726-728; 1275pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cao Y,
                  Weitz CJ,
                                                        (HARD ) HARVARD COLLEGE.
                                                                                                 07-MAY-1998;
                                                                                                                                       06-MAY-1999;
                                                                                                                                                                             11-NOV-1999.
                                                                                                                                                                                                                   W09957137-A1
                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse clock cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5345 BP; 1288 A; 1232 C; 1539 G; 1286 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                        fertility; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 pGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-476164/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drmanac RA,
                     Gekakis N, Staknis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                              9808-0084610
                                                                                                                                       99WO-US10072
                                                                                                                                                                                                                                                                         Location/Qualifiers
389..2956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.00
3.067
68.182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 36.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
                     Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Werhman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            χŞ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV61401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAZ34627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-471-276-831_COPY_1_16 x AAZ34627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5598 CTGCTTCTGTATGGGGTGACTTGGGGT 5624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-box-linked genes. The drugs are used to treat conditions such as 
jet lag, sleep disorders, depression (seasonal affective disorder) 
and infertility. The invention also provides BMALI and CLOCK 
proteins with which to stimulate the transcription of an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mechanism regulating genes responsible for the establishment and/or maintenance of the circudian clock, is useful for the assay of novel drugs aimed at restoration of a nomal circulan cycle, the drugs being modulators of BMAL1-CLOCK-mediated transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (see ANY32214). CLOCK activates the transcription of the perl gene when present in combination with BMAL1 (see ANY32209). The invention, based on the discovery of the transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of murine cDNA encoding CLOCK protein (see AAY32214). CLOCK activates the transcription of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel heterodimeric composition for identifying modulators used in diagnosing and treating circadian clock disruption disorders -
                                                                                                                                                                                                                                                                                                               Cos
                                                                                                                                                                                                                                                                                                                                                                                                           Clock gene; circadian rhythm; mouse; seasonal affective disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 15A-B; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY32214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-052938/04.
WPI; 1998-520828/44
                                        Pinto LH, Takahaski JS,
                                                                                                                 30-JUN-1997;
13-MAR-1997;
                                                                                                                                                                                                                   17-SEP-1998.
                                                                                                                                                                                                                                                         W09840514-A1
                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse Clock gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV61401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV61401 standard; DNA; 7498 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7478 BP; 2177 A; 1534 C; 1616 G; 2151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E-box-linked gene which regulates the circadian clock.
                                                                           (NOUN ) UNIV NORTHWESTERN
                                                                                                                                                                          13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                 97US-0885291
97US-0816693
                                                                                                                                                                             98WO-US05114.
                                                                                                                                                                                                                                                                                                               Location/Qualifiers 389..2956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.00
5.111
                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 9
Gencent Identity: 88.889
                                        Turek F;
                                                                                                                                                                                                                                                                                                                                                                                                              jet lag; sleep-wake
diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                disorder;
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seq_documentation_block:
ID AA121916 standard: DNA: 128 BP.
XX AA121916;
XX 12-0CT-2001 (first entry)
XX Probc #11849 for gene expression
XX Probc: human; microstray; gene e
KW cgrvical cancer; ss.
XX W0230157278-A2.
XX W0230157278-A2.
XX 10-10M-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-471-276-831_COPY_1_16 x AAV61401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI21916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 5.111
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5598 CTGCTTCTGTATGGGGTGACTTGGGGT 5624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenotypic resous of Clock, and make expression of conditate genes
by Northern analysis in Clock mutant versus wild type mice The
human Clock gene (see Aw66/450) has also been identified The
invention provides isolated and purified CLOCK polyapitides. Per
polymicleotides (Including antisense), vectors and host cells. The
polymicleotides or polyapitides can be used to treat disorders of
altered or disrupted circulation rhytms e.g., jst-lag, sessonal of
altered arother sleep-wake cycle disorders such as mood states,
stress, neurological disorders, to regulate diet and food intake
especially for disbetes, to treat cardiovascular, respiratory
liver or endocrine disorders, and for diagnossis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circadian rhythmicity. Identification and isolation of the Clock geno involved: genetic mapping of the mouse genome (mid portion of chromosome 5); physical mapping of the Clock region; transcription unit analysis in the Clock region by (a) direct screening of SCN cDNA libraries with BAC clones as probes, (b) hybridisation selections of cDNAs from SCN libraries using BAC clones as driver, and (c) shutgun sequencing random Mid libraries made from BAC clones; transgenic mouse expression of an isolated BAC clone and the clone in the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (see AAW79529) that acts as a transcription factor. The Clock generating the strength of the circalan clock system: the intrinsic circadian period and the persistence of circadian rhythmicity. Identification and isolation of the Clock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the complete nucleotide sequence of the murine Clock game based upon genomite axon sequences; splice donor and acceptor sites are provided in Anv61403-48. It encodes a 855-amino acid polypept (see ANV91929) that acit as a transcription factor. The Clock genome
                                                                                                                                                                                                                                                                                                                                                              Probe: human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe #11849 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7498 BP; 2197 A; 1534 C; 1616 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormal cell division such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 8.1-8.8; 154pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel mouse and human circadian rhythm gene, clock - useful for treating e.g. jet-lag, sleep-wake disorders, abnormal cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW79529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is the complete nucleotide sequence of the murine Clock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide
Clock gene
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
  Sequence 128 BP;
                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                            microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithellal cells. By measuring gene expression, the probes are therefore useful in grading and/or staging
                                                                                                                                                                                                              Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                            27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
                               at ftp.wipo.int/pub/published_pct_sequences.
                                                                               of diseases of the cervix, notably cervical cancer.
                                                                                                                                          The present invention relates to human single exon nucleic acid probes (SEMP). The present sequence is one such probe. The SEMPs are derived from human Heia cells. The SEMPs can be used to produce a single exon
                                                                                                                                                                                                                                             analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                             WPI; 2001-488901/53
                                                                                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                               SG
                                                                                                                                                                                                           SEQ ID No 11849; 487pp; English.
                                                                                                                                                                                                                                                                                                                            Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                              2000GB-0024263
18 A; 40 C;
                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                                                                                                                                                                                                            Chen W,
  37
                                                                                                                                                                                                                                                                                                                            Rank DR
G; 33 T; 0 other;
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alignment_block:
US-09-471-276-831_COPY_1_16 x AAT21916
seq_documentation_block:
ID AAI47201 standard;
                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA147201
                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                       Align seg 1/1 to: AAI21916
                                                                                                                                                                                                                                            Percent Similarity:
  AAI47201 standard; DNA; 128 BP
                                                                                     74 GTCCTCTTGCTCCTGCTGGGGGTGTGGGTGG 106
                                                                                                                      5 ValValPheLeuLeuTrpGlyValThrTrp 15
                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                             Ratio
                                                                                                                                                                                                                                          5.000
81.818
                                                                                                                                                                                                                                                                           45.00
                                                                                                                                                       from: 1 to:
                                                                                                                                                                                                                                            Percent Identity:
                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                        11
0
63.636
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genetic disorder;

microarray;

Probe #15887 used to measure gene expression in human placenta sample.

human; placenta; antenatal diagnosis;

AAI47201;

17-OCT-2001 (first entry)

04-FEB-2000; 26-MAY-2000; 30-JUN-2000;

2001WO-US00663. 2000US-0180312. 2000US-0207456.

Homo sapiens.
wo200157272-A2
09-AUG-2001.
30-JAN-2001; 2

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seq_documentation_block:
ID AAI07604 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAI47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-471-276-831_COPY_1_16
                                                         04-FEB-2000; 2000US-0180312
26-MAY-22000; 2000US-0207456
30-JUN-22000; 2000US-0508408
03-MG-2000; 2000US-032366
21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
04-CCT-2000; 2000US-0234587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
          Penn
                                                                                                                                                                                      09-AUG-2001.
                                                                                                                                                                                                                                                             Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                Probe #7595 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                            09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 128 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                              WO200157270-A2
                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                           29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                                                                                                                                                                                                           74
                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ValValPheLeuLeuLeuTrpGlyValThrTrp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to single exon nucleic acid probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                         GRECTETTTGTCCTGCTCTGGGGGTGTGGGTGG
          SG,
                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AA107604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel DK,
          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID No 15887; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.00
5.000
81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 A; 40 C;
                                                                                                                                                                                                                                                                                                                                                                            DNA; 128
          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x AAI47201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37 G;
          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 11
Gaps: 0
Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           106
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alignment_block:
US-09-471-276-831_COPY_1_16 x AAI07604
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Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXCCCCCCCCCCCCXXXTTXXX
PT XXX PXX PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA10193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAI07604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring human game expression in a human breast sample where the probability tridings at this straingney to a nucleic acid expressed in the human breast me probes are useful for predicting, disposing profing, steping, monitoring and prophosing diseases of the human breast particularly those diseases with polygenic settlology religious and prophosing diseases include; breast cancer diseases of development, inflammatory diseases include; breast cancer diseases of development, included the prophosing diseases and profine the press includes the property of the prophosic prophosic profiles and the prophosic prophosic profiles are the property of the prophosic prophosic profiles and profiles are profiles are profiles and profiles are profil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 128 BP; 18 A; 40 C; 37 G; 33 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-carcinoma tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to novel single exon nucleic acid p
The present sequence is one such probe. The probes are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel single exon nucleic acid probe used to measuring gene expression
in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxicological response marker; rat; liver; expression pattern; toxicity screening; toxic compound; polycyclic aromatic hydroc PAH; benzo(a)pyrene; clofibrate; acetaminophen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat liver toxicological response marker,
                                                                                                                                                                                                                                                                                                                                    28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200012760-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA10193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA10193 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ValValPheLeuLeuLeuTrpGlyValThrTrp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCCTCTTTGTCCTGCTCTGGGGGGTGTGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; SEQ ID No 7595; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                      98US-0141825
98US-0172108
                                                                                                                                                                                                                                                                                                                                                                                                99WO-US19768
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81.818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 11
Gaps: 0
Percent Identity: 63.636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO:86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         part of the printed
directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrocarbon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          where the probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes.
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Isolated and purified nucleic acid molecules used as toxicological response markers for detecting and diagnosing a potential toxicological

WPI; 2000-237888/20.

(INCY-) INCYTE

PHARM INC.

Zweiger

GB,

Panzer

SR,

Seilhamer

98US-0172711

response in a mammalian subject to a test compound or molecule

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seq_documentation_block:
ID_AASOB124 standard: cD
XX
AC AASOB124;
XX
AC AASOB124;
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AC AASOB124;
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AMAMBALIAN toxicologic
XX
AMAMBALIAN toxicologi
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US-09-471-276-831_COPY_1_16 x AAA10193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS08124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AN10201 and AN10205 ware 11 impressible to the recomposite stransfer with Krown Carlo compounds relative to uniterest samples. Shill sequences which Krown AN10150, AN10159, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marker expression pattern in untrested control samples, and the toxicity of the test compound determined rhe tissue sample is preferably selected from liver, kidney, brain, spleen, pancrous and bung. The nucleic acid molecules and methods of the invention may also be used for screening libraries of molecules for specific binding affinity, and for the first of time-funing of treatment regimens which use drugs with toxic side-effects such that the side-effects are minimised without compromising the efficacy of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hybridiation were only observed between the sample mRNA and sequences AAA10108-A10224. In particular, sequences AAA10110, AAA10116, AAA10117, AAA10126, AAA10133, AAA10138, AAA10140, AAA10147-A10144, AAA10146, AAA10149, AAA10164, AAA10174, AAA10185, AAA10188, AAA10189, AAA10166, AAA10174, AAA10185, AAA10188, AAA10189, AAAI0189, AAA10189, AAA10189, AAA10189, AAA10189, AAA10189, AAA1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a toxic compound (e.g., clofibrate, acetaminophen or polycyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequences AAA10108-A10224 represent rat liver toxicological response markers. These were identified by their pettern of at least twofold upregulation or downregulation of expression in rat liver treated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 65;
                                                                                                                                                 16-NOV-2000; 2000WO-US31743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian toxicological response marker; antigen; antibody; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian toxicological response marker #13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS08124 standard; cDNA; 285 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 ATGTCTCTGCTGACTACTGCTACTTCTCTGGGGTTTCATTCTGGGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA10193
                           99US-0443184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.00
3.750
75.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7bpp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to:
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Caps: 0
Percent Identity: 56.250
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above method is also useful for preventing a coxtoological response by initiating transcription of a gene comprising a down regulated muclet cacid molecule of the invention. Protoins senceded by the nucleic acids of the invention are useful for producing antibodies The nucleic acids of molecules are useful for producing antibodies The nucleic acids immobilised on a substrate as hybridisshle array element in a microarray forms may be used to characterise aper appreciation patterns associated with novel compounds to elucidate any toxicological esponses. The nucleic response to toxic compounds any be expected in the transcription of the producing methods of the nucleic cacids are useful for various hybridistics and to end of the nucleic acids are useful for various hybridistics.
                                           is useful for designing hybridisation probes. The nucleic or its fragment, or a protein encoded by the nucleic used to purify a ligand from a sample.
                                                                                                                                                                                                                                                                                                                                                                              The sequence is a novel mammalian nucleic acid molecule whose levels are up regulated or down regulated following treatment with a toxic compound. Dolynucleotide sequences complementary to the sequences of the invention are useful for preventing a toxiconjogical response by acting against one or more up regulated nucleic acid molecules. An agonist identified by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel mammalian nucleic acid molecules whose levels are up regulated or down regulated following treatment with a toxic compound, useful for detecting metabolic and toxicological responses and in monitoring drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 41; 89pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        action -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-355646/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cunningham MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zweiger GB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Azimzai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaser MR,
Y, Lal P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panzer SR,
                                                                   The nucleic acid molecule nucleic acid molecule may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seilhamer JJ;
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Sequence 285 BP; 58 A; 78 C; 79 G; 70 T; 0 other;

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seq_documentation_block:
ID AAI12735 standard;
                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
us-09-471-276-831_COPY_1_16 x AAS08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI12735
                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAS08124
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Probe; human; microarray; gene expression; cervical epithelial cell;
                                       Probe #2668 for gene expression analysis in human cervical cell sample
                                                                                 12-OCT-2001
                                                                                                                                                                                                                                                                   14 ATGTCTCTGCTGACTACTGTACTACTTCTGGGGGTTTCATTCTGGGC 61
                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                          standard; DNA; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              45.00
3.750
75.000
                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 56.250
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cervical cancer;

88

30-JAN-2001; 2001WO-US00670

09-AUG-2001 WO200157278-A2

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI34086
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-471-276-831_COPY_1_16 x AAI12735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                  _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04 - FEB-
26 - MAY -
30 - JUN-
03 - AUG-
21 - SEP-
27 - SEP-
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                  Probe #2772 used to measure gene expression in human placenta sample
                                                                                                                                                                                                                                                                                     AAI34086 standard; DNA; 472 BP
                                                                                                                                                                                                                                                                                                                                                        380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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                                                    30-JAN-2001;
                                                                                 09-AUG-2001
                                                                                                         WO200157272-A2
                                                                                                                                   Homo sapiens.
                                                                                                                                                              genetic disorder;
                                                                                                                                                                         Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                  17-OCT-2001
                                                                                                                                                                                                                                                          AAI34086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 472 BP; 102 A; 121 C; 145 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                 5 ValValPheLeuLeuTrpGlyValThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                       GTCCTCTTTGTCCTGCTCTGGGGGTGTGGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
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2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.

2000US-0236359.
2000US-0180312.
2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                (first entry)
                                                    2001WO-US00663
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5.000
81.818
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                                                                                                                                                                                                                                                                                                                                                                                                           from: 1 to: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 11
Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in human cervical epithelial cells
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAI02644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAI34086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-471-276-831_COPY_1_16 x AAI34086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                           26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53.
                                      (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                  04-FEB-2000;
                                                                                                                                                                                                        09-AUG-2001
                                                                                                                                                                                                                                  W0200157270-A2
                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                        Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                              Probe #2635 used to measure gene expression in human breast sample
                                                                                                                                                                                                                                                                                                                                                           09-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   AAI02644 standard; DNA; 472 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID No 2772; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
           Penn SG,
                                                                                                                                                                             29-JAN-2001; 2001WO-US00661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCCTCTTTGTCCTGCTCTGGGGGGTGTGGGTGG 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                               2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000CB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000GB-0024263.
                                                                                                                                                  2000US-0180312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.00
5.000
81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W. Rank DR.
         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 11
Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 G; 104 T; 0 other;
           Rank
           DR;
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blignment_block:
US-09-471-276-831_COPY_1_16 x AAI02644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                steging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to movel single exon nucleic acid probes. The present sequence is one such probe. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the properties at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, predicting, diagnosing, grading, and present.
  Primer sets for synthesizing polynucleotides, particularly the 5602
                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (3'-primer) SEQ ID NO:7283
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH10448 standard; cDNA; 576 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 GYCCTCTTTGTCCTGCTGCTGCGGTGTGGGTGG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 472 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25;
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                                                                                                                                                                                                                           28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValValPheLeuLeuLeuTrpGlyValThrTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l single exon nucleic acid probe used to measuring gene expression human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH10448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                           Isogai T, Nishikawa T,
, Sugiyama T, Wakamats
                                                                                                         HELIX RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: AAI02644
                                                                                                                                    99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                           detection; diagnosis; antisense therapy; gene therapy; ss
                                                                                                                                                                                               99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.00
5.000
81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 A; 121 C; 145 G; 104 T; 0
                                                               Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity:
                                                             ۶
                                                                           Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                             Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11
0
: 63.636
                                                                           Saito K,
                                                               Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     part of the printed
directly from WIPO
                                                               Н
                                                                           Yamamoto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes.
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in gone therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. ARM3166 to ARM3528 and ARM3533 to ARM31673 represent human amino acid sequences; and ARM3639 to ARM31633 represent busine manio acid sequences; and ARM3639 to ARM31633 represent busine manio acid sequences; and ARM3639 to ARM31633 represent oligonucleotides, all of which are used in the exemplification for the protein and the acid sequences.
                                                                                                                                                                                                                                                                                                                                                                                            sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence, complementary to the
                                                                                                                                                                                                                                                                                                                                 the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; SEQ ID 7283; 2537pp + CD ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length cDNAs defined in the specification, and and/or diagnosis of the abnormality of the proteins
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encoded by the
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alignment_block:
US-09-471-276-831_COPY_1_16 x AAH10448
                                                                                                                                                       alignment_scores:
                                                 Align seg 1/1 to: AAH10448
                                                                                                                Percent Similarity:
                                                                                                                                                                                             Sequence 576
                       2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp
AACCTCTTAACTTCTTTTGTGATTTTGTGGGGAACAATCTGG
                                                                                                                                          Quality:
                                                                                                                             Ratio:
                                                                                                                                                                                             BP;
                                                                                                                45.00
3.750
85.714
                                                                                                                                                                                             116 A;
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                                                  from: 1 to: 576
                                                                                                                Percent Identity: 42
                                                                                                                                                                                             G
                                                                                                                                                                                             148
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                                                                                                                                            Length:
                                                                                                                           Gaps:
                                                                                                                                                                                             156 T; 3 other;
                                                                                                                14
0
:. 857
324
                       15
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of the present invention

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAF10038

cDNA; 632 BP

283

22-MAR-2000; 2000WO-US07781

99US-0273623

expressed sequence teg; Fusarium venenatum; Aspergillus nider; expressed sequence teg; Fusarium venenatum; Aspergillus oryzae; Trichoderma necest; identification; recombination; culture condition; environmental stress; spore morphogenesis;

metabolic pathway engineering; catabolic pathway engineering;

Multiple gene expression; filamentous fungal cell; EST;

Fusarium venenatum EST SEQ ID NO:2561

(first entry)

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alignment_block:
US-09-471-276-831_COPY_1_16 x AAF10038/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX24234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AAF10038 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
AAX24234 standard; DNA; 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    niger; ARPI1854 to ARPI4878 represents ESTs from Aspergillus oryzae; and AAPI4879 to ANPI3337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rarray equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07178 to AAF1127 represents ESTs from Fusarium renematum. AAF11248 to AAF11853 represents ESTs from Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (F) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                             Gram positive bacteria; covalent coupling; pathogenicity factors LPXTG-motif dependent C-terminal anchorage; cell surface; antiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 86; Page 1320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrate of expressed sequence tags
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   WO9916900-A1
                                                   Unidentified
                                                                                                       therapeutic agent; extracellular
                                                                                                                                                                                                          W09916900 Seq ID 4
                                                                                                                                                                                                                                                                 01-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 TCAGCGTCATTGATTTTCAAAAGACTATGGGGAAANAGCTGGGGC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 632 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how ff cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovered, possible functions of unknown open reading frames can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
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                                                                                                                                                                                                                                                                 (first entry)
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4.500
66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 A; 175 C; 118 G; 156 T; 5 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3161pp; English.
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                                                                                                          matrix; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
0
46.667
                                                                                                                                cell surface; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAX24250 standard;
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particularly pathogenicity factors, to the cell surface. The pro
of the invention have antibacterial activity and are potentially
userially les therapeuric agents, inhibiting binding of bacteria to
                                                                                                                                                                                                                                               that encodes a polypeptide which affects covalent coupling of polypeptides to the surface of Gram-positive bacteria. The method identifies mutations in bacterial factors that (In)directly interact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-255104/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1997;
27-SEP-1997;
   Sequence 748 BP;
                                                                               extracellular matrix.
This sequence is represented in the
                                                                                                                                                                                                                    with the LPXTG-motif dependent C-terminal anchorage of polypeptides,
                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for identifying a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                       Claim 17; Page 41-42; 58pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EVOT-) EVOTEC BIOSYSTEMS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying nucleic acid that affects adhesion of Gram positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pohlner J,
                                                     the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97EP-0118755.
97EP-0116841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-EP06136.
216 A; 113 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strauss A,
   170
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   င္ပ
                                                                               Seq ID listing but does not
   238 T;
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   11 other
                                                                                                                                                                                      The products
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alignment_scores:

Ouality: 45.00

Ratio: 6.429
Percent Similarity: 87.500
Percent Similarity: 87.500

Percent Similarity: 87.500

Percent Identity: 87.500

Alignment_block:

US-09-471-276-831_COPY_1_16 x AAX24234 ...

Align seg 1/1 to: AAX24234 from: 1 to: 748

9 | LeuLenTrpGlyValThrTrpGly
| 1 | | | | | | | | | | |
| 58 CTTTTGTGGGCCCCACCTGGGGT 608

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX24250
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DNA; 748 BP

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CC AAX24250;
CC AAX24250;
CC Ol-JUL-1999 (first entry)
CY Ol-JUL-1999 (first entry)
CY OVER A CLIVE agent; covalent coupling; Gram-positive bacteria; Inhibitor;
CY ACTIVE agent; covalent coupling; Gram-positive bacteria; Inhibitor;
CY ADAMSANCE ATTROCHIUNARY MATTER ACTIVE AC
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(EVOT-) EVOTEC BIOSYSTEMS

AG

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seq_documentation_block:
ID AAQ87927 standard; DNA; 794 BP
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US-09-471-276-831_COPY_1_16 x AAX24250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/gcneseq/geneseqn/NA1995.DAT:AAQ87927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAX24250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describe a novel method for identifying an active agent that affects covalent coupling of polypeptides to the surface of Gram-positive bacteria. The agents identified inhibit polypeptide-induced adhesion of bacteria to extracellular matrix in the host. The active agent effects the LPXTG motifiedependent anchorage of pathogenically factors to the bacterial coll wall and are potentially useful as therepeutic agent, inhibiting binding of bacteria to the pathogenically factors to the bacterial coll wall and are potentially exfracellular matrix in the host.
          Claim 5; Page 5-6; 6pp; Japanese
                                     A gene expressed specifically in anther(s) - used for the preparation of male sterile Cruciferae plants
                                                                                       WPI; 1995-135897/18
                                                                                                                  (MITS ) MITSUBISHI CORP.
(MITU ) MITSUBISHI KASEI CORP
                                                                                                                                                               20-AUG-1993;
                                                                                                                                                                                          20-AUG-1993;
                                                                                                                                                                                                                          07-MAR-1995
                                                                                                                                                                                                                                                       JP07059573-A.
                                                                                                                                                                                                                                                                                    Brassica napus
                                                                                                                                                                                                                                                                                                                   pollen
                                                                                                                                                                                                                                                                                                                             Anther
                                                                                                                                                                                                                                                                                                                                                            Anther speciic gene promoter element.
                                                                                                                                                                                                                                                                                                                                                                                       22-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          585 CTTTTGTGGGGCCCCACCTGGGGT 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 748 BP; 216 A; 113 C; 170 G; 238 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 38-39; 51pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-255102/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying agents that affect adhesion of Gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 LeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the sequence ID listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                             specific gene; Brassica napus; antisense RNA; Cruciferae; formation; male sterile plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pohlner J,
                                                                                                                                                               93JP-0206459
                                                                                                                                                                                            93JP-0206459
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6.429
87.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 8
Gaps: 0
Percent Identity: 87.500
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នន្តន្តន្តន្ត្
                                      This sequence was used for the expression of an anther specific gene derived from Brassica napus. This sequence caused expression of the anther specific gene as antisense RNA in acrualferee plant causing pollen formation to be modified. This is esp. useful in the production of male sterile plants.
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Sequence 794 BP; 258 A; 157 C; 137 G; 228 T; 14 other;

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alignment_block:
US-09-471-276-831_COPY_1_16 x AA087927/rev
                                                                                                                                                                                                              alignment_scores
                                                                    Align seg 1/1 to reverse of: AAQ87927
                                                                                                                                                           Percent Similarity:
763 TCTTGCTTTGTGATATTTTTGTGTGTTTATGGCCCTTTTATGGGGG 719
                                2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                        45.00
3.750
80.000
                                                                                                                                                 Length: 15
Gaps: 0
Percent Identity: 46.667
                                                                    from: 1
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P03326 Q9s214 P75362 P18464 Q28125 P19785

6 fujinami sa 4 streptomyce 2 mycoplasma 4 homo sapien 5 bos taurus

P39285

s fatty aci saccharopol mus musculu homo sapien mus musculu homo sapien homo sapien 097939 P12255 P03402 P12504

bordetella sus scrofa arabidopsis arabidopsis didelphis m

mus musculu human immun human immun

Result No. Database Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 Minimum DB Maximum DB Total number of hits satisfying chosen parameters: Scoring table: Sequence: Title: Perfect score: Run on: OM protein - protein search, using Searched: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score seq length: 0 length: 2000000000 Match US-09-471-276-831 661 January 7, 2002, 16:45:58; Search time 16:52 Seconds (vithout alignments) 279:647 Million cell updates/sec SwissProt_39:* Gapop 10.0 , Gapext 0. BLOSUM62 100059 segs, 36664827 residues GenCore version Copyright (c) 1993 - 2000 MSMLVVFLLLWGVTWGPVTE.... Length В VWF_PIG BLAC_MYCTU VP19_VZVD VIE_HV1JR OSL3_ARATH 1B55_HUMAN Y4PA_RHISN NRAM_IAQIT
PARC_ECOLI
GUXB_CELFI
CP2B_HUMAN
CA14_MOUSE
1B25_HUMAN S24B_ARATH
BUB1_HUMAN
CA14_HUMAN
1C12_HUMAN
1C13_HUMAN
1C13_HUMAN
1C14_HUMAN VIF_HV1RH MM02_CHICK FCG1_MOUSE RSFA_BACSU VIF_HV1MA 1C04_HUMAN 1C15_HUMAN AFX1_HUMAN HEM1_HELMO A1BG_HUMAN EPPL_HUMAN IRF7_HUMAN 1B16_HUMAN SW summaries SUMMARIES model 4.5 Compugen Ltd. ...LLELTGPKVLACSLALDGAS P02462 P30505 P30507 P30507 Q07584 P20082 P50899 P50899 P50463 P02463 P02463 P30471 P30508 P30508 Q28833 Q10670 Q10670 P09276 P98177 P39650 P04599 Q9m081 Q9zgg6 Q92985 P58107 P19373 P20877 P50700 P30492 P55610 Q90611 P26151 Description homo sapien homo sapien homo sapien homo sapien homo sapien homo sapien influenza a escherichia homo sapien bacillus su human immun homo sapien homo sapien homo sapien sus scrofa homo sapien rhizobium s heliobacill homo homo sapien arabidopsis homo sapien mycobacteri varicella-z arabidopsis gallus gall mus musculu cellulomona human immun sapien sapien sapien sapien

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	1020 1247 1247 1247 1591 1591 1592 192 3593 309 323 309 323 323 362 362 1572 594 477 9172 362 362 1572 1572 1572 1572 1572 1572 1572 157
11 H C	029_HUM CAA1_ARA LA7_ARA LA7_ARA LA7_ARA HA3_DID YA1_MOU YA1_MOU YA1_MOU YA1_MOU YA1_MOU YA1_HOU YA1_HOU YA1_HOU YA1_HOU HOU RAM

P35799
P03989
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y escherichia
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homo sapien

ALIGNMENTS

P30482 P30491 P30496 P30386 P30386 P30387 P30504 P30504 Q10978 P49000 Q10978 Q10978 Q10978 Q10978

mus musculu homo sapien haemophilus

rattus norv mycobacteri homo sapien rattus norv streptococc

09cd48 050580 P47539 P10320 P30481

rattus norv hemitripter

human 1mmun

5 human immun 8 mycobacter; 0 pseudomonas 9 mycoplasma 0 homo sapien 1 homo sapien 6 porilla gor 7 gorilla gor 7 gorilla gor 7 dorilla gor 1 homo sapien

GG95_HUMAN

RESULT

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10 A18G, HUNAN
10 A18G, HUNAN
10 A18G, HUNAN
10 A18G, HUNAN
11 AC 10 A18G, HUNAN
10 20 ANA
10 20 ANA
10 20 ANA
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11 A18G, A1
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Best Local S
Matches 71
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P04217;
                                         VIE_HVIRH STANDARD: PRT: 192 AN P05900; Rel. 09, Created) 01-NOV-1988 (Rel. 09, Created) 01-NOV-1988 (Rel. 20, Last sequence update) 01-JUL-1993 (Rel. 26, Last annotation update VIRION INPECTIVITY FACTOR (SOR PROTEIN).
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
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DOMAIN
Viruses;
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SMART: SM00410; IG_like; 4.
Immunoglobulin domain; Glycoprotein; Plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ishloka N., Takahashi N., Putnam F.W.;
"Anino acid sequence of human plasma alpha 1B-glycoprotein:
to the immunoglobulin supergene family.";
Proc. Natl. Acad. Sci. U.S.A. 83:2363-2367(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1987 (Rel. 04,
20-MAR-1987 (Rel. 04,
20-AUG-2001 (Rel. 40,
ALPHA-1B-GLYCOPROTEIN
                    Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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InterPro: IPR003598; Ig_c2.
InterPro: IPR003600; Ig_11ke.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID~9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-86205955; PubMed-3458201;
                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               22
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SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE V-TYPE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PLASMA GLYCOPROTEIN OF UNKNOWN FUNCTION
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                                                                                                                                                                                                                                                                                  KHQFLLTGDTQGRYRCRSGLSTGWTQLSKLLELTGPKSL 95
                                                                                                                                                                                                                                                                                                                           KHOFFLTGDTOGRYRCRSGLSTGWXQLSKLLELTGPKVL 116
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71.78;
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  Retroviridae; Lentivirus
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Pred. No. 4e-27;
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                    (RF/HAT isolate) (HIV-1).
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01-NOV-1997
20-AUG-2001
72 KDA TYPE
                  MEDILNE-91161603; Pubbed-1848840;
Chen J.-M., Almes R.T., Ward G.R., Youngleib G.L., Quigley (
"Isolation and characterization of a 70-kba metalloprotease
(gelatinase) that is elevated in Rous sarcoma virus-transfor
chicken embryo fibroblasts ",
J. Biol. Chem. 266:5113-5121(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last senotation update)
70-NOC-2001 (Rel. 40, Last annotation update)
72 KNA TYPE W COLLACEMASE PREUERSOR (EC 3 4.24, 24) (72 KDA
GELATINASE) (MATRIX METALLOPROTEINASE-2) (MMP-2) (GELATINASE
                                                                                                                                                                                                                                                                               MEDLINE-94280397; PubMed-8010954;
Almas R.T., French D.L., Quigley J.P.;
"Cloning of a 72 kbm matrix metalloproteinase (gelatinase) frechicken embryo fibroblasts using gene family PCR: expression
                                                                                                                                                                                                                                gelatinase
Biochem. J.
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE Embryo
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InterPro; IPR000475; Viral_infect
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or send an email to license@isb-sib.ch).
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PRINTS; PR00349; VIRIONINFFCT
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CATALYTIC
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                                                                                                                                                                             AND 107-122
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Neognathae; Galliformes; Phasianidae; Phasiani
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CLEAVAGE OF
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ephs S.F., Gal
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lo R.C.,
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PRINTS, PRODO138; MATRIXIN
PRODON; PD000995; FN_Type_I
SMART; SM00595; FN.2; 3.
SMART; SM00120; HX; 4.
SMART; SM00235; ZnMc: 1.
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PROSITE: PS00024; HEMOPEXIN, 1.
PROSITE: PS000142; ZINC_PROTEASE; 1.
PROSITE: PS00546; CYSTEINE_SWITCH; 1.
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Pfam; PF00045; hemopexin; 4.
Pfam; PF00413; Peptidase_M10;
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                                                                                                                                                                                                                                                                                               SEQUENCE
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Collagen d
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InterPro: IPR001818; Matrixin.
InterPro: IPR000130; Zn_MTpeptdse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; MIU.003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P08253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U07775; AAA19596.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000562;
581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COPACYON: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
SUBUNT: LICAND FOR INTEGRIN ALPHA-V/BETA-3.
TISSUE SPECIFICITY: PRODUCED BY MORMAL SKIN FIBROBLASTS.
SIMILARITY: COMPAINS 1 HEMODEXIN. LIKE DOMAIN.
SIMILARITY: CONTAINS 3 FIBROBCTIN TYPE 11-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 FIBROBCTIN TYPE 11-LIKE DOMAINS.
SIMILARITY: BELONGS TO PETIDASE FAMILY MIDM. CINC
METALLOPROFURSED ALSO MORN AS MATRIXIN SUBMAILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILE-ALA-GLY-GLN
                                         VHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACS 119
                                                                                                                                 PVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPG-----PPGDSRLPAVQEWGAQEP 69
                                                                                                                                                                                Similarity
26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V, VII, X. CLEAVES THE COLLAGEN-LIKE SEQUENCE PRO-GLN-GLY-|-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e; Metalloprotease;
degradation; Extra
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KKTY I FSGDRYWKYN --
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                                                                                        -AGNEYWYYTASNLDRGYPKKLTSLGLPPDYQRIDAAFNWGRN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Extracellular matrix;
                                                                                                                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc; Zymogen;
                                                                                                                                                                                                   Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
P -> Q (IN REF. 2).
F -> I (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYSTEINE SWITCH (POTENTIAL)
ZINC (CATALYTIC) (BY SIMILA
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIBRONECTIN TYPE-II
FIBRONECTIN TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLAGEN-BINDING
COLLAGENASE-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 KDA TYPE IV CC
COLLAGENASE-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMOPEXIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIVATION PEPTIDE
                                                                                                                                                                                                                                                                                                                  -> Q (IN REF. 2).
-> T (IN REF. 2).
-> I (IN REF. 2).
                                                                                                                                                                                                                                                                                               8D6FDA4E67C3EBCA CRC64;
                                                                                                                                                                                Mismatches
EEKKKMELATPKFIADS
                                                                                                                                                                                                   DB 1; Length 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IV COLLAGENASE
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                                                                                                                                                                             37;
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                                                                                                                                                                                34;
                                                                                                                                                                             Gaps
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RESULT 4
FCG1_MOUSE
                        CARBOHYD
CARBOHYD
                                                                       CARBOHYD
CARBOHYD
                                                                                                                TRANSMEM
DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and chromosomal location of the human Fc gamma RI gene.";
J. Immunol. 148.1570-1575(1992).
-1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS GAMMA. HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMB outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Sears D.W., Osman N., Tate B., McKenzie I.F.C.,
"Molecular cloning and expression of the mouse!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FCG1_MOUSE
P26151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-- TISSUE SPECIFICITY: MACROPHAGE-SPECICIC.
-- SIMILARITY: CONTAINS 3 IMMUNOLOBULIN-LIER C2-TYPE DOMAINS.
-- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92166399; PubMed=1531670;
Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor for IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FCGR1 OR FCG1
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SMART; SM00408; IG:
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A43511; A43511.
PIR; A46480; A46480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M31314; AAA40056.1; ..
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                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                    IgG-binding protein; Receptor;
Immunoglobulin domain.
                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00410; IG_like; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:95498; Fcgrl
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                                                                                                                                                                                                                                                                                                                                                                                         ig; 3.
IGc2; 1.
      297
320
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404
124
216
28
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168
249
IG-LIKE CZ-TYPE DOMAIN 1
IG-LIKE CZ-TYPE DOMAIN 2
IG-LIKE CZ-TYPE DOMAIN 2
IG-LIKE CZ-TYPE DOMAIN 3
IG-LIKE CZ-TYPE DOMAIN 3
IG-LIKE CZ-TYPE DOMAIN 3
IG-LIKED (GLCHAG. . ) (POTENTIAL)
N-LIKED (GLCHAG. . ) (POTENTIAL)
                                                                                                                                      POTENTIAL,
POTENTIAL,
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC 12
                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                      HIGH AFFINITY IMMUNOGLOBULIN RECEPTOR I.
                                                                                                                                                                                                                                                                                                                                             Transmembrane; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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RECEPTOR
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mouse high affinity Fc
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                                                                                                                                                               (TRUNCATED).
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RESULT
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Best Local Similarity
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OSLJ_ARATH STANDARI
P50700;
01-OCT-1996 (Rel. 34, (
01-OCT-1996 (Rel. 34, 1
20-AUG-2001 (Rel. 40, I
OSMOTIN-LIKE PROTEIN OS
OSM34.
                                                                                             ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (JRCSF isolate) (HTV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
01-JUL-1993 (Rel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                           AIDS
                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00559; Vlf;
                                                                                                                                                                                                                                                                                                                                                                                                           HIV; M38429; VIFSJRCSF
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M38429; AAB03746.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-11688;
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                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                      æ
                                                                                                                                                                                                                              8 LLLMGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anagi S., Chen I.S.Y.;
mitted (DEC-1988) to the HIV data bank.
FUNCTION: DETERMINES VIRUS INFECTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                          QEWGAGEPVHLDSPAIKHOFLLTGDTOGRYRCRSGLSTGW 101
                                                                                                                                                                                                      MIVWQVDRMRIRTWNSLVKHHMYISGKAKGWIYKHHYESTNPRVSSEVQIPLGDARLVIT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                            192 AA;
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                                                                                  STANDARD;
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26, Last annotation u
FACTOR (SOR PROTEIN)
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              OSM34 PRECURSOR.
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Pred. No. 2.3;
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Pred. No. 3.4;
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                                                                                                                                                                                  1855_UMAN STANDARD; PRT; 362 AA.
P30492;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last semestation_update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         osmotin-like protein from Arabidopsis thaliana.
Gene 191:51-56(1997).
                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-54(BW-22) B*5401 ALPHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X89008; CAA61411.1; -. HSSP; P25871; 1AUN.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Enkaryota: Viridiplantae: Streptophyta; Embryophyta; Trachoophyta;
Spermatophyta, Magnollophyta; endicotyledons; core endicots; Rosidae;
eurosids II. Brassicales; Brassicaceae; Arabidopsis.
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nes 25; Conserv
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Pred. No. 3.5;
4; Mismatches
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCB1_TaxID 9606 Homo sapiens (Human). HLA-B OR HLAB. CHAIN PRECURSOR.

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RESULT 8
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"HLA-Bw22: a family of molecules with identity to HLA-B7 in the alpha
                     PUTATIVE TRANSCRIPTIONAL Y4PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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SMART; SM00407; IGC1; 1.
PROSITE; PS00290; IG_MHC; 1.
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MEDLINE-92148136; PubMed=1737933;
   Rhizobium
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InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
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RESULT 9
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InterPro: IPR002197; HTM; F1S;
InterPro: IPR0021978; Sig54_Interact;
IPR05178; Sig06575; SIGMA54_INTERACT_1; F7
PR05178; PS00676; SIGMA54_INTERACT_2; F7
PR05178; PS006688; SIGMA54_INTERACT_3; F7
PR05178; PS00688; SIGMA54_INTERACT_3; F7
PR05178; PS00688; SIGMA54_INTERACT_4; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-I- SIMILARITY: THE CENTRAL REGION CONTAINS A SIGNA-INTERACTION AFE-BINDING DOMAIN.
-I- SIMILARITY: IN THE N-TERMINAL, TO YAOT AND YAOV
KEDLINE-99061957; PubMed-9843979;
Xiong J., Inoue K., Bauer C.E.;
"Tracking molecular evolution of photosynthesis by characterization
a major photosynthesis gene cluster from Heliobacillus mobilis.";
                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
GLUTAMYL-TRNA REDUCTASE (EC 1.2.1.-) (GLUTR)
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Q9ZGG6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Transcription regulation;
ATP-binding; Plasmid.
ATP-binding; Plasmid.
ATP-GOMAIN 313 533 ATGMA-54 FACTOR INT
NP_BIND 395 404 ATP (FOTENTIAL)
DAN_BIND 78 597 H-T-H MODIF (BY SI)
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between the Swiss Institute of Bioinformatics and the BW
the Buropean Bioinformatics Institute. There are no restr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobiaceae; Rhizobium.
NCBI_TaxID=394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid sym pNGR234a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular basis of symbiosis between Nature 387:394-401(1997).
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                             Heliobacterium gr
NCBI_TaxID=28064;
                                                                                                                                                                                                                      Bacteria; Firmicutes;
                                                                                                                                                                                                                                                Heliobacillus mobilis.
                                                                                                                                                                                                                                                                              HEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRFRRGEAARYLGISR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIKSEH-LPPLGDANADAPHPHPGEER----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         609
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                                                                                                                                                                                        group; Heliobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                  Bacillus/Clostridium group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha subdivision; Rhizobiaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL).
H-T-H MOTIF (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8CC727E67D508F36 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EW--
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                                                                                                                                                                                                                                                                                                                               update)
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Best Local Similarity
Matches 34; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7_HUMAN
IRF7_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRP7_HUMAN STANDARD: PRT: 503 AA. 992985; 000331; 000332; 000333; 075924; 01-MOV-1997 (Rel. 35, Created) 01-MOV-1997 (Rel. 35, Last sequence update) 20-MOV-2001 (Rel. 40, Last annotation update) INTERFERENCH REGULATORY FACTOR 7 (IRF-7).
                         MEDLINE-99003279; PubMed-9786932; AUW.-C., Moore P.A., LaFleur D.W., Tombal B., Pitha P.M.; Characterization of the interferon regulatory factor-7 and its potential role in the transcription activation of interferon A
                                                                                                                                                                                                                                              Palang L., Pagano J.S.;
"IRF"), a new interferon regulatory factor associated with Epstein-Barr virus Datancy."
Mol. Cell. Biol. 17:5748-5757(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Grossman A., Nicholl J., Antonio L., Luethy R., Sutherland G.R., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the swiss institute of sloinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 95:14851-14856(1998).

-- CATALYTIC ACTIVITY: GUUTANLI-TRANGCUJ + NADPH -- GLUTAMATE-1-
SEMIALDEHYDE + NADP(+) + TRNAGUJ)

-- SPATHAY: FIRST STEP IN PORPHYRIN BIOSYNTHESIS BY THE C5 PATHWAY.

-- SIMILARITY: BELONGS TO THE GLUTAWIL-TRWA REDUCTASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS A; B MEDLINE:97459673; PubMed:9315633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF080002; AAC84013.1; -. HSSP; Q42843; 1B29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entitics requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FISSUE Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 SNGIVNTWFQ 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00745; GlutR;
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Pred. No. 11
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MBL outstation -
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OS OS

EPPK1 OR EPIPL

HOMO Sapiens

(Human).

EPPLAUNAN STANDARD: PRT: 5065 AA. PS107; MAC-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last senotation update) 20-AUG-2001 (Rel. 40, Last senotation update) EPIPLAKIN (450 KDA EPIDERMAL ANTIGEN).

RESULT 11 EPPL_HUMAN

224 CAGGPGLPAGELYGWA-----VETTPSPGPQPAA 252

TOGRYRCRSGLSTGWXQLSKLLELT---GPKVLA 117

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Best Local
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1. FUNCTION: TRANSCRIPTIONAL ACTIVATOR. BINDS TO THE INTERFERON-
STINULATED RESPONSE ELEMENT (ISRE) IN IFN PROMOTERS AND IN THE O
PROMOTER (OP) OF EBY NUCLEAR ANTIGEN-1 (EBNA1).

1. SUBCELLUAR LOCATION: NUCLEAR (POTENTIAL).

1. ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHONN HERE). B/BETA, C/GAMMA
1. ALTERNATIVE PRODUCTS: 4 ISOFORMS: A (SHONN HERE). B/BETA, C/GAMMA
1. ALTERNATIVE PRODUCTS: EXPRESSED PREDONINANTLY IN SPLEEN, THYMUS, AND
1. TISSUE SECTIONITY: EXPRESSED PREDONINANTLY IN SPLEEN, THYMUS, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SAISS-PROT entry is copyright. It is produced through a collaboration between the Saiss Institute of Bioinformatics and the BMBL outstation - between the Saiss Institute of Bioinformatics and the BMBL outstation on its use by non-profit institutions as long as its content is in no way modified and this steement is not removed. Usage by and for commercial modified and this steement is not removed. Usage by and for commercial modified and this steement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U73036; AAB17190.1; -.
EMBL; U53830; AAB80686.1; -.
EMBL; U53831; AAB80688.1; -.
EMBL; U53832; AAB80690.1; -.
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                                                                                                                                                                                                               SEQUENCE
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HSSP; P23906; 11RG.
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hes 37; Conserv
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Q -> R (IN REF. 3).
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"Epiplakin, a novel member of the plakin family originally identified
as a 450 kba human epidermal autoantigen: structure and tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21201183; PubMed=11278896; Fujiwara S., Takeo N., Otani Y., P
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TISSUE-Cervical carcinoma
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TISSUE SPECIFICITY: HOLELY EXPRESSED MITH HIGHEST LEVELS IN LIVER, SMALL INTESTINE, COLON, SALLVARY GLANDS, STOMACH AND APPENDIX. SIMILARITY: COMTAINS 65 PLECTIN REPENTS.
SIMILARITY: BELONGS TO THE PLAKIN OR CTFOLINKER FAMILY.
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                            Choo S.Y., St John T., Orr H.T., Hansen J.A.;
"Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703)
Identifies a unique single anino acid substitucion.";
Hum. Immunol. 21:209-219(1988).
1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE INMUNE SYSTEM.
1- SUBMUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                       Taid HUMAN STANDARD: PRT: 362 AA.
p19373:
01-NOV-1990 (Rel. 15. Created)
01-NOV-1990 (Rel. 15. Last sequence update)
20-AUG-2001 (Rel. 40. Last annotation update)
HLA CLASS INTSTOCOMPATIBILITY ANTIGEN, B-27 B+2703 ALPHA CHAIN
PRECURSOR (B-27D).
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SWISS-PROT entry is copyright.
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Swiss Institute of Bioinformatics

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SEQUENCE OF 397-553 FROM I
MEDLINE-93356762; PubMed-I
Lavergne J.M., Piso Y.C.,
Bahnak B.R., Meyer D.;
                                                                                                    SEQUENCE FROM N.A.
Seaman W.T., Read M.S.,
Submitted (MAR-1998) to
                                                                                                                                                                                    Mammalia; Eutheria;
NCBI_TaxID-9823;
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                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                    Bellinger D.A., Nicho the EMBL/GenBank/DDBJ
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                    Ferreira
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17; Mismatches
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N-LINKED (GLCNAC.
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Pred. No.
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B-77 B-773 ALPHA CHAIN.
EXTRACELULIAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
EXTRACELLULAR ALPHA-3.
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(FRAGMENT)
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10;
                    Kerbiriou-Nabias
                                                                                                    Nichols T.C.;
k/DDBJ databases
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Pfam; PF00094; vwd; 3
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InterPro;
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EMBL; S64541; AAB27829.2; -.
HSSP; P04275; IATZ.
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                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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SIMILARITY: CONTAINS 3 VARC DOMAINS.
SIMILARITY: CONTAINS 1 C-TERMINAL CYSTINE KNOT-LIKE DOMAIN SIMILARITY: CONTAINS 7 C SILKWORM HEMOCYTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRE000359; Cys_knot.
FRE000561; DGF-11ke.
FRE001928; Endochin_Cox.
FRE001928; Endochin_Cox.
FRE002919; TIL.
FRE001907; WAFC.
FRE001806; Wdd.
FRE002035; WAFA.
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NYCTU STANDARD; PRT; 307 AA.

110670;
1110671.1996 (Rel. 34, Created)
1010671.1996 (Rel. 34, Created)
1010671.1996 (Rel. 34, Last sequence update)
201-NHG-2001 (Rel. 40, Last sequence update)
201-NHG-2001 (Rel. 40, Last sequence update)
201-NHG-2001 (Rel. 40, Last sequence update)
8ETA-LACTANSES PRECURSOR (RC 3.5.2.6) (PERUICILLINASE).
8ELAA.OR BLAC OR RYZ0068C OR NYZ128 OR NYCY49.07C.
                                                            SEQUENCE FROM N.A.

STRAIN-ATCC 201 / H37RA;

MEDLINE-97291283; PubMed-9145897;

MEDLINE-97291283; PubMed-9145897;

"Cloning and sequence analysis of a class A beta-lactamase Mycobacterium tuberculosis H37Ra.;

Aptimicrob. Agents Chemother. 41:1182-1185(1997).
                                                                                                                                                                                                                          Actinomycetales;
NCBI_TaxID+1773;
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  SEQUENCE FROM N.A
STRAIN~H37RV;
                                                                                                                                                                                                                                                                     Bacteria;
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                                                                                                                                                                                                                                                                     Firmicutes; Actinobacteria; Actinobacteridae;
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9; Mismatches
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MEDLINE-98295987: PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglandster K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Comnor R., Bautes R., Devlin K., Feltwell T., Gentles S., Hanlin N., Holtoyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Rutter S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seaper K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.:

"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CDC 1551 / Oshkosh;
Pleischmann R.D. Alland D., Elsen J.A., Corpenter L., White O.,
Pleischmann R.D. Alland D., Elsen J.A., Corpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Oshin M.L., Hatt D., Hickey E.,
Kolonay J.F., Nelson N.C.. Umbyam L.A., Emolaeva M.D., Salzberg
peicher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
                                                                                                                     or send
                                                                                                                                                          entities requires a
                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laboratory strains.";
Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Whole genome comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complete genome sequence.
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                S SMISS-PROT entry is copyright. It is produced through a case the Swiss Institute of Bioinformatics and the EMBL. European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nitted (APR-2001) to the EMBL/GenBank/DDBJ databases CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)0 = A SUBST
                      U67924; AAB07556.1; -. 273966; CAA98216.1; -.
                                                                                                                 s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
AAK46408
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                                                                                                                                                                                     Usage
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Query Match
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Matches 36
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EMBL; Z73966; CA
EMBL; AE007063;
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BINDING
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InterPro; IPR001466; Beta_lactam.
InterPro; IPR000871; Beta_lactam_A.
Pfam; PF00144; beta-lactamase; 1.
                                                                                                                            SEQUENCE
                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                              Complete
                                                                                                                                                                                                                            Hydrolase;
                                                                                                                                                                                                                                          PROSITE; PS00146;
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                                                                                                                                                                                                                                                                       PRINTS; PRO0118;
                                                                                                                                                                                                                                                                                                                                         TIGR; MT2128; -
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 128
GMT1GQLCDAAIRYSDGTAANLLLADLGGPGGGTAAFTGYLRSLGDTVSRLDAEEPELNR
                           GVTWGPVTEAAIFYE--TQXSL-----WAESEHXLKTLG----QCDADVP----
                                                                  Similarity
                                                                                                                                                                                                             proteome.
                                                                                                                            307
                                                                                                                                                                                                                            Antibiotic resistance; Membrane;
                                                        Conservative
                                                                                                                            AA;
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252
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                                                                      9.8%;
27.9%;
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                                                        17;
                                                      Score 65; DB
Pred. No. 11;
17; Mismatches
                                                                                                                                        SUBSTRATE (BY SIMILARITY).
                                                                                                                                                      BETA-LACTAMASE.
N-ACYL DIGLYCERIDE (POTENTIAL).
BY SIMILARITY.
                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                          Lipoprotein; Signal;
                                                                                  Length 307
                                                        Indels
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LSKLLELTG

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P09276;
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFXI HUMAN STANDARD: PRT: 304 AA.
P98177: 01370; 03881;
01-007-1399 (Rel. 34, Creeted)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last sequence update)
                                                                                   Peters U., Haberhausen G., Kostrzewa M., Nolte D., Muellor "AKXI and p54nrb: fine mapping, genomic structure, and excleandidate genes of X-linked dystonia parkinsonism."; Hum. Genet. 100:569-572(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation — the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way entitled and this statement is not removed. Usage by and for commercial entitled and this statement is not removed. Wisage by and for commercial entitled and this statement is not removed. Wisage by and for commercial entitled and this statement is not removed.
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01-MAR-1999 (Rel. 10, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CAPSID ASSEMBLY AND DNA MATURATION PROTEIN (CAPSID PROTEIN VP19C).
SEQUENCE FROM N.A.
MEDLINE 97163401; PubMed~9010221;
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Capsid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davison A.J., Scott J.E.;
"The complete DNA sequence of varicella-zoster virus.";
J. Gen. Virol. 67:1759-1816(1986).
-i- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Varicella-zostor virus (strain Dumas) (VZV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                MEDLINE-98001080; PubMed-9341872;
                                                                                                                                                                                                                                                 TISSUE-Blood;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUTATIVE FORK HEAD DOMAIN TRANSCRIPTION FACTOR MLLT7 OR AFX1 OR AFX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X04370; CAA27903.1; -. PIR; B27343; WZBE20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-86306657; PubMed 3018124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alphaherpesvirinae;
NCBI_TaxID 10338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 SRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBEDDED. BINDS DNA (BY SIMILARITY).
SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANIPACVFWDVDKDLHLSADGLKHVFLVFVYTQRRQREGVRLHLALSQLNE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CE 483 AA; 53971 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD
                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Varicellovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB
Pred. No. 18;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding.
A584CF73D689BF91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           483 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFX1
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RSFA_BACSU
ID RSFA_B
AC P39650
DT 01-FEB
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Best Local S
Matches 33
RSFA_BACSU STANDARD;
P39650;
01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genes Chromosomes Cancer 11:79-84(1994).
-:- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-:- TISSUE SPECIFICITY: HEART, BRAIN, PLACENTA,
MUSCLE, KIDNEY AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-byllosa, ....
Parry P., Wei Y., Evans G.;
"Cloning and characterization of the t(x:11)
"Cloning and characterization of the text o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Y11284; CAA72156.1;
EMBL; Y11285; CAA72156.1;
EMBL; Y11286; CAA72156.1;
EMBL; X93996; CAA63819.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and characterization of AFX, the gene that fuses to MLL in acute leukemias with a t(X;11)(q13;q23).";
Oncogene 14:195-202(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosomal translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; DNA-binding; Nuclear protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00658; FORK_HEAD_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00657; FORK_HEAD_1; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0053; FORKHEAD. SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00250; Fork_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 300033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U10072; AAA82171.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- DISEASE: INVOLVED IN ACUTE LEUKEMIAS BY A CHROMOSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95118921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE .. Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHROMOSOMAL TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borkhardt A., Repp R., Haas O.A.,
Hammermann J., Henn T., Lampert F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001766; Fork_head
                                                                                                                                                                                         386
                                                                                                                                                                                                                                    65 GAQEPVHLDSPATKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLAL
                                                                                                                                                                                                                                                                                                                                           12 GVTWGPV--TEAAIFYETQXSLWA-----ESEHXLKTLGQCDADVPGPPGDSRLPAVQEW 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSLOCATION T(X;11)(Q13;Q23) THAT INVITHE RESULT IS A ROGUE ACTIVATOR PROTEIN
                                                                                                                                                                                                                                                                                         GVT-GPLHTYSSSLFSPAEGPLSAGEGCFSSSQALEAL--LTSDTPPPPADVLMTQV---
                                                                                                                                                                                      ---DPILSQAPTL----LLLGGLPS----SSKLATGVGLCPKPLEAPGPSSLVPTLSM
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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78
108
421
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                                                                                                                                                                                                                                                                                                                                                                                                                   9.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53470 MW;
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                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P -> S (IN REF. 2).
A -> G (IN REF. 2).
L -> F (IN REF. 2).
P -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDPGNENSATEAAAIIDLDPDFEPRAVPLLHLA -> PQKAAAIIDLDPDFEPQSRPRSCTWP (IN REF. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORK-HEAD
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37767944FD32B8C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leis T., Harbott J., Kreuder J.,
                                                         258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INVOLVES
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 504
                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LUNG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              forkhead
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                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from
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                                                                                                                                                                                                                                                                                                                                                                                                 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKELETAL
                                                                                                                                                                                                                                                                                         385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRIQ
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MEDLINE-86245056; PubMed-2424612;

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RESULT 18
VIF_HV1MA
ID VIF_HV1MA
AC P04599;
DT 13-AUG-1987
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Best Local Similarity
Matches 25; Conser
                                                                                             13-AUG-1987
01-JUL-1993
VIRION INFEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification and characterization of a new prespore specific regulatory gene, rsfA, of Bacillus subtilis.";
J. Bacteriol. 182:418-424 (2000).
-i- FUNCTION: REGULATOR OF TRANSCRIPTION THAT FINE-TUNES GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Bacillus subtilis genome project: cloning and sequencing of the
kb region from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Presecan E., Santana M., Schneider Rapoport G., Danchin A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales M.,
Hullo M.P., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.
Presecan E., Santana M., Schmeider E., Schweizer J., Vertes A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PRESPORE SPECIFIC TRANSCRIPTIONAL ACTIVATOR RSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; SEQUENCE 258 AA; 29728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X73124; CAA51648.1;
EMBL; Z99123; CAB15789.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20096685; PubMed=10629188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95020537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSFA OR IPA-92R
                                               Viruses; Retroid viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S39747; S39747.
SubtiList; BG10638; rsfA.
SEQUENCE FROM N.A
                             NCBI_TaxID=11697;
                                                             Human immunodeficiency virus type 1 (MAL isolate) (HIV-1).
                                                                                                                                                                                                                                                              102 QETAAEEPVKTETPSVENEQPLMSGE 127
                                                                                                                                                                                                                                                                                              62
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SIMILARITY: TO B. SUBTILIS YLBO.
                                                                                                                                                                                                                                                                                         QEWGAQEPVHLDSPAIKH-QFLLTGD 86
                                                                                                                                                                                                                                                                                                                              GFRWNAVVRHQ--YEKALQLAKKQRKQRMRALGN-----GQPAKKRLLYQPPAVDPEII 10:
                                                                                                                                                                                                                                                                                                                                                           GVTWGPVTEAAIFYETQXSL-WAESEHXLKTLGQCDADVPGPPGDSRL----PAV----- 61
                                                                                               INFECTIVITY
                                                                                                          (Rel. 05, Created)
(Rel. 05, Last sequence update)
(Rel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=7934828;
                                                                                               FACTOR (SOR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                           9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator; DNA-binding; Complete proteome MW; 67C65A0483BF8B5C CRC64;
                                               Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 64.5; D
Pred. No. 9.9;
                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                              192
                                               Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 258;
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68 TYWGLQ------TGEKD--WHLGHGVSIEWRQ

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Q.
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                                                                                                                                                                                                                                                       Matches
                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-slb.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                       Pfam; PF00559; Vif; 1
                                                                                                                                                                                                                                                                                        HIV; K03456; VIF$MAL.
InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                            EMBL; X04415; CAA28013.1; -. EMBL; A07116; CAA00620.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on
                                                                                                                                                                                                                                   ProDom; PD000063; Viral_infect;
                                                                                                                                                                                                                                                          PRINTS;
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62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQ 103
                                     œ
                                                                    8 LLLWGV-----TWGPVTEAA1FYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                   MIVWQVDRMRIRTWHSLVKHHMYVSKKAKNWFYRHHYESRHPKVSSEVHIPLGDARLVVR 67
                                                                                                                                                                                                                                                          PR00349; VIRIONINFECT
                                                                                                                                                                                                  192 AA;
                                                                                                            Conservative
                                                                                                                           9.7%;
                                                                                                                                                                                                  22723 MW; 1926C410DB92E255 CRC64
                                                                                                            15; Mismatches
                                                                                                                           Score 64; DB Pred. No. 7.9;
                                                                                                                                             DB 1; Length 192;
                                                                                                            42;
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                                                                                                            24;
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S24B_ARATH RESULT 19 294B_KARTH STANDARD: PKT; 1009 AA.

09M0B1 065535;
20-AHG-2001 (Rel. 40, Created)
20-AHG-2001 (Rel. 40, Last sequence update)
20-AHG-2001 (Rel. 40, Last sequence update)
20-AHG-2001 (Rel. 40, Last sequence update)
40-AHG-2001 (Rel. 40, Last s Eukaryofa; Viridiplantae: Streptophyta; Embryophyta: Tracheophyta: Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis. NCBI_TaxID=3702 core eudicots; Rosidae, AT4G32640

STRAIN=CV. COLUMBIA;

SEQUENCE FROM N.A

MEDLINE=20083488; PubMed=10617198;

Ax Mayer K.F.X. Schweller C. Wembuit R. Murphy G. Volckert G. Ax Pohl T. Duestcrhoeft A. Stickema W. Entlan K.-D. Terryn M. Ax Harris B. Masorge W. Brandt P. Grivell L.A. Rieger M., Meller M. Weichselgerner M., de Simone V. Obermaler B. MacHe R. Mueller M. Kreis M. Delseny M. Pulgdomeer. P. Watson M. Schmidthein! T. Ax Kreis M. Delseny M. Pulgdomeer. P. Watson M. Schmidthein! T. Ax Reichert B. Portetelle D. Perez Alonso M. Bourry M. Bancroft I. Ax Vos P. Hoheisel J. Zimmermann W. Wedler H. Ridley P. Ax Langham S.-A. McCullagh B. Billham L. Robben J. Vandenbussche F. Ax Langham S.-A. McCullagh B. Billham L. Robben J. Vandenbussche F. Ax Langham S.-A. McCullagh B. Billham L. Robben J. Vandenbussche F. Ax Langham S.-A. McCullagh B. Billham L. Robben J. Vandenbussche F. Ax Langham S.-A. McLilens I. Voot M. Bastlaans I. Aert R. Defoor E. Ax Langham S.-A. McLilens I. Voot M. Bastlaans I. Jack H. Braun M. A. Moljman P. Klein Lankborst R. Rose M. Hauf J. Koetter P. Ax M. Holzer E. Benoth A. Peters S. van Staveren M. Dir J. Koetter P. Ax Bernelser S. Hempel S. Feldpausch M. Lamberth S. Van den Daele H. Be Keyser A. Buryshaert C. Gielen J. Villarroel R. De Clercq R. Van Montagu M. Rogers J. Cronin A. Ouall M. Bray Allen S.

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RA Chlefdor F. Cooke R. Berger C. Monfort A. Casacuberia E.

RA Clabbons T. Weber N. Vandenbol M. Barguas M. Terol J. Torres A.

RA Percz-Perez A. Purnelle B. Bent E. Johnson S. Tacon D. Jesset T.

RA Helijen L. Schwarz S. Scholler P. Hebor S. Francs P. Weleke C.

RA Frishman D. Hasse D. Lemcke K. Mewes H.-W. Stocker S. Weleke C.

RA Frishman D. Hasse D. Lemcke K. Mewes H.-W. Stocker S. Spiegel L.

RA Parnell L. Debhla N. Gnoj L. Schutz K. Huang E. Spiegel L.

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RA Parnell L. Debhla N. Graves T. Harmon G. Edwards Johnson D.

RA Stocking T. Kalleki J. Graves T. Harmon G. Edwards J. Johnson D.

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RA MAIN P. Bentley D. Polton B. Miller N. Greco T. Wellow D.

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RA MAIN J. Johnson A. Wellow J. Wellow J. Wellow J. Wellow J.

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Pottett A. Rejandreum M. A., Lyne M., Benes Y., Rechmann S.,
Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
Dose S., de Hann M., Maarse A.C., Schaefer M., Mueller-Auder S.,
Gabel C., Fuchs M., Fertmann B., Granderth K., Danner D., Herz
Neumann S., Argiriou A., Vitale D., Liguori R., Pirawandi E.,
Massenet O., Oyldley F., Clabauld G., Muendlein A., Felber R.,
Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the EURopean Bioinformatics Institute, There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AL022537; CAA18597.1; ALT_SEQ. EMBL; AL161581; CAB79981.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Transport; Protein transport; Golgi stack;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:769-777(1999)
                                                                                          318
91
                                                                                                                                                                              42 LGQCDADVPGP------PGDSRLPAVQEWGAQEPVHLDSPAIKHQFLL-TGDTQGR 90
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                                                                                   MGQPGATVPGPSRIDPNQIPRPGSSSSPTVFETRQSNQANPPPPATSDYVVRDTGNCSPR 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reticulum; Multigene family.
430 455 ZINC FINGER
55 60 POLY-PRO.
                                                                                                                                                                                                                                                                                     Conservative
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--LSTGWXQLSKLLE
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344
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                                                                                                                                                                                                                                                                               Score 64; DB
Pred. No. 58;
B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-PRO
MW; 81CD
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                                                                                                                                                                                                                                                                                                                                                                         Length 1069;
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378 YMRCTINQIPCTVDLLSTSGMQLALMVQ 405

RESULT 20 BUB1_HUMAN

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Cahill D.P., Lengauer C., Yu J., Riggins G.J., Willson J.K. Markowitz S.D., Kinzler K.W., Vogelstein B.;
"Mutations of mitotic checkpoint genes in human cancers.";
(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUB1_HUMAN STANDARD;
O415883; O60625; O415483; O43430;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
30-MAY-2000 (Rel. 39, Last sequence up
                                                                                                                                                                                                                                                                                                                         Genomics 46:379-388(1997).
                                                                                                                                                                                                                                                                                                                                       "Mammalian BUB! protein kinases: map positions and in vivo expression.";
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE .. 98110573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cahill D.P., da Costa L.T.,
Vogelstein B., Lengauer C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS A MEDLINE~99296833; PubMed~10366450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Taylor S.S., Ha E., McKeon F.; required for kinetochore localization The human homologue of Bub3 is required for kinetochore localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouyang B., Lan Z., Meadows J., Pan H., Fukasawa K., Li W., Dai W., "Human Bubj: a putative spindle checkpoint kinase closely linked to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT TYR-492 MEDLINE-98180623; PubMed-9521327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MITOTIC CHECKPOINT SERINE/THREONINE-PROTEIN KINASE BUB1 (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 276-1085 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE 98327111; PubMed 9660858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeley T.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99005160; PubMed-9790499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HBUB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of MAD2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_TaxID~9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol.
                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR IN INTERPHASE CELLS. KIRPTOCHORE
LOCALIZATION IS REDUIRED FOR NORMAL MITOTIC TIMING AND CHECKPOINT
RESPONSE TO SPIMILE DAMAGE (BY SIMILARITY).
TISSUE SPECIFICITY: HIGH EXPRESSION IN TESTILS AND THYMUS, LESS IN
COLON, SPLEEN, LUNG AND SWALL INTESTINE: EXPRESSED IN FETAL
                                                                                                                                                                                                                                                                                        FUNCTION: INVOLVED IN CELL CYCLE CHECKPOINT ENFORCEMENT. CAN INTERACT AND PHOSPHORYLATE BUB3.
                        SIMILARITY: CONTAINS 1 CD1
                                                                                                                      THYMUS. BONE MARROW, HEART, LIVER, SPLEEN AND THYMUS. EXPE
IS ASSOCIATED MITH CELLS/TISSUES MITH A HIGH MITOPIC INDEX
INDUCTION: INHIBITED BY PHORBOL 12-MYRISTATE 13-ACETATE (PR
                                                                                                                                                                                                                                                                          ENZYME REGULATION: AUTOPHOSPHORYLATED WHEN THE CELLS ENTERS
                                            BUB1 SUBFAMILY
                                                          SIMILARITY: BELONGS
                                                                            DISEASE: DEFECTS IN
                                                                                                           DOMAIN: CD1 DOMAIN DIRECTS KINETOCHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR BUBLL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proliferation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and a Mad3/Bub1-related protein kinase."
                                                                                                                                                                                                                                                                                                                                                                                                                                     58:181-187(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Differ.
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                                                                                                                                                                                                                                                                                                                                                                                    PubMed - 9441741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND VARIANTS ASP-36 AND ARG-648
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                                                          BUB1 ARE ASSOCIATED WITH TO THE SER/THR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carson-Walter E.B., Kinzler K.W.,
                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other mitotic spindle checkpoint
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                                                                                                             LOCALIZATION AND BINDING
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                                                            PROTEIN KINASES
                                                                            TUMOR FORMATION
                                                                                                                                                                                                                                                                                                                                                                      Spencer F.;
                                                                                                                                                          EXPRESSION
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RESULT 21
CA14_HUMAN
ID CA14_HUMAN
AC P02462;
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DOMAIN
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InterPro; IPR002290; Ser_th_kin_actsite.
InterPro; IPR002290; Ser_th_kin_actsite.
PR0SITE: PS00101; PR0TEIN_KINASE_DOW; 1.
PR0SITE: PS00107; PROTEIN_KINASE_ST: 1.
PR0SITE: PS00108; PR0TEIN_KINASE_ST: 1.
Transferase; Serine/threonine-protein_kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         LWGV-----TWGPVTEAAIFYETQ-XSLWAESEHXLK-----TLGQ 44
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                                                                                                                                                                 RLTDTDAAIAEDPPDAIAGLQAEWMQMSSLGTVDAPNFI
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S -> T (IN REF. 5).
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P -> R (IN COLORECTAL CANCER).
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ATP (BY SIMILARITY).
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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K -> IRHE (IN REF.
38AE5E1F88C53BDC
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[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-89340433; PubMed-2701944;
Soininen R., Huotari M., Ganguly A.,
Soininen R., Huotari M., Ganguly A.,
                                                                                                                                                              MEDIJNE-65216555; PubMed-2583422;
Brinker J.M., Gudas L.J., Loidl H.R.,
Kefalides N.A., Myers J.C.;
"Restricted homology between human al
procollagen chains."
                                                                                                                                                                                                                                                                                                                                             Pilliajaniemi T. Tryggwason K. Myers J.C., Kurkinen M., Lebo F
Cheung M.-C., Prockop D.J., Boyd C.D.;
P.DNA clones coding for the pro-alphal(IV) chain of human type
procollagen reveal an unusual homology of amino acid sequences
halves of the carboxyl-terminal domain.*;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure of human-basement membrane (type IV) collagen. Complete amino-acid sequence of a 914-residue-long pepsin fragment from the alpha 1(IV) chain.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glanville R.W., Qian R.Q., Siebold B., "Amino acid sequence of the N-terminal region (75 domain) of the alpha 1 (IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deutzmann R., Kuehn K.;

"Completion of the amino acid sequence of the alpha 1 chain

"Completion of lite amino acid sequence of the alpha 1 chain

"Completion of the amino acid sequence of the alpha 1 chain

"Completion of the alpha 1 chain

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01-FEB-1996 (Rel. 33, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
                                                                SEQUENCE OF 1-28 FROM N.A. MEDLINE-89034231; PubMed-3
                                                                                                                                    procollagen
Proc. Natl.
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MEDLINE-85003629; Pul
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FDBS Lett. 225:188-194(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88083584; PubMed=3691802;
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                                                                                                                                                           chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143:545-556(1984).
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                                                                                                                                    Sci.
                                                                PubMed=3182844;
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                                                                                                                                    U.S.A.
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                                                                                                                                    82:3649-3653(1985)
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alpha 1-chain of human basement
                                                                                                                                                                                 alpha 1 type
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                                                                                                                                                                                                                           S. -Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D.J.,
alpha
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1 chain of
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Soininen R., Huotari M., Hostikka S.L., Prockop D.J., "The structural genes for alpha 1 and alpha 2 chains

divergently encoded on opposite DNA strands and have

chains of

Tryggvason K.;

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EMBL;
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1- FUNCTION: TYPE IV COLLAGEN IS THE MAJOR S.
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J. Biol. Chem. 263:17217-17220(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM. LYSINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT ARE HYDROXYLATED IN ALL CASSS AND BIND CARBOHYDRATE.

THE ROLLNES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.

THE TYPE IV COLLACENS CONTAIN HUREROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12 THESE, LOCATED IN THE NCL DOMAIN. AND FORCEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: THERE ARE SIX "YPE IV COLLAGEN ISOFORMS, ALPHA I(IV)-
ALPHA 6(IV), EACH OF WHICH CAN ORM A TRIPLE HELIX STRUCTURE
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS
DOMAIN (NCI)) AT THEIR C-TERMINUS, EREGUENT INTERUPTIONS OF THE
G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH MAY
CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHOPT N-TERMINAL
TRIPLE-HELICAL JS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: TYPE IV COLLACEN IS THE MAJOR STRUCTURAL COMPONENT GLOMERULAR BASEMENT MEMBRANES (GEM), PORTING A 'CHICKEN-HIRE MESHWORK TOGETHER WITH LAMININS, PROTEOCLYCANS AND ENTACTIN',
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          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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PROSITE: PS00290; IG_MIC; 1.
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"The molecular basis for reactivity of anti-Cwl and an alloantisera with HIA-B46 haplorypes.";
Tissue Antigen 39.249-257(1992)
-i- PUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN
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HSSP; P30460;
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                                                                                                                                                                   DAASPRGEPRAPWVEQEG---PEYWDRETQKYKRQAQTDRVSLRNLR-----GYYNQSEA 114
                                                                                                                                                                                            DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                                                                                     MAPRILILLISGALALTETWACSHSMRYFY-TAVSRPGRGEPRFIAVGYVDDTQFVQFDS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003006; Ig_MHC IPR003597; Ig_c1. IPR001039; MHC_I.
   (Rel.
                                                                                                                                                                                                                                                                                                                                       110
366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gumperz J.E., Hildebrand W.H., Ward F.E.,
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA59688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1AGB.
                                                     STANDARD;
   25,
40,
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206
298
308
333
366
188
                                                                                                                                                                                                                                                                                                                                       40772 MW;
                                                                                                                                                                                                                                                                                 9.5%;
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                   CYTOPLASHIC TAIL.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

1, 2A64041389A0465A CRC64;
                                                                                                                                                                                                                                                                                   Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          CW-8 CW+0801 ALPHA CHA)
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                     PRT;
                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW*0801 ALPHA CHAIN
                                                   366 AA
                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                1,
                                                                                                                                                                                                                                                                       67;
                                                                                                                                                                                                                                                                                                Length 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and anti-Cw3
                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marsh S.G.
                                                                                                                                                                                                                                              --- QCDA 47
                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO
                                                                                                                                                                                                                                                                     Gaps
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Pfam; PF00047; ig; i.
Pfam; PF00129; MHC_I; 1.
ProDom; PD0000050; MHC_I; 1.
SMART; SM00407; IGCL; 1.
PR05ITE; PS00220; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alloantisera with HLA-B46 haplotypes. Tissue Antigens 39:249-257(1992).
                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/mnnounce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams R.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                               DOMAIN
                                                                                                                                        CHAIN
                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                  MIM; 142840
                                                                                                                                                                                                                                                                                             EMBL; M84173; AAA59687.1; -. HSSP; P30460; IAGB.
                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - !- FUNCTION: INVOLVED IN THE PRESENTATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The molecular basis for reactivity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zemmour J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE-93031775; Pubmed=1384166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-C OR HLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW-8 CW*0802 ALPHA CHAIN PRECURSOR (CW8.2).
                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                       MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE IMMUNE SYSTEM
                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                         IPR003006; Ig_MHC.
IPR003597; Ig_cl.
IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gumperz
                        25
115
207
207
299
309
334
125
227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parham P.;
                       114
206
298
308
333
366
188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.E., Hildebrand W.H.,
                                                                                                                                                                 Glycoprotein; Signal.
                                                                                                               CW-8 CW*0802 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-Cw1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ward F.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and anti-Cw3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marsh S.G.,
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
Loutstation -
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RESULT
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Best Local S
Matches 34
                                            115
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  24
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                                                                                                                                                                                        MSMLVVFLLLWGV-----TWGPVTEAAIFYETOXSLWAESEHXLKTLG-----OCDA 47
                                            GSHTLQRMYGCDLGPDG
                                                                      LELTGPKVLACSLALDG
                                                                                                                                                            MAPRTLILLLSGALALTETWACSHSMRYFY-TAVSRPGRGEPRFIAVGYVDDTQFVQFDS
                                                                                                   DAASPRGEPRAPWVEQEG---PEYWDRETQKYKRQAQTDRVSLRNLR---
                                                                                                                             DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                 9.5%;
                                            131
                                                                                                                                                                                                                                 Score 63;
Pred. No.
                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                 DB 1; Length 366;
21;
                                                                                                                                                                                                                      67;
                                                                                                                                                                                                                    Indels
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DISULFID DISULFID CARBOHYD TRANSMEM DOMAIN DOMAIN

DOMAIN

EXTRACELLULAR ALPHA-3.
EXTRACELLULAR ALPHA-3.

PEPTIDE

SEQUENCE

3

40871

MW.

BY SIMILARITY BY SIMILARITY N-LINKED (GLC) CYTOPLASMIC TAIL. BY SIMILARITY.

-LINKED (GLCNAC. . .) (BY SIMILARITY). D343B054568EA32C CRC64;

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                                                                                                                                                                                                                                                             Matches
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Best Local
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InterPro; IPR001039; MIC_I.
Pfam: PP00047; Ig; 1.
Pfam: PP00120. ....
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
10-AUG-2001 (Rel. 40, Last annotation update)
11A. CLASS I HISTOCOMPATIBILITY ANTIGEN, CM-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-C OR HLAL.

HOMO saplens (Human).

Larvota; Metazoa; Chordata;

Larvota; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 19; 1.
Pfam; PF00129; MHC_1; 1.
ProDom; PD000050; MHC_1; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the RMBL outstation— the Buropean Bloinformatics Institute, There are no restrictions on its use by non-profit institutions as long as its concent is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Belich M.P., Madrigal J.A., Hildebrand W.H., Zemmo Williams R.C., Luz R., Petzi-Erler M.L., Parham P. "Onusual HLA-B alleles in two tribes of Brazilian Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRECURSOR.
HLA-C OR HLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 142840; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92269955; PubMed-1317015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID 9606;
   108 LELTGPKVLACSLALDG 124
                                                     63
                                                                                                    48
                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICROCLOBULIN).
                                                                                                                                                                                                        MSMLVVFLLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLG-----OCDA 47
                                                  DAASPRGEPRAPWVEQEG---PEYWDRETQKYKRQAQTDRVSLRNLR-----GYYNQSEA 114
                                                                                                    DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                      MAPRILILLSGALALTETWACSHSMRYFY-TAVSRPGRGEPRFIAVGYVDDTQFVQFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P30460; 1AGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                25
115
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                                                                                                                                                                                                                                                                                      9.5%;
                                                                                                                                                                                                                                                                                                                                                                                              40872
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                                                                                                                                                                                                                                                                                                                                                                                              ME
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                                                                                                                                                                                                                                                                                                                                                                                          CYYODLASHIC TAIL.
BY SIMILARITY
BY SIMILARITY
N-LINKED (GLUNG. . .) (BY SIMILARITY).
; COLSDPANSBBL4866 CRC64;
                                                                                                                                                                                                                                                                                      Score 63;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CW-8 CW*0803 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                          21:
                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                             67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zemmour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CW*0803 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                               Length 366
                                                                                                                                                                                                                                                             indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indians.";
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                                                                                                                                                                                                                                                             Caps
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                                                 Query Match
Best Local S
Matches 37
                                                                                                                                                                                                                                                                                                                                        DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed, Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 193:868-876(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Influenza A virus (strain A/Quail/Italy/1117/65).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEURAMINIDASE
NA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel.
01-FEB-1995 (Rel.
01-FEB-1996 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRAM_IAQIT
Q07584;
                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000431; Neur;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L06587; AAA43373.1; HSSP; P06820; 11NH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE~93212520;
                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Phylogenetic analysis of the N8 neuraminidase gene of influenza A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Influenza virus A and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND FROM THE SITE OF INFECTION.

CATALYTIC ACTIVITY: CLEAVE THE TERMINAL STALIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 34 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCULT: HOMOTETRAMER. FORMS SUBCELLULAR LOCATION: VIRAL MEMBRANE. FORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: PREVENT SELF-AGGREGATION BY REMOVING THE CARBOHYDRATE FROM THE VIRAL ENVELOPE. FACILITATE THE MOBILITY OF THE VIRUS TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPIKE ON THE SURFACE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEURAMINIC ACID) FROM CARBOHYDRATE CHAINS
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   WGVTWGPVTEAA1FYETQXSLWAESEHXLKTLGQCDADVPGP------PGDSRLPAV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00064; neur;
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3212520; PubMed-8460490;
Kawaoka Y., Webster R.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001860; Neur.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycosidase;
7 38
                                                 Conservative
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Rel. 31, Last sequence update)
Rel. 33, Last annotation update)
(EC 3.2.1.18).
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ANCHOR (BY SIMILARITY).
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                                                                                                                                                                         X.
                                                 19;
                                                                                                                                                                                                                                    HEAD OF NEURAMINIDASE.
BY SIMILARITY
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LINKED (GLCNAC. .
9F743833EAC7F1C2 C
                                                 Mismatches
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RDNWTGTNRPILVISPDLSYRVGYLCAGLPSDTPRGVDAQFTGSCTSPMGNQGYGVKGFG

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01-FEB-1991
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20-AUG-2001
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                                                                                                                         Hayashi T., Wakino K., Ohnishi M., Kurokawa K., Ishii K., Yokoy, Han C.-G., Ohtsubo E., Makayama K., Murata T., Tanaka M., Tobe 'Ilda T., Takami H., Bonda T., Sasakawa C., Ogasawara N., Yasunaw Khhara S., Shiha T., Hattori M., Shinagawa H., "Complete genome sequence of enterohemorrhagic Escherichia coli 137:H7 and genomic comparison with a laboratory strain K-12."; DM, Res. 8 11.7-22(2011)
                                                                                                                                                                                                                                                                                                                                 Perna M.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Crotheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Mantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / MG1655;
MEDLINE-9746501; Puhwed-9278503;
MEDLINE-9746501; Puhwett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Pede C.K., Mayhew G.F. Gregor J., Dayls N.W., Klirkpatrick H.A., Goedden M.A., Rose D.J., Gregor J., Dayls N.W., Klirkpatrick H.A., Goedden M.A., Rose D.J.,
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01-MUG-1992 (Rel. 23). Last sequence updat
10-AUG-2001 (Rel. 24). Last annotation upd
TOPOISOMERASE IT SUBUNITY A (ECC 5.99). 1. ).
PAKC OR BJ019 OR Z4373 OR ECS5903.
"Characterization of the Escherichia coli gene l-acyl-sn-glycerol-3-phosphate acyltransferase Mol. Gen. Genet. 232:295-303(1992).
                                                                                                                                                                                                                                                                                     -Genome sequence of enterohaemorrhagic
Nature 409:529-533(2001).
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Cell 65:1289-1290(1991).
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                                                             Coleman J.;
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MEDLINE=21156231; PubMed=11258796;
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MEDLINE-21074935; PubMed-11206551;
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Escherichia.
                                                                             MEDLINE-92212294;
                                                                                            SEQUENCE
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topoisomerase essential for chromosome
63:393-404(1990).
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                                                                             OF 724-752 FROM N.A.
92212294; PubMed=1557036;
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Tanaka M., Tobe T.,
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n E. coli.";
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Best Local
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EMBL. M53401 AAA4395.1.
EMBL. M53401 AAA4395.1.
EMBL. AB00391 AAA69187.1.
EMBL. AB00391 AAA69185.1.
EMBL. AB00591 AA659185.1.
EMBL. AB00591 AA65918.1.
EMBL. AB00591 AA65918.1.
EMBL. AB00591 AA65919.1.
EMBL. AB00591 AA65980.1.
EMBL. AB00591 AA65980.1.
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EMBL. AB0071, AB0075.
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01-0CT-1996 ()
01-0CT-1996 ()
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EXOGLUCANASE ()
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J. BIOL. Chem. 768:24481-72484(193).

11 FUNCTION: TOPOISOMERASE IV IS ESSENDENCE CHROMOSOME
SERERGANION. IT HAS RELAXATION OF SUPERIAL FOR CHROMOSOME
PERFORMS THE DECATEMATION EVENTS REQUIRED DURING THE REPLICATION
OF A CIRCULAR DAY ADLECULE.
OF A CIRCULAR DAY ADLECULE.
PARC AND PARE.
SUBSELLLIAR LOCATION: MEMBRANE-ASSOCIATED.
THE SUBSELLIAR LOCATION: MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   MEDLINE-96003898: PubMed-7575482;
Shen H., Gilkes N.R., Kilburn D.G
                                                        SEQUENCE FROM N.A.,
STRAIN-ATCC 484;
                                                                                                                                                                                                                    Cellulomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                     GUXB_CELFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00434; TOP4C; 1.

TOPOLSSOmerase: Isomerase; DNA-binding; Complete proteome.

ACT_SITE 120 120 DNA CLEAVAGE (BY SIMILARITY)
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InterPro; IPR002205; DNA_topoisoIV
Pfam; PF00521; DNA_topoisoIV; 1.
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                                                                                                                                      Actinomycetales; Micrococcineae; NCBI_TaxID=1708;
                                                                                                                                                                                          Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                         (1,4-BETA-CELLOBIOHYDROLASE B)
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                                                                                                                                                                                                                                              OR CENE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                        (Rel. 34, Last sequence update)
(Rel. 34, Last annotation update)
E B PRECURSOR (EC 3.2.1.91) (EXOCELLOBIOHYDROLASE
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ococcineae; Cellulomonadaceae;
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D.G.,
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THE REPLICATION
   Warren R.A.J.;
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Query Match
Best Local S
Matches 33
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InterPro; IPR001777; FN_III;
InterPro; IPR001555; Glyco_hydro_48.
Pfam; PF00553; CBD_2: 1.
Pfam; PF0041; fn3; 3.
Pfam; PF0041; fn3; 3.
Pfam; PF00041; fn4; GLyco_hydro_48: 1.
PRINTS; PR00844; GLHYDRLASE48.
                                                                       ACT_SITE
DISULFID
SEQUENCE
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DOMAIN
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between
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MeLinke A. Gilkes N.R., Kilburn D.G., Miller R.C. Jr., M. Cellulose-binding polypoptides from Cellulomonas fimi: D. (CenD), a family A beta-1.4-glucanase.*;
J. Bacteriol. 175:1910-1918(1933).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CenE, a member of a new family of beta-1,4-glucanases."; Blochem. Biophys. Res. Commun. 199:1223-1228(1994),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cellobiohydrolase B, a second exo-cellobiohydrolase from the cellulolytic bacterium Cellulomonas fimi."; Blochem. J. 311:67-74(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shen H., Tomme P., Meinke Warren R.A.J., Miller R.C.
                                                                                                                     DOMAIN
                                                                                                                                                                                                           PROPEP
                                                                                                                                                                                                                                       Cellulose
                                                                                                                                                                                                                                                     PROSITE; PS00561;
                                                                                                                                                                                                                                                                 SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P07986;
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L38827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN CELLULOSE AND CELLOTETRAOSE, RELEASING CELLOBIOSE PRO
REDUCING ENDS OF THE CHAINS
SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS
SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: HUDROLYSE CELLOHEXAOSE TO A MIXTURE OF CELLOTERAOSE. CELLOTRIOSE AND CELLOTROSE, WITH ONLY A TRACE OF GLUCOSE. IT HYDROLYSED CELLOPENPAGSE TO CELLOTROSE AND CELLOTROSE, WITH CELLOTERIOSE TO CELLOTROSE. BUT IT DID NOT HUDROLYSE CELLOTRIOSE. HAS ALSO HEAR ENCOCLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS HAS ALSO HEAR ENCOCLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS HAS ALSO HEAR ENCOCLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC BONDS HAS ALSO HEAR ENCOCLUCANASE ACTIVITY. HYDROLYSES GLUCOSIDIC LINKACES.
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                9.5%;
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  19;
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Score 63; DB
Pred. No. 76;
L9; Mismatches
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                                                                                                                               CATALYTIC (BY SIMILARITY).
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
                                                                                                   CELLULOSE-BINDING (BY SIMIL NUCLEOPHILE (BY SIMILARITY)
                                                                                       BY SIMILARITY
                                                                                                                                                                                                                         POTENTIAL.
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                                                                         046BB9D956F2F399 CRC64;
                                                                                                                                                                                                                                     Glycosidase; Repeat; Signal.
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O15528;
15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
20-AUG-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                    mutations causing vitemin D-dependent rickets type 1.";
1. Endocrinol. 11:151-1370(1997).
-1- FUNCTION: CATALYZES THE CONVERSION OF 25-HYDROXYVITAMIN MODERN CATALYZES THE CONVERSION OF 25-HYDROXYVITAMIN DID (1,25(0H)2D)
IMPORTAMI ROLE IN CRUCIAL ROLE IN NORMAL BONE GROWTH, CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IS-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sanctation update)
20-MUG-2001 (Rel. 40, Last annotation update)
25-HYDROXYUTAMIN D-1 ALPHA HYDROXYLASE, MITOCHONDRIAL PRECURSOR
(EC 1.14.---) (25-GHD-1 ALPHA HYDROXYLASE) (25-HYDROXYUTAMIN D3
ALPHA-HYDROXYLASE) (VD3 1A HYDROXYLASE) (P450C1 ALPHA) (P450VD1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Cloning of human 25-hydroxyvitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98075882; PubMed-9415400; Fu G.K., Lin D., Zhang Y.H., Bikl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fu G.K., Portale A.P., Miller W.L.; "Complete structure of the human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-hydroxyvitamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suda T., Hayashi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monkawa T., Yoshida T., Wakino S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE~98008873; PubMed~9344864;
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MEDLINE-98089075; PubMed--9428799;
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                          s SMISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics institute. There are no restr
                                                                                                                                                                                                                                               METABOLISM, AND TISSUE DIFFERENTIATION.
PATHWAY: SECOND STEP IN THE COMPRESION OF VITAMIN
ACTIVE FORM (1-ALPHA, 25-DIHYDROXYVITAMIN D(3)).
SUBCELLULAR LOCATION: MITOCHONDRIAL.
TISSUE SPECIFICITY: KIDMEY.
                                                                                                                                     DISEASE: DEFECTS IN CYP27B RICKETS TYPE 1 (VDDR-1), A WEAKNESS AND RICKETS. SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NISTOGAS
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xyvitamin D3 1 alpha-hydroxylase.*;
Blophys. Res. Commun. 239:527-533(1997).
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                                                                                                                                        BELONGS TO THE CYTOCHROME P450 FAMILY.
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DISEASE CHARACTERIZED E
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nt rickets type 1.";
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                                                         a collaboration .
MBL outstation -
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01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.
                                                                                                                         wood L., Theirman, completing cons completing
                                                                                                                                                                                 MEDLINE-88112221; PubMed-3338568; Wood L., Theriault N., Vogeli G.
                                                                                                                                                                                                                                                                                        Muthukumaran G., Blumberg B., Kurkinen M.;
"The complete primary structure for the alpha 1-
collagen IV. Differential evolution of collagen
J. Biol. Chem. 264:6310-6317(1989).
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-89197932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
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                         SEQUENCE OF 1149-1424 FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTWGPVTEAAIFYETOXSLWAESEHXLKTLGQCDADVPGPP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --GLSTG----WXQLSKLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRWAPELGASLGYR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264700;
                                                                                                       mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR001128; Cyt_P450
PF00067; P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR00385; P450.
PR00408; MITP450.
; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport; Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-2703490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508
455
56504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -EWGAQEPVHLDSPAIKHQFL-----
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chain of baseme
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITOCHONDRION (POTENTIAL)
25-HYDROXYVITAMIN D-1 ALP
HEME (BY SIMILARITY).
; 7F0511EFAD1B5C1C CRC64;
                                                                                                                         of basement membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                  the alpha 1-chain of mouse
of collagen IV domains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae; Murinae;
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(type
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"Mogeli G., Voss T., Siebold B., Glanville R.W., Kuhn K.,
"Amino acid sequence of the non-collagenous globular domain (NC1) of
the alpha [17] chain of basement membrane collagen as derived from
complementary DNA.";
                                                                                                                                                                                                                                                                                                                 *Structure of the amino-terminal portion of collagen chain and the corresponding region J. Biol. Chem. 25:8706-9709(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1276-1669 FROM N.A. MEDLINE-85127033; PubMed-2578961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic oligodeoxynucleotide.
Gene 43:301-304(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-129 FROM N.A. MEDLINE-88243724; PubMed-3379041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Alpha 1(IV) and alpha 2(IV) collagen genes are regulated bidirectional promoter and a shared enhancer.", proc. Natl. Acad. Sci. U.S.A. 85:9679-9682(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burbelo P.D., Martin G.R., Yamada Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-28
MEDLINE-89071759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Raytes P., Wood L., Theriault N., Kurking "Head-to-head arrangement of murine type J. Biol. Chem. 263:19274-19277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-28 FROM N.A. MEDLINE-89066738; PubMed-3198626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collagen
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"Alpha 1 type IV collagen gene evolved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE FROM N.A. MEDLINE-86196099; PubMed-3009468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Extensive homology between the carboxyl-terminal
alpha 1(IV) and alpha 2(IV) collagen.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1441-1669 FROM N.A. MEDLINE-87250460; PubMed-3597383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biol.
SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOPOMS, ALPHA I(IV) ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCTURE WITH 2 OTHER CHANS TO GENERATE TYPE IV COLLAGEN NETWORK. DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A MONOCLAGENUS SOMAIN (NCI) AT THEIR C-TERMINIS, FREDUER'I INTERUPTIONS OF THE G-X-Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOMAIN (WHICH CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL TO DOMAIN.
                                                                                                                                                                                                                                                    TUNCTION: TYPE IV COLLAGEN IS THE MAJOR STRUCTURAL COMPONENT GLOMEBULAR BASEMENT MEMBRANES (GEM), FORHING A "CHICKEN-WIRE MESHMORK TOGETHER WITH LAMININS, PROTEOGLYCANS AND ENTACTIN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghem.
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cDNA clone using a
                                                                                                                                                                                                                                                                                                                                                                      y Y.;
f the murine a
n of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen genes.";
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This SWI modified entities use e European B SMISS-POT entry is copyright. It is produced through heen the Swiss Institute of Bioinformatics and the Ex European Bioinformatics Institute. There are no rest non-profit and this st institutions as long is not removed agreement (See as its content http://www.isb-sib Usage by restrictions and EMBL a collaboration - MBL outstation for .ch/announce, outstation no 9

PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS PTM: TYPE IV COLLACEMS CONTAIN MUNEROUS CYSTEINE RESIDUES WHICH ARE INVOLVED IN INTER- AND INTRAMOLECULAR DISULFIDE BONDING. 12

IV COLLAGENS

LOCATED IN THE

NC1 DOMAIN, ARE CONSERVED

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MEDLINE-86301886; PubMed-3755692;

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1825_UIUMAN STANDARD: PRT: 362 AA.

P10471;
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InterPro: IPR000087; Collagen
Pfam; PF01413; C4; 2.
Pfam; PF01391; Collagen; 21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00111; C4: 2. Extracellular matrix; Connective tissue; Basement membrane:
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SMART; SM00111; C4; 2.
   Eukaryota; Metazoa;
                         Homo sapiens (Human)
                                               HLA-B OR HLAB
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AAA51625.1; -.
AAA50292.1; -.
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-; NOT_ANNOTATED_CDS.
AAA37344.1; -.
AAA37345.1; -.
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COLLAGEN ALPHA 1(IV) CHAIN.
TRIPLE-HELICAL RECION
NONHELICAL RECION (NCI).
OR 1546 (BW SIMLLARITY).
OR 1551 (BW SIMLLARITY).
BY SIMILARITY.
OR 1665 (BW SIMLLARITY).
BY SIMILARITY.
OR 1665 (BW SIMLLARITY).
BY SIMILARITY.
OR 1665 (BW SIMLLARITY).
DY SIMILARITY.
OPTOMINATION.

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6; Mismatches
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   Craniata; Vertebrata; Euteleostomi;
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1C04_HUMAN
P30502;
P30502;
O1-APR-1993
O1-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for common entities a linear and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belich M.P., Madrigal J.A., Hildebrand M.H., Zemmour J.,
Williams R.C., Luz R., Petzl Erlor M.L., Barham P.,
Vinusual HA-B alleles in two tribes of Brazilian Indians.";
                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation - the European Bioinformatics institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 357:326-329(1992).
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MEDLINE-92269955; PubMed-1317015;
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                                                                                                                                                                RTEPRAPWIEQEG---PEYWD----RNTQIFKTNTQ-TYRESLRNLRGYYNQSEAGSHTL
                                                                                                                 QSMYGCDLGPDG
                                                                                                                                         PKVLACSLALDG
                                                                                                                                                                                                                                       VFLLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLG------QCDADVPGP 52
                                                                                                                                                                                        PGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTG
                                                                                                                                                                                                                   VLLLLWGAVALTETWAGSHSMRYFY-TAMSRPGRGEPRF1AVGYVDDTQFVRFDSDAASP
                                                                                                                                                                                                                                                                              Similarity
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IPR003597; Ig_c1.
IPR001039; MHC_I.
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EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3505 ALPHA CHAIN.
                                                    PRT;
                                                                                                                                                                                                                                                                   Mismatches
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RESULT 32
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=89235215; PubMed=2715640;
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or send an email to license@isb-sib.ch).
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ProDom; PD000050; MHC_I; 1.
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InterPro; IPR003597; Ig_cl.
InterPro; IPR001039; MHC_I.
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SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
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                                                                                                                         GSHTLQRMYGCDLGPDG 131
                                                                                                                                                                                                                       DAASPRGEPRAPWVEQEG---PEYWDRETQKYKRQAQTDRVNLRKLR-----GYYNQSEA 114
                                                                                                                                                                                                                                                                                                                     MAPRTLLLLLSGALALTETWACSHSMRYFY-TAVSRPSRGEPHFIAVGYVDDTQFVRFDS
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PS00290; IG_MHC; 1
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EXTRACELLULAR ALPHA-1.
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62

Query Match Best Local Matches

Local Similarity

9.48;

Score 62; DB Pred. No. 27; 15; Mismatches

67;

Indels

22;

Gaps

5

Length 366;

Conservative

15;

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P30508;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CW+12
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DISULFID
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MHC I; T:
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           CARBOHYD
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Pfam; PF00129; MHC_I; 1.
ProDom; PD000050; MHC_I; 1.
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                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
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Submitted (JUN-1992) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and analysis of HLA class I cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takata H., Inoko H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-88330144; PubMed-2843461;
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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PS00290; IG_MHC; 1.
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N-LINKED (GLCNAC. . .) (BY SIMILARITY).; E6A7DA16117A7B46 CRC64;
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                                                                                 CW*1201 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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Catarrhini; Hominidae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CW*1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                      as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bodmer J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOREIGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                           (BETA-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        new HLA-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tsuji K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Inoko H.;
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밁 Ş 밁

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RESULT 34
Y029-HUMAN
ID Y029-H
AC 015032
DT 15-JUL
DT 15-JUL
DT 20-ANG
DE HYPOTH
GN KIAAOG
OS HURDO'S
OC Eukory
OC Mammal
                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GG95_HUMAN
Q08379;
01-NOV-1997
01-NOV-1997
                                                                         15-JUL-1998
15-JUL-1998
20-AUG-2001
                                                                                                                         Y029_HU
Q15032;
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  GOIGI Stack: Coiled coil
DOMAIN 5 336
DOMAIN 352 510
POMAIN 67 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAMOH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fritaler M.J., Hamel J.C., Ochs R.L., Chan E.K.L.;
Modecular characterization of two human autoantigens: unique cDNAs encoding 95- and 160-kD proteins of a putative family in the Golyi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOLGIN-95.
                                                              HYPOTHETICAL PROTEIN KIAA0029
              Eukaryota; Metazoa;
                               Homo sapiens (Human)
                                              KIAA0029
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM; 602580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L06147; AAA35920.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb•sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Exp. Med. 178:49-62(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93301617; PubMed-8315394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                            26 ETQXSLWAESEHXLKTL----GQCDADVPGPPGDSRLPAVQE------WGAQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: GOLGI AUTO-ANTIGEN: MAY HAVE A FUNCTION IN THE PROCESSING AND TRANSPORT OF PROTEINS THROUGH THE GOLGI. DOWAIN: EXTENDED ROD-LIKE PROTEIN WITH COLLED-COIL DOWAINS. SIMILARITY: HIGH, TO RAT CIS-GOLGI MATRIX PROTEIN GM130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSHTLQRMYGCDLGPDG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LELTGPKYLACSLALDG 124
                                                                                                                                                                                                                 EVEQQLQAEAEHLRKELEGLAGQLQAQVQDNEGLSRLNREQEERLLELERAAELWGEQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAASPRGEPRAPWVEQEG---PEYWDRETQKYKRQAQADRVSLRNLR-----GYYNQSEA 114
                                                                                                                                       HUMAN
    Eutheria;
                                                                         (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                        9.4%;
    Primates;
              Chordata;
                                                                                                                                                                                                                                                                                                                                                      70472 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                           ۲.
                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                   COILED COIL COILED COIL POLY-PRO. POLY-GLU.
  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                      54B31A0FBB42BFC8 CRC64
                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                          No.
                                                                                                                                       971 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            620
                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                        Length 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                  ACAL_ARATH STANDARD; PRP; 1020 AA.
037145; 037146; 042517 (042587, 042587)
20-ANG-2001 (Rel. 40 Created)
20-ANG-2001 (Rel. 40 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoj
Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                               ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SMISS-PROT entry is copyright. It is produced through
between the Swiss Institute of Bioinformatics and the Bu
the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y., Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.; Prediction of the coding sequences of undentified human genes. The coding sequences of 40 new genes (KIAAOOOI-KIAAOO4O) deduced
                             Proc.
                                                                                                                                                                                                                                                                         ACA1 OR PEA1 OR AT1G27770 OR T22C5.23 OR F28L5.1.
Arabidopsis thallana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01424; R3H; 1.
SMART; SM00393; R3H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Bone marrow;
MEDLINE-96051387; PubMed-7584026;
                                                          REVISIONS.
                                                                                                      "Characterization of a gene encoding a the plastid envelope.";
                                                                                                                                     MEDLINE~94052104; PubMed~8234257;
Huang L., Berkelman T., Franklin A.E.,
                                                                                                                                                                     STRAIN-CV. COLUMBIA;
                                                                                                                                                                                 PRELIMINARY SEQUENCE FROM N.A., AND PARTIAL
                                                                                                                                                                                                               NCBI_TaxID 3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein DOMAIN 461 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001374; R3H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D21852; BAA04878.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 1:27-35(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        analysis of randomly sampled cDNA clones from human immature myeloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGAGETVVGKVLEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---GWXQLSKLLELT 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ-----GRYRCRSGLST- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPG-QGDSRYPLL-----GQPLQYNPPAVLHGHIPNQQGQPGSRHGNRGRRQAKKAASTD 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               line KG-1
                       Natl. Acad. Sci.
                                                                                            Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   non-profit institutions as long
                                              Berkelman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694
971 AA;
                                                                                            Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480
698
                                              ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107673 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.4%;
                                                                                         U.S.A. 90:10066-10070(1993)
                             U.S.A. 91:9664-9664(1994).
                                              Franklin A.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB
Pred. No. 85;
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-PRO.
W; D07684D368955108 CRC64;
                                                                                                                     Hoffman N.E.;
Ca(2+)-ATPase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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C
                                                                                                                                                                                                                                                             Tracheophyta
                                                                                                                                                                                                                                                                                                                       3.8.3.8)
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                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for commercial
                                                                                                                                                                                                                                              Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RA Thologis A., Ecker J.R., Pelderspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Borman C.L., Brooks S.Y.,
RA White E., Chan A., Chao G., Chen H., Check R.F., Chin C.W.,
RA Buehler E., Chan A., Chao G., Chen H., Check R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Hans B., Hansen N.F., Hudphes B., Hulzar L.,
RA Gill J.E., Goldsmith A.D., Hans B., Hansen N.F., Hudphes B., Hulzar L.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
RA Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
RA Lin X., Liu S.A., Luros J.S., walti R., Warzlall A.,
Lin X., Liu S.A., Luros J.S., walti R., Warzlall A.,
RA Lin X., Liu S.A., Luros J.S., walti R., Warzlall R.,
RA Hilischer J., Miranda M., Nguyen M., Nierman W.C., O'Sborne B.I.,
RA Hilischer J., Miranda M., Nguyen M., Neoney T., Rowley D.,
RA Hilscher J., Manney G., Tochuni M.J., Town C.D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Tochuni M.J., Town C.D.,
RA Hilb., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
L., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
L., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
L., Yun G., Walker H.,
RA Willer G. W., Walker M.,
RA Willer G. W., Walker M.,
RA Willer G. W., Walker M.,
RA Walker M., Walker M.,
RA
                                                                          Mendel: 16033 Arath:2439;16033
Mendel: 16034 Arath:2439;16034
Mendel: 22293 Arath:2439;22293
Mendel: 22293 Arath:2439;22293
Mendel: 32294 Arath:2439;262294
Mendel: 36857 Arath:2439;36858
InterPro: PRRO01757: E1-E2_AFPase.
InterPro: PRRO01757: E1-E2_AFPase.
InterPro: PRRO01859; HATPase.
InterPro: PRO01859; HATPASE.
PRINTS: PRO0119: CATATPASE.
PRINTS: PRO0119: CATATPASE.
PRINTS: PRO01101: MATPASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Bt the European Bioinformatics Institute. There are no resti
Hydrolase; Calcium transport; Transmembrane; Phosphorylation; ATP-binding; Metal-binding; Magnesium; Chloroplast;
                                                   PROSITE; PS00154; ATPASE_E1_E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:816-820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: THE N-TERMINUS CONTAINS AN AUTOINHIBITORY CALMODUL.
BINDING DOMAIN, WHICH BINDS CALMODULIN IN A CALCIUM-DEPENDIFASHION (BY SINLLARITY).
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OUT OF THE CELL OR INTO ORGANELLES.

CATALYTIC ACTIVITY: ATP + H(2)0 + CA(2+)(CIS) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (E1-E2 ATPASES). SUBFAMILY IIB. CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENVELOPE (INNER MEMBRANE) (PROBABLE).
TISSUE SPECIFICITY: EXPRESSED AT HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN: CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA(2+)(TRANS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THIS MAGNESIUM DEPENDENT ENZYME OF ATP COUPLED WITH THE TRANSLOCATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOUNDARIES PREDICTED FROM THE GENOMIC SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENZYME REGULATION: ACTIVATED BY CALMODULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LO8469;
D13983;
D13984;
X69940;
X69941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L08468; AAD10211.1; -. L08469; AAD10212.1; -. D13983; BAA03090.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11719; 1EUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC012375; AAF24958.1; ALT_SEQ. AC079280; AAG50579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAA49559.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAA03091.1; -. CAA49558.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIGHER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CALCIUM FROM THE CYTOSOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A CALCIUM-DEPENDENT
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                                                               Sato S., Wakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.,
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Seq
features of the regions of 4,504,664 bp covered by sixty Pl and T
                                                                                                                  STRAIN=CV. COLUMBIA;
MEDLINE-20277480; PubMed-10819329;
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Pred. No. 89;
10; Mismatches
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PHOSPHORYLATION (BY SIMILARITY).

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MAGNESIUM (BY SIMILARITY).

P-> S (IN REF. 1; AAD10211 AND
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                                                                                 DM43_DIDMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB019229; BAB02320.1; ALT_SEQ. InterPro; IPR001757; E1-E2_ATPase. InterPro; IPR001454; Hydrolase.
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Unpublished o
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FUNCTION: INVOLVED IN TRANSPORT OF PHOSPHOLIPIDS (POTENTIAL)

CATALYTIC ACTIVITY: AFP + H(2)F0 - ADP + PHOSPHATE.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN

SINILARITY: BELONGS TO THE CATION TRANSPORT AFPASES FAMILY
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CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO WRONG
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    METALLOPROTEINASE
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  INHIBITOR DM43
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                      Score 62;
Pred. No.
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W; 07E323DB71B6D9FB CRC64;
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PHOSPHORYLATION (BY SIMILARITY).
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-1- SIMILARITY: TO HUMAN ALPHA-1B-GLIXCOPSOTEIN
-1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE V-TYPE DOWAINS
INTERPRO: IPR003306; T9_MIC.
INTERPRO: IPR003309; T9_MIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neves-Ferreira A.G.C., Perales J., Fox J.W., Shannon J.D., Makino D.L., Garratt R.C., Domont G.B.,
"Structural and functional analyses of DM43, a snake venom metalloproteinase inhibitor from Didelphis marsuplatis serum.";
Submitted (FER-2001) to the SMISS-PROT data bank.
1- FUNCTION: METALLOPROTEINASE INHIBITOR.
                                                                                                                                                                                                                                                                                                                                SMART; SM00410; IG_like;
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Eutel
                                                                                                                                                                                                                                                                                                                   Metalloprotease inhibitor;
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-!- PTM: ALL THE "X" ARE PROBABLY GLYCOSYLATED
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64 VTADNRGIYRCRILTSENDWTPLSAPVEVTGKEPL 98
                                   83 LTGDTOGRYRCRSGLS-TGWXQLSKLLELTGPKVL 116
                                                                                                                                                                                                                                                                                                                                                                         PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                            IPR003600; Ig_like
                                                                              Conservative
                                                                                                                                                                                                                                 domain.
21 81
26 272
28 74
                                                                                                                                                                             AA;
                                                                                                                                                                           163
265
32374
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                                                                                               429
                                                                                               9 8
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IG-LIKE V-TYPE DOMAIN 2.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 1889D62F1A28288D CKC64;
                                                                                                                                                                                                                                                                                                                   Venom;
                                                                                               Score 61.5;
Pred. No. 24;
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Didelphidae; Didelphis.
                                                                                                                  DΒ
                                                                                                                  1.
                                                                              14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASPARAGINE
                                                                                                                  Length
                                                                              Indels
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                                                                            <u>;</u>.
                                                                            Gaps
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RESULT 38
EYAL MOUSE STANDARD; PRT; 591 AA.
AC P97767.008818; STANDARD; PRT; 591 AA.
DT 15-7UL-1998 (Rel. 36, Last sequence update)
DT 16-7UL-1998 (Rel. 36, Last sannotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
Abdelhak S., Kalatzis V., Hellig R., Compain S., Samson D. Vincent C., Beil D., Craud C., Sahly r., Leibovici M., Bitner-Glindzicz M., Francis M., Lacombe D., Vigneron J., Charachon R., Boven K., Bedbeder P., van Regemorter N., Weissenbach J., Petit C.;
                                                                                                                                                 STRAIN-CB/20;
MEDLINE-97172972; PubMed-9020840;
                                                                                                                                                                                                                                                                      Xu P.-X., Woo I., Her H., Beier D.R., Maas R.L.;
"Mouse Eya homologues of the prosophila eyes absent gene require Pax6
for expression in lens and nasal placode.";
Development 124:219-231(1997).
                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97158722;
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYA1
                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYES ABSENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOY10MOH
                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9006082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                    2
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Query Match
Best Local Similarity
                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage here or no or send an email to a license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borsani G., DeGrandi A., Hallabio A., Bulfone A., Bernard L.,
Banfi S., Gettuso C., Mariani M., Dixon M., Donai D., Metcali
Winter R., Robertson M., Axton R., Brown A., van Heyningen V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Inner ear and kidney anomalies caused by IAP insertion in an intron of the Eyal gene in a mouse model of BOR syndrome."; Hum. Mol. Genet. 8:645-633(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99172074; PubMed=10072433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99105912; PubMed-9887327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 431-549 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paradies N.E., Friedman R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Johnson K.R., Cook S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human homologue of the Drosophila eyes absent gene underlies anchio-oto-renal (BOR) syndrome and identifies a novel gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: EXTENSIVELY EXPRESSED IN CRANTAL PLACODES, BRANCHIAL ARCHES, CNS AND DEVELOPING EYE AND NOSS.
DISEASE: DEFECTS IN EYAL ARE THE CAUSE OF THE EYAL-BOR MUTATION AN AUTOSOMAL RECESSIVE DISORDEN WHICH RESEMBLES HUMAN BOR SYNDROME. THE CONDITION IS CHRACTERIZED BY GROSS MORPHOLOGICAL ABBORDALITIES OF THE INNER EAR AND DYSMORPHIC OR MISSING KIDNEY ABBORDALITIES OF THE INNER EAR AND DYSMORPHIC OR MISSING KIDNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE EYA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MAY BE INVOLVED IN DEVELOPMENT OF THE EYE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGI:109344; Eyal
                                                                                                                                                                                                                                                                                                                                                                                                    Lopmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U61110; AAB48017.1; -. Y10263; CAA71312.1; -. AF097544; AAD19355.1;
                                                                                                                                                                                                                                                                                                                                                                                                                 PF00702; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ007995; CAA07818.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a novel vertebrate gene related to Drosophila eyes absent." pl. Genet. 8:11-23(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001454; Hydrolase
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163
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S > I (IN REF. 2).

R - G (IN REF. 2).

LL - VV (IN REF. 2).
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Pred. No. 54;
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1B7B433027F47176
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SSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                    V (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND DYSMORPHIC OR MISSING KIDNEYS
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Signal;
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                                                                                                                            EMBL;
                                                                                                                GlycoSuiteDB; 097939;
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                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fukae M., Tanabe T., Murakami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simmer J.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Enamel epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENAMELIN PRECURSOR
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20-AUG-2001
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20-AUG-2001
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                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Primary structure of porcine 89 kda enamelin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97350624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE FROM N.A., PARTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hu C.-C., Fukae M., Uchida T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98040070; PubMed=9372788;
                                                                                                    InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
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                                                                                                                                                                                        European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: EXPRESSED BY SECRETORY-PHASE AMELOBLASTS INTACT ENAMELIN AND LARGE-MOLECULAR-WEIGHT ENAMELINS ARE LIM
                                                                                                                                                                                                                                                                                                                                                                                            PUNCTION: PEPTIDES DERIVED FROM THE PARENT ENAMELIN ARE COMP
OF ENAMEL, A UNIQUE AND HIGHLY MINERALIZED ECTODERMAL TISSUE
COVERING VERTEBRATE TEETH.
                                                                                                                                                                                                                                                       OCCURS SOON AFTER SECRETION.
                                                                                                                                                                                                                                                                  PTM: PARENT ENAMELIN IS PROTEOLYTICALLY CLEAVED INTO SMALLER POLYPEPTIDES. CLEAVAGE OF N-TERMINAL REGION (
                                                                                                                                                                                                                                                                                                                                           TO THE MOST SUPERFICIAL LAYER OF THE DEVELOPING ENAMEL MATRIX, WHILE LOW-MOLECULAR-WEIGHT ENAMELINS ARE OBSERVED IN DEEPER
                                                                                                                                                                                                                                                                                          TRANSITION STAGE
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                                                                                                                                                                                                                                                                                                                               ENAMELIN. PREFERENTIAL LOCALIZATION
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                                                                                                                            U52196; AAD10837.1; -.
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                                                                             Enamel;
                                                                                         PR01217;
                                                                                                                                                                                                                the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Yamakoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                   Res. 10:111-118(1996)
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76:1720-1729(1997)
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                                                                           Glycoprotein; Hydroxylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y., Murakami
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ENAMELIN.
56 KDA ENAMELIN.
89 KDA ENAMELIN.
142 KDA ENAMELIN.
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ami C., D
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whi N., S
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                                                                             Phosphorylation
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                                                                                                                                                                                                                                                                                                                                 THE
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                                                                                                                                                                                                                                                                                                                                 CHRYSTALLITES
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RESULT 40
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation.—
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                                                                                                                                                                                                                                                             MEDLINE-89202384; PubMed-2595956; Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., "Filamentous hemagyluthini of Bordetcila pertussis: nuc sequence and crucial role in adherence."; sequence and crucial role in adherence."; Proc. Natl. Acad. Sci. U. U.S.A. 86-2567-2561(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Relman D.A., Domenighini M., Tuomanen E. "Genetic characterization of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE 90355839; PubMed 2388559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
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    -I - SUBCELLULAR LOCATION: SURFACE

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RESULT 41
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EMBL: M60351; AAA22975.1; ALT_INIT
EMBL: M60351; AAA22976.1; ALT_INIT
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21-JUL-1986 (Rel. 01, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation updat
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                                                                                                                                             SEQUENCE
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                                                                                                                                                                                 InterPro; IPR000475; Viral_infect
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFECT.
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or send an email to license@isb-sib.ch).
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-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-85090453; PubMed 2578227; Sanchez-Pescador R., Power M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW
                                                    LLLWGV-----TWGPVTEAA1FYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VIF_HV1N5
P12504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
01-FEB-1956 (Rel. 33, Last annotation update)
VIRION INFECTIVITY FACTOR (SOR PROTEIN).
                                                                                                         GAG_FULSY STANDARD: PRT; 309 AA.
P03326: 085558
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
20-AUG-2001 (Rel. 40, Last sanotation update)
GAG_POLYPROTEIN (CONTAINS: CORE PROTEIN P19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@idb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (New Viruses; Retroid viruses; Retroviridae;
                                             Fujinami sarcoma
Viruses; Retroid
NCBI_TaxID=11885
MEDLINE-83050964; Pul
Shibuya M., Hanafusa
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M38431; AAB04038.1; -. HIV; M19921; VIF$NL43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M19921; AAA44989.1; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases -- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J. Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=11698;
                       SEQUENCE FROM N.A.
                                                                                                PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theodore T.,
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                     68
                                                                                                                                                                                                                                                         62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
                                                                                                                                                                                                                                                                                   8 MIVWQVDRMRINTWKRLVKHHMYISRKAKDWFYRHHYESTNPKISSEVHIPLGDAKLVIT 67
                                                                                                                                                                                                                                                                                                          8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                  P27]
                                                                                                                                                                                                                                                                                                                                                                                               192 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Buckler-White A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD
                                                           viruses;
                                                                         virus.
             PubMed=6291784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLONE PNL4-3)
                                                                                                                                                                                                                                                                                                                                                                                                 22699 MW;
                                                                                                                                                                                                                                                                                                                                                9.2%;
                                                                                                                                                                                                                                   LHTGERD--WHLGQGVSIEW 89
                                                             Retroviridae;
                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                              Score 61;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                              2830B3233E8ECD16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (New York-5 isolate) (HIV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192
                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lentivirus
                                                           Alpharetrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                            CORE PROTEIN P10; CORE
                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                          Length 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCoy J.;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                  ω
 B
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176

57

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Query Match
Best Local
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The Buropean Bioinformatics Institute There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                            Cell 30:787-795(1982)
                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            other sarcoma viruses.";
                                                                       SEQUENCE
                                                                                        CHAIN
                                                                                                       CHAIN
                                                                                                                                                           PIR; A03926; FOFVF.
                                                                                                                                                                          EMBL; J02194; AAA42402.1; ALT_TERM.
                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb~sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of Fujinami sarcoma virus: evolutionary relationship of its transforming gene with transforming genes
Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-FPS
                                                                                                                                                                                                                                                                                                                                                         POLYPROTEIN.
                                                                                                                                          protein;
                                                                       309
                                                                                      236
                                                                                                                                       Polyprotein
                                                                                      235
308
                                                                       32082 MW;
                                                                     CORE PROTEIN P19.
CORE PROTEIN P10.
CORE PROTEIN P27.
; 4FA60BC95B618A5C CRC64;
                 Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                of.
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TGPKVLACSLAL
                                                                                                                                                 PATERRIDKGETTVQRDTKMAPEETATPKTVGTSCYHCGTAIGCNCATASAPPPPYVGSG
                                                                                                                                                                                   PVTEAAI -----FYETQXSLWAESEHXLKTLGQ------CD---ADVPGPP--GDS 56
TGPPMVAMPVVI 239
                                                                       LYPSTAGVGEQQGQGGDTP-----RGAEQPRAEPGRTGLAPGPALTDWARIREELAS
                                                                                                            RLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYR-CRSGLSTG-----WXQLSKLLEL 110
                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                        9.2%;
                                                                                                                                                                                                                          17;
                                                                                                                                                                                                                                             Score 61;
Pred. No.
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          7;
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Matches

17

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RESULT 44
PIP_STRCO
                                                                                                                                                                               PIP_STRCO STANDARD; PRT; 323 AA.

0952L4;
20-MUG-2001 (Rel. 40, Created)
20-MUG-2001 (Rel. 40, Last sequence update)
20-MUG-2001 (Rel. 40, Last sequence update)
20-MUG-2001 (Rel. 40, Last annotation update)
PROBABLE PROLINE IMINOPEPTIDASE (BC 3.4.11.5) (PIP) (PROLYL
NCBI_TaxID=1902;
                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                            Streptomyces coelicolor.
                                                                                                                               SC7H2.03C
                                                                                                                                                     AMINOPEPTIDASE) (PAP).
                              Streptomyces
```

Rejandream M.A.;
Submitted (AWG-1999) to the EMBL/GenBank/DDBJ databa
Submitted (AWG-1999) to the EMBL/GenBank/DDBJ databa
FUNCTION. SPECIFICALLY CATALYZES THE REMOVAL OF
RESIDUES FROM PEPTIDES (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: RELEASE OF

A N-TERMINAL PROLINE FROM (BY SIMILARITY).

PEPTIDE

SUBCELLULAR LOCATION: CYTOPLASMIC

BELONGS TO PEPTIDASE FAMILY S33.

SIMILARITY:

Saunders D.C., Harris D., Bentley S.D.,

Parkhill J.,

Barrell B.G.,

databases

N-TERMINAL PROLINE

STRAIN-A3(2); SEQUENCE FROM N.A

the

ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a by non-profit institutions as long as i

There are no rest

restrictions

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RESULT
FTSY_MY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULT 45
Y_MYCPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FTSY_MYCPN
P75362;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-NUG-2001 (Rel. 40, Last annotation update)
CELL DIVISION PROTEIN PTSY HOMOLOG.
ETSY OR MPN425 OR MP15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstailon. The EMPL potenties institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial continues a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial methics requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              -1- FUNCTION: FUNCTIONAL HOMOLOG OF SRP RECEPTOR, PROBABLY INVOLVED THE RECEPTION AND INSERTION OF A SUBSET OF PROTEINS AT THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
ProDom; PD000819; SRP54; 1.
PROSITE; PS00300; SRP54; 1.
                                      InterPro; IPR000897; SRP54.
Pfam; PF00448; SRP54; 1.
                                                                                         EMBL; AE000040; AAB96064.1; ... HSSP; P10121; 1FTS.
                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        MEMBRANE (BY SIMILARITY).
--- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED (BY SIMILARITY).
--- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycoplasmataceae: Mycoplasma.
NCBI_TaxID-2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00561; abhydrolase; 1. PRINTS; PR00793; PROAMNOPTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL109732; CAB52045.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         interpro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 LPPDARDGNLPAAYNRLLESP----DPAVRER 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 LVMGVSWGSVLGLRYAQTHPGVVTELVLTGVATGSNAEVALLTRGLGNIFPEAHERFLAE 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 LLWGVTWGPV-----TEAAIFYE---TQXSLWAESEHXLKTLGQCD------AD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ipr000073; Abhydrolase.
ipr000379; Est_lip_thioest_actsite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002410; Pro_amnoPTase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
271
299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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271
299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOPHILE (BY SIMILARITY).
BY SIMILARITY.
PROTON DONOR (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7BEF00133B353EEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Signal recognition particle;

GTP-binding; RNA-binding; Membrane;

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                                                                                    Matches
                                                                                                       Query Match
                                                                                                                                                UP_BIND
UNIB_GN
DAIB_GN
                                                                                                                                                                   NP_BIND 143 150 GTP
                                                                                                                                       SEQUENCE
 227
                                         182
                    88
                                                                                              Local
                                                               28
                    QGRYRCRSGLSTGWXQLSKLLE-LTGPKVLACSLALDGAS 126
                                         QLAEWAQ-----RIG-CDIVLPNPKEET--PAVIFRGVQQGIQNE----YDFVLC-DT 226
                                                              QXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDT 87
SGRLQNKTNLMNELKKIYQIVQKVSSAKPQETLLVLDGTT
                                                                                             Similarity
                                                                                                                                       348 AA;
                                                                                                                                                289
                                                                                    Conservative
                                                                                                                                      229
292
38775 MW;
                                                                                             9.2%;
                                                                                  23;
                                                                                             Score
Pred.
                                                                                                                                               GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
                                                                                                                                       8A14C4DB9E1EAE29 CRC64;
                                                                                    Mismatches
                                                                                             61; DB 1;
No. 33;
                                                                                  36;
                                                                                                       Length 348
                                                                                    Indels
                                                                                    16;
                                                                                  Gaps
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6

Search completed: January Job time: 275 sec 7, 2002, 16:50:33

of:

US-09-471-276-831_COPY_1_16 to: EST:*

out_format :

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pb_est1: M25099
pb_est1: M25240
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pb_est1: M25240
pb_est1: M25240
pb_est1: M25250
pb_est1: M25250
pb_est1: M17127
pb_est1: M1712
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Database sequences: 11351937
Database length: 1077921985
Search time (sec): 1532.110000
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AL51425 AL51425 [VI NIL WGC.2]
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AM252470 UI R-BUO-det d-l'10-UI
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LOCUS W25099
DEFINITION zb68b07.rl s
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                                             v zb6bb7.rl soares_fetal_lung_NbHL19W Homo sapiens IMAGE 308725 5 Similar to Sw:2180_BUMAN p04217 ALPHA-1B-GIFCDP07EIN. [1] :, mRMA sequence. W25099 1 GI:1302954 EST.
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Ratio: 5.438
Percent Similarity: 100.000
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                                                                                              AL531425 612 bp mRNA EST 13-FEB-2001
AL531425 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODMOO2YF08
prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL: contact the
TMGE Consortium (infoOlmage.llnl.gov) for further information.
Insert Length: 1951 SET 6:00
Seq.primer: mob. REGA+ET
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/dev_stage~"19_weeks"
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Contact: Genoscope
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1 (bases 1 to 612)
Li,W.B., Gruber,C.,
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                 Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nlh.gov/.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 712)
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BG389779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG389779 712 bp mRNA EST 12-MAR-2001 602415155F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4523701 5',
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                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG389779.1 GI:13283215
                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax: (1) 301 610
3371 Email: fliang@ifetech.com_RRL:
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/db_xref-"taxon:9606"
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The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonalide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify It as a clone from the normalized AV canal at 13 opt library cONA Library Preparation:

M. B. Soares Lab Clone distribution: Clones will be available through Research Genetics (www.respen.com) The following repetitive clements were found in this cDNA sequence: 1-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Iowa
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.uiowa.edu
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/clone="IMAGE:4523701"
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                                                                                      Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Azakawa, T., Carrinci, P., Endo, T., Fikuda, S., Fakunishi, Y., Hara, A., Huyatsu, N., Izawa, M., Kadota, K., Kagwa, I., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagwa, I., Kai, C., Kawa, I.J., Kikuchi, N., M., Kiyosawa, H., Kadota, K., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Abkamura, M., Oda, H., Okazaki, Y., Cono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Soqabb, Y., Sugahara, Y., Shigemoto, Y., Shinagawa, A., Tokahashi, F., Tominaga, N., Toya, S., Tayawa, A., Tokahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamanura, T., Yamanaka, I., Yano, R., Yasunishi, A., Vokota, T., Yoshida, K., Yoshiki, A., Yoshino, H., Sain, Y., Yamanaka, J., Yano, R., Yasunishi, A., Vokota, T., Yano, H., Shi, Yashi, Yananaka, J., Yana, R., Yashi, M., A., Yashi, Y., Yananaka, J., Yananaka, J., Wananaka, J., Wananaka, J., Wananaka, J., Wananaka, M., Wananaka, M., A., Washi, Yananaka, J., Yananaka, J., Wananaka, Wananaka, J., Wananaka, J., Wananaka, J., Wananaka, Wananaka
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BB048712 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus cDNA clone 6430596A08 3', mRNA sequence.
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Seq primer: M13 Forward
RIKEN Mouse ESTs (Konno,H., et al.) Unpublished (2000)
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Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
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TAG_LIB-UI-R-BJ0
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/clone="UI-R-BJ0-adt-d-11-0-UI"
/clone_11b="UI-R-BJ0"
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seq_name: gb_est2:BG177264
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Ratio: 5.273
Percent Similarity: 100.000
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                                                                                                      ValPheLeuLeuTrpGlyValThrTrpGly 16
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URL:http://genome.gsc.riken.go.jp/
Carnincl.P. Nishlyama.Y. Westover,A. Itoh,M. Nagaoka,S., Sasaki
AN. Okazaki,Y. Muramarsu,M. and Hayashlzaki,Y.
Phormostabilization and thermoattvation of thermolabile enzymes by
Trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U. SA. 95 (2), 520-524 (1988)
Tioh.M. Kitsunai,T. Akiyama.J. Shibata.K. Izawa.M. Kowai,J.
Tioh.M. Kitsunai,T. Akiyama.J. Shibata.K. Izawa.M. Kowai,J.
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC). Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High-efficiency full-length cDNA cloning, Methods Enzymol, 303
                                                                                                                                                              to: BB048712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepared by using trehalose thermo-activated reverse
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/db_xref-"taxon:10090"
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/dev_stage~"adult"
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LOCUS BG177264
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                 805 GTTGTGTTTCTTGCTGTTTGGGGTGTGGCGTGGGGG 770
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Rattus.
1 (bas
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                       Norway rat.
Rattus norvegicus
                                                                                                                                      EST
                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                           DRA05G03 Rat DRG Library Rattus norvegicus cDNA clone DRA05G03 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://lmage.llnl.gov
Plate: LLAM10157 row: g column: 14
High quality sequence stop: 703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Proparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 898)
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BG177264
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                                                                                                                                                            BG662957.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
   (bases 1 to 581)
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/clone_Lib_mill_MGC_85_cell line*
/clone_Lib_mill_MGC_85_cell line*
/close_Type_Tlymphoma_cell line*
/lab_hosr_Type_Tlymphoma_cell line*
/lab_hosr_Type_Tlymphoma_cell line*
/note=00gnn, lymphomactesistant);
/note=00gnn, lymphomactesistant);
Sile_2: Sall: Cloned unidirectionally; oligo-TT primed.
Sile_2: Sall: Cloned unidirectionally; oligo-TT primed.
Autorigo_1: Sall: Cloned unidirectionally; oligo-TT primed.
full: nngth clones and committee; oligo-TT primed.
Note: Type_Tlymphomactesistant.
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5.091
91.667
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                                                                                                                                                            GI:13884879
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Caps: 0
Percent Identity: 75.000
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; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 t
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REFERENCE
AUTHORS
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KEYWORDS
SOURCE
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US-09-471-276-831_COPY_1_16 x BG662957/rev
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                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                               seq_name:
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                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                   568
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                                                                                                                                                                                                                                                                                                                                                                                                              gb_gss:A2675056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        induced by peripheral nerve axotomy Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xiao, H.S.,
                                                                                                                                                                                    Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
                                                                                                                                                                                                                                                                                                        AZ675056 1031 bp DNA GSS 14-DEC-2000 ENTHH08TFB Entamoeba histolytica Sheared DNA Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is also available at Chinese National Human Genome Center at Shanpilanghai, 351 Guo Shoujing Road, Zhanpilang Hi-Tech Park, Pudong New Area, P.R.China, Please contact with Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031,
Tel: 86-21-64748700-121
Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Distinct gene expression profiles of rat dorsal root ganglion
              9712 Medical Center Dr., Rockville, Tel: 301 838 0200
                                                 Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                   Contact: Brendan J Loftus
                                                                                                   Unpublished (2000)
                                                                                                                 LOCIUS, B., Van Aken.S. and Fraser.C.
Determination of clone end sequences from Entamoeba histolytica
HM1: IMSS sheared DNA library
                                                                                                                                                                                                                       Entamoeba histolytica
                                                                                                                                                                                                                                                           A2675056.1 GI:11812202
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                                                                                                                                                                                                                                                                                        genomic, DNA sequence
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POLYA-No.
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BACKWARD: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: xu.zhang@ion.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lao,H.S., Han,Z.G., Zhang,F.X., Huang,Q.H., Lu,Y.J., Bao,L., Fu,G. Guo,C., Yan,Q., Jin,S.X., Zhu,Z.D., Xu,X.R., Li,N.G., Chen,Z. and
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5.500
90.909
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/db_xref="taxon:10116"
/clone="DRA05G03"
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175 c 115 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Rat DRG Library"
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0200
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                                 MD 20850, USA
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81.818
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alignment_block:
US-09-471-276-831_COPY_1_16 x AZ675056
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LOCUS AI712777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est1:AI712777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LeuValValPheLeuLeuLeuTrpGlyValThrTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1712777 136 bp mRNA EST 08-JUN-1999 UI-R-AF1-aax-d-07-0-UI sl UI-R-AF1 Rattus norvegicus cDNA clone UI-R-AF1-aax-d-07-0-UI 3', mRNA Scyuence.
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first \,
                                                                                                                                 451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                       Program for Rat Gene
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 136)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI712777
AI712777.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: shotgun
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Seq primer: Ml3-Forward
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                  Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Normalization and subtraction: two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Norway rat
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/Strain="MALINESS"
/Alb_xref="taxon:5759"
/Alb_xref="taxo
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113 c 393 g 404 t
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Gaps: 0
Percent Identity: 69.231
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                                                                                                                                                                                                                                                                                                      Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    approaches to
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elignment_block:
US-09-471-276-831_COPY_1_16 x AI712777/rev
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ORIGIN
                                                                        COMMENT
                                                                                                                                                                                                                            REFERENCE
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LOCUS AI010058
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Ratio: 5.400
Percent Similarity: 100.000
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                                                                                                JOURNAL
                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheLeuLeuTrpGlyValThrTrpGly 16
   Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand CDMA and therefore this may represent a bonefide poly A tail. The sequence tag present in the CDMA between the MOII site and the oligo-df track served to verify it as a clone from the normalized AV canal at 15 dpc library CDMA Library Preparation: M.B. Scares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                          EST204509 Normalized rat lung, RLUBT10 3' end, mRNA sequence.
                                                                                            Unpublished (1998)
                                                                                                                                             Rat Genome Project: Generation of a Rat
                                                                                                                                                                     Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                    Rattus.
                                                                                                                                                                                                                                                                        Mammalia; Euthoria;
                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                        Rattus sp.
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Seq primer: M13 Forward
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                                                                                                                                                                                                                        (bases 1 to 252)
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(301)-838-3529
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//lab_lost."DB/DB/(Life Technologies)*
//notc."Woctor: pT/730-Pac (Pharmacia) with a modified
//notc."Woctor: pT/730-Pac (Pharmacia) with a modified
polyplinker: site_i: Not I: Site_2 Beo RI; The UI-Pa-RI
library is a normalized library constructed from 15 dpc
not exclude the commalized library constructed and the
not exclude the present between the Not I site and the
olipo-UT track. The library was constructed as described
by Bonaldo, Leanon and Spares, Genome Research 0: 791-806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ:GAAGG"
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/clone_lib~"UI-R-AF1"
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/db_xref·~"taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _TISSUE AV canal at 15 dpc
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Gaps: 0
Percent Identity: 80,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rat lung, Bento Soares Rattus
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SOURCE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-471-276-831_COPY_1_16 x AI010058/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 TTTTTGTTTGGGGGAGTTACTTGGGGG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AM233137 255 bp mRNA EST 17-DEC-1999 UI-R-BJ0-aet-a-03-0-UI-S UI-R-BJ0 Rattus norvegicus cDNA clone UI-R-BJ0-aet-a-03-0-UI 3′, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21
                                                                                                                                                                               M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41,
                                                                                                                                                                                                                                                  Buall: mscares@bluc.weg.ulowa.edu
The sequence contained an oligo-off track that was present in the
Oligonucleotide that was used to prime the syntaxic first
strand cDNA and therefore this may represent a bonaide poly A
and the oligo-off track served to identify it as clone from the
normalized wentricle at, 16.5. dpc library cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa
451 Eckstein Medical Research Building Towa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
Rattus norvegicus
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                                                                                                                   POLYA Yes.
                                                                                                                                         Seq primer: M13 Forward
                                                                                                                                                               >POLY_A#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Program for Rat Gene Discovery and Mapping
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/note."Organ: lung; Vector: pT/T3Pac; Site_1: EcoRi;
Site_2: NotI"
a 51 c 18 g 54 t
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/db_xref "taxon:10118"
/clone~"RLUBT10"
/organism:"Rattus norvegicus"
/strain:"Sprague-Dawley"
/db_xref:"taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soares,
                                                                                         Location/Qualifiers
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seq_documentation_block:
LOCUS AI176065
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Ratio: 5.400
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                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel. (301)-838-3529
Tel: (301)-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1998)
Other_ESTs: TC52105
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EST219642 Normalized rat ovary
ROVBK09 3' end, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee,N.H., Glodek,A., Chandra,I., Mason,T.M.,
Kerlavage,A.R. and Adams,M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-*Wector: pT/T30-Bac (Pharmacia) with a modified polylinker; Site 1: Not 1, Site 2: Roo RI. The UI-R-B30 library is a subtracted library derived from the UI-R-B31 UI-R-B1. UI-R-B
                                                                                                                                                                                                                                                                                                                                                                                            nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_SEQ=GTTCG", 49 c
/db_xref="ARCC (inhost):2031135"
/db_xref="sarcc (inhost):2031135"
/db_xref="sarcc (inhost):2031135"
/clone="ROVBK09"
/clone="ROVBK09"
/clone="Toyan: overy: Vector: pT773Pac; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_LIB-UI-R-BJO
TAG_TISSUE-ventricle
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/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="UI-R-BJO-aet-a-03-0-UI"
/clone_lib="UI-R-BJO"
                                                                                                                                                                                                                           /organism="Rattus sp."
                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rat ovary, Bento Soares Rattus sp. cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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FEATURES

/lab_host-"DH10B (Life Technologies)"
/note-"Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Stte_1: Not I; Stte_2: Eco RI: The UI-R-E1 library is a subtracted library derived from the UI-R-E0

/dev_stage="adult"

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

SOURCE KEYWORDS VERSION ACCESSION DEFINITION

ORGANISM

BASE COUNT ORIGIN

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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-471-276-831_COPY_1_16 x AI176065/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est1:AA956508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
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                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA956508 364 bp mRNA EST Q4-UL-1999 UI-R-E1-fk-9-09-0-UI.sl UI-R-E1 Rattus norvegicus cDNA clone UI-R-E1-fk-9-09-0-UI.sl UI-R-E1 Rattus norvegicus cDNA clone Human DNA sequence from PAC 244F1 on chromosome 64j6.1-16.3. Contains nucleophosmin (nucleolar phosphoprotoin, PSJ3, NPN1, numatrin) like pseudogene, ESTs and an STS with a CAC repeat
                                                                                                                                                                                                            I.M.A.G.E. Consortium at LLNL (info@lmagg.llnl.gov). IMAGE ID=1779665 The following repatitive elements were found in this CDNA sequence: 1732, >POLY_A*Simple_repeat
                                                                                                                                                                                                                                                                                                            Damail: msoares@blue.weeg.miowa.edu
The sequence tog present in the CONA between the NotI site and the
The sequence tog present in the CONA between the Not site and the
Oilgo-di track served to identify it as a clone from the normalized
adult 12-bay-Embryo library. cDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones.will be available through
                                                                                                                                                                                                                                                                                                                                                                                                                               451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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AA956508
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                                                                                                                                                                                            Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                        Research Genetics This clone is also available through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on May 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 364)
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1 61 c
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/strain="taxon:10116"
/clone="UI-R-EI-fk-g-09-0-UI"
/clone_lib="UI-R-EI"
                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.00
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alignment_block:
US-09-471-276-831_COPY_1_16 x AA956508/rev
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                                                Email: usoarcséblue weeg.ulowa.cdu
The sequence contained an oligo-off track that was prosent in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
toll. The sequence tag present in the cDNA between the Not! site
and the oligo-off track served to verify it as a clone from the
normalized Eye library cDNA Library Preparation: M.B. Soarcs lab
clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                        Program for Nat Come Discovery and Mapping University of Towa 451 Eckstein Medical Research Building Towa City, IA 52242, USA Tol: 319 335 8250 Fax: 319 335 9555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Al76409 366 bp mRNA EST 25-UUN-1999 UI-R-YO-acy-g-11-0-UI-I UI-R-YO Rattus norvegicus cDNA clone
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Elkatryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Seq primer: M13 Forward
                              Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      discovery
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Bonaldo, M.F., Lonnon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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5.400
100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               llbrary. The UI-R-E0 llbrary consisted of a mixture of individually the constructed from a library constituence from the constructed from 8, 12 and 18 day embryo. The tag is a string of 3.5 muclocities present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B
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library. This procedure has been previously described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Bonaldo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
Percent Identity:
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COMMENT

AUTHORS

TITLE MEDLINE JOURNAL

SOURCE VERSION DEFINITION

ORGANISM

KEYWORDS ACCESSION BASE COUNT ORIGIN

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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est1:AI408881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AI764098 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-471-276-831_COPY_1_16 x AI764098/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity: 100.000
                                                                                                          TITLE
                              JOURNAL
                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTGTTTGTTTGGGGAGTTACTTGGGGG 73
                         Gene Index
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST237172 Normalized rat ovary, Bento Soares Rattus sp. cDNA clone ROYER35 3' end, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                     Rat Genome Project:
                                                                                                                                         Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                  Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                      AI408881.1 GI:4252385
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI408881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1408881
                                                                                                                                                                                                                                                    Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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//dev_srack.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult.redult
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62 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE Eye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacteria (Life Technologies) to generate the UI-R-Y0
library. This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain. "Sprague-nawley"
/db_xref. "taxon:10116"
/clone. "Ut.R-Y0-acy-g-11-0-UI"
/clone_lib. "UI-R-Y0"
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                                                                                                     Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                        Chordata: Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
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                                                                                                                                                                             Quackenbush, J.,
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REFERENCE
AUTHORS
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KEYWORDS
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ORIGIN
                                                            BASE COUNT
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Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI101493 379 bp mRNA EST210782 Normalized rat brain RBRBP87 3' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: nhlee@tigr.org
Seq primer: M13-21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Other_ESTs: TC52105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
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9712, Medical Center Drive, Rockville, MD 20850, USA
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(301)-838-0208
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/clone="movER35"
/clone_ib="movER35"
/clone
                                             /organism="Rattus sp."
//db_xref="ATCC (inhost):2024108"
//db_xref="taxon:10118"
//db_xref="taxon:10118"
//clone="BBRBP87"
//clone="1b="Normalized rat brain, Bento Soares"
//clone=ib="Normalized rat brain, Bento Brain, B
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Rodentia;
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Sclurognathi; Muridae; Murinae;
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alignment_block:
us-09-471-276-831_COPY_1_16 x AH101493/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity: 100.000
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 PheLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A1704632 388 bp mRNA EUI-R-AB1-yw-d-05-0-UI-S1 UI-R-AB1 Rattus UI-R-AB1-yw-d-06-0-UI 3', mRNA sequence. A1704632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence contained an oligo-off track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag tresent in the cDNA hetween the NotI site and the oligo-dirack served to verify it as clone from the normalized ventricle at 16.5 dpc library DNA library Preparation: N.B. Soarces and Clone distribution: clones will be available through Research Generics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lenno
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EST.
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Seq primer: M13 Forward
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.ulowa.edu
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                                                                                                      /ibb.bot*-nniub (Life Technologies)*
//ibb.bot*-nniub (Life Technologies) with a modified //octa-vector. pf7701-9co (Pharmacab) with a modified polylinker; Site_1 not I. Site_2 not RI: He HIT - 18 In Life of RI: HIT - 18 In Life of RI
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University of Iowa.
TAG_LIB=UI-R-AB1
TAG_TISSUE=ventricle at 16.5 dpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="UI-R-AB1-yw-d-06-0-UI"
/clone_lib="UI-R-AB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="Sprague-Dawley"
/db_xref="taxon:10116".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence contained in oligo-dy track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonside poly A tall. The sequence tag present in the cDNA between the NCI site and the oligo-dy track served to identify it as a clone from the normalized Ay canal at 15 dpc library cDNA tibrary Preparation: M. B. Searces Lab Clone distribution: clones will be available through Research Generics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AWJ51200 390 bp mRNA EST 17-DEC-1999 U1-R-BJO-adf-d-02-0-U1.sl U1-R-BJO Rattus norvegicus cDNA cione U1-R-BJO-adf-d-02-0-U1 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Program for Rat Gene Discovery and Mapping
University of lowa
451 Eckstein Medical Research Building Towa City, IA 52242, USA
Tel: 319 335 8256
Fax: 319 335 9555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW251200.1 GI:6594791
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoarcs@blue.weeg.uiowa.cdu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
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Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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primer: M13 Forward
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/dev_stage.*.dult
/dev_stage.*.dult
/lab_host.*DniDB/IJF acchnologies)*
/note.*Vector: pT730-Pac (Pharmacla) with a modified
/note.*Vector: pT730-Pac (Pharmacla) with a modified
/note.*Vector: pT730-Pac (Pharmacla) with a modified
/note.*Vector: pT740-Pac (Pharmacla) with a modified
/note.*Vector: pT740-Pac (Pharmacla) with a modified
/note.*Api, UT-R-ACI, UT-R-ACI, UT-R-ACI, UT-R-ACI, IDT-ACI (UT-R-ACI) with a modified in the modified of the
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a 62 c
                                                                                                                                                                                                                                                                                          /strain."Sprague-Dawley"
/db_xref."taxon:10116
/clone."U[-R-BJO-adf-d-02-0-UI"
/clone_1lb."U[-R-BJO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism·*Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; Cranlata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e9 g
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VERSION
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US-09-471-276-831_COPY_1_16 x AW251200/rev
                                                                                                                                                                                                                                                                                              FEATURES
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ORIGIN
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Ratio: 5.400
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTGTTTGTTTGGGGAGTTACTTGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 393)
Bonaldo, M.F., Lenno
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                         POLYA-Yes
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62 c
                      /clone."UI.R-BS1-azd-d-09-0-UI"
/clone_lib-"UI.R-BSI"
/dew_stage."embryonic 13 dpc"
/lab_host."DH10B (Life Technologies)"
                                                                                                                                                      /strain~"Sprague-Dawley"
/db_xref~"taxon:10116"
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                                                                                                                                                                                                                          ∕organism⊶"Rattus norvegicus"
                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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seq_documentation_block:

DOUGLE BEIO930 93 bp mRNA EST 13-JUN-2000

DEFINITION U1-R-BS1-azd-d-09-0-U1.S1 U1-R-BS1 Rattus norvegicus cDNA clone
U1-R-BS1-azd-d-09-0-U1 3', mRNA sequence.

ACCESSION BEI0930 9
The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the Not1 site and the oligo-dT track served to verify it as a clone from the normalized embryo at 13 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                             451 Eckstein Medical Research Building Towa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                         Program for Rat Gene Discovery and Mapping University of Iowa
                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Chordata; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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cDNA clone

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alignment_block:
US-09-471-276-831_COPY_1_16 x BE109230/rev
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Quality:
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                                                                BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are available from Research Genetics (Info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
seq primer: Mi3-21
class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ112808 438 bp DNA GSS 29-AUG-1998 CIT-HSP-2382K1.TF CIT-HSP Homo sapiens genomic clone 2382K1, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ112808.1 GI:3488929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ы
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TAG_TISSUE=embryo at 13 dpc
TAG_SEQ=AATCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pT/73D-Pac (Pharmacia) with a modified polylinker; site_i wot i; Site_2: Eoo RI; The UI.R-BSI library is derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web site at
                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ratest.eng.uiowa.edu.
                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="2382K1"
                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .438
                                                                                                                                                                                                                            /sex-"Male"
                                                                                                                                                                                                                                                            /clone_lib="CIT-HSP"
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Gaps: 0
Percent Identity: 80.000
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                                                                                                84 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MD 20850, USA
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AQ112808 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValPheLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence contained an oligo-dT track that was present in the oligonucleotida that was used to prime the synthesis of first strand DNA and therefore this may represent a benafide byte tail. The sequence tay tracks that in the DNA between the NCI Site and the oligo-drawk is greed to destify it was close from the normalized AV canals at greed to the tity it was a close from the normalized AV canals at greed to the oligo-dNA bilary Preparation. The ormalized the contains a contains closes will be available through Research Genetics (www.resgen.com) The following reputitive a newestary are found in this CNA sequence: 1-41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW251345 470 bp mRNA EST 17-

UI-R-BJO-adh-a-11-0-UI 31 UI-R-BJO Rattus norvegicus

UI-R-EJO-adh-a-11-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW251345.1 GI:6594936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 470)
                  /lab_bost="bHIOB (Life Technologies)" // Lib bost="bHIOB (Life Technologies)" // Life Technologies) // Life Technologies // Life Techno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.00
5.400
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="UI-R-BJO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Sprague-Dawley
/db_xref="taxon:10116"
described by Bonaldo, Lennon and Soares,
                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UI-R-BJ0-adh-a-11-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
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Gaps: 0
Percent Identity: 72.727
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KEYWORDS
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligonucleotide that was used to prime the synthesis of first strind cDNA and therefore this may represent a bonafide poly A tail. The sequence top present in the cDNA between the NoI site and the oligo-dr track served to identify it as a clone from the normalized ventricle at 16.5 dpc library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 1-41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV$252673 4/75 bp mRNA EST 17-DEC-1999 UI-R-BJO-aeb-c-05-0-UI-3 UI-R-BJO-aeb-c-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Towa
451 Eckstein Medical Research Building Towa City, 1A 52242, USA
Tel: 319 335 B250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 475)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalla; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: Ml3 Forward POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  >POLY_A#Simple_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.ulowa.edu
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Program for Rat Gene Discovery and Mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
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TAG_LIB-UI-R-BJO
TAG_TISSUE AV canal (
TAG_SEQ-GAAGG*
TAG_SEQ 104 9
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/dev_stage."adult"
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/db_xref·"taxon:10116"
/clone-"UI-R-BJO-aeb-c-05-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism·"Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from:
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VERSION KEYWORDS

ACCESSION

DEFINITION FOCUS

SOURCE

ORGANISM

COMMENT

JOURNAL

REFERENCE

AUTHORS

TITLE

FEATURES

source

BASE COUNT ORIGIN

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-471-276-831_COPY_1_16 x AW252673/rev
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Mammalia; E
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A1176739
A1176739.1 G1:3727377
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville,
Tel: (301)-938-3529
Fax: (301)-938-0208
Email: nhlee@tigr.org
                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Lee, NH
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI176739 479 bp
EST220332 Normalized
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Ratio:
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TAG_SEO.GTTCG"
a 76 c 106 g
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                                                                                                                                                                                                                           Organism "Rattus sp."
//db_xref."ATCC (inhost):2031503"
//db_xref."taxon:10118
//db_xref."toxon:10118
//clone."Br070W32"
//clon
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54.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Rodentia;
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Length:
Gaps:
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alignment_block:
US-09-471-276-831_COPY_1_16 x AII76739/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTTGTTTGGGGGAGTTACTTGGGGG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss:A2776969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2M0011K05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0011K05 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 0011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
Email: ddundgenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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AZ776969.1 GI:12905099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria;
L (bases 1 to 550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: AI176739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                           10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pND42 (91/4732114/gb)AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was liquted with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnarcs/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclestide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The captured DNA was purified and size-selected for a 9.5 to
adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host*"E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone-"UUGC2M0011K05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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US-09-471-276-831_COPY_1_16 x AZ776969
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ORIGIN
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence contained an oligo-off track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNN and therefore this may represent a bonafide poly A tail The sequence trap present in the DNNA between the Moult 18 the and the oligo-off track served to verify it as a clone from the normalized rat eye library cDNN Library Preparation: M.B. Soores Lab Clone distribution: clones will be available through Research cenetics (www.respen.com) The following repetitive elements were cound in this cDNN sequence: 1-12.3 ANT_cthildoc_complexity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: M13 Forward POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Res. 6 (9), 791-806 (1996)
                      /lab.host**DH108 (Life Technologies)*
//note-"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; CVZ is a subtracted library derived from a normalized eye library (nREZ); constructed occording to the procedure described by Bonaldo, Lennon & Soares (Genome Research Genome 6: 79-806, 1996). For construction of the CVZ library, plasmid DNA from the normalized rat eye library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.400
83.333
electroporated into competent bacteria for production of
                                                                                                                                                                                                                                             /dev_stage="ADULT"
                                                                                                                                                                                                                                                                            /clone="UI-R-CV2-chn-g-10-0-UI"
/clone_lib="UI-R-CV2"
                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 75.000
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Rodentia;
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Sciurognathi;
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thi; Muridae; Murinae;
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COMMENT

TITLE

SOURCE

VERSION

ORIGIN

BASE COUNT

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seq_documentation_block:
LOCUS BF339365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 MetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            602038716F1 NCI_CCAP_Brn64 Homo sapiens cDNA clone IMAGE:4186610
5', mRNA sequence.
BF339365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordeta; Cranieta; Verrebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo
l (bases l to 741)
                                                                                                                                                                                                                                                                                                                                                      Plate: LLAM9507 row: p column: 03 High quality sequence stop: 646.
                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.linl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF339365.1 GI:11285832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 numan
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"Ath aretve taxon: 9606"

Aclone. "IMAGE. Al98610"

Aclone. Lib. "NGI_GCAP_BIN64"

/Lissue_type. "Jikblastona with SGPR amplification."
/lab_lost. DH100 (TI phage-resistant).
/note-Osgnn: brain; vector: pGMV-SFORTS; Site_1; NotI;
Site_1: SAII: cloned unidirectionally. Primer: Olio dT
sverzage insert size 1.57 Nb. Constructed by Life
Technologics. Note: his is a NCI_CCAP_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAG_TISSUE rat eye
TAG_SEQ CAGCC"
63 c 60 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represented 80% of the final driver population. TAG_LIBOUTR-CV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single-stranded circular DNA. This was then used as a
                                                                                                                                                                                                                                                                       /organism·"Homo sapiens"
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
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REFERENCE AUTHORS TITLE

COMMENT

JOURNAL

FEATURES

source

Percent Similarity:

ACCESSION VERSION

DEFINITION

SOURCE KEYWORDS

ORGANISM

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SOURCE
ORGANISM
                                                                       alignment_scores:
Quality:
                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
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LOCUS BF673019
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US-09-471-276-831_COPY_1_16 x BF339365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 ValPheLeuLeuTrpGlyValThrTrpGly 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nth.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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Kammalia: Eutheria; Primates: Catarrhini; Hominidae; Homo.
1 (basos 1 to 873)
NIH-MGC http://mgc.nci.nih.gov/
National_Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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Clone distribution: MGC clone distribution information can
                                                 Ratio:
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                                                                                                                                                                                                                                                                             5'-ATTCTAGÁGGCCGÁGGCGGCGACATG-dT(30)BN-3' (where B ·· A, C, G or T). Average insert size (c, or G and N ·· A, C, G or T). Average insert size (1.55 kb (range 1.04-6, kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Paio Alto, CA). (2)

Alto, CA). 204 g 171 t
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//ab_bost-bH108 (TI phage-resistant)*
//ab_bost
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5.889
81.818
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92.308
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/db_xref·"taxon:9606"
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Gaps: 0
Percent Identity: 72.727
Gaps: 0
Percent Identity: 61.538
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JOURNAL
REFERENCE
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US-09-471-276-831_COPY_1_16 x BF673019/rev
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  seq_name: gb_gss:CNS043FU
                                                                                                                               alignment_block;
US-09-471-276-831_COPY_1_16
                                                                                                                                                                                                                                     alignment_scores:
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                                                                                                   Align seg 1/1
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                                  CTGAATGTTCTTCCCTTCTTGTCTCTGTGGGGGCCTTCTGTGGGGG
                                                                 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly
                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMHL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.org.fr/Petraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F., Saurin,W. and Meissenbeh,J.
Human gene number estimate provided by genome wide analysis using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostoni;
Actinopteryil: Meopteryyil: Teleostei: Euteleostei: Neoteleostei:
Acanthomorpha: Acanthopterygil: Percomorpha: Tetraodontiformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Tetraodon nigroviridis.
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Coneti
                                                                                                   to: CNS02MAW
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                                                                                                                                                                                                                                                                                                                                  /organism-"Tetraodon nigroviridis"
/db_xref-"taxon:99883"
/clone="148pil"
/clone=1b-"G"
                                                                                                                                                                                  53.00
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Gaps: 0
Percent Identity: 50.000
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end of clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fisher, C.,
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REFERENCE
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LOCUS BE108A72
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LOCUS CNS043FU
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Rattus norvegicus
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alignment_block:
US-09-471-276-831_COPY_1_16 x CNS043FU
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Roteleostei;
Actinopterygii; Neopterygii; Percomorpha; Tetraodontiformes;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                         BEJ08872 152 bp mRNA EST 13-JUN-2000
UL-R-BS1-ayz-d-04-0-UL-S1 UL-R-BS1 Rattus norvegicus cDNA clone
UL-R-HS1-ayz-d-04-0-UT 3', mRNA sequence.
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Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using
retracion nigroviridis DNA sequence
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Tetraodon nigroviridis.
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/note="Genoscope
209 c 259
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/clone="070"""
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GI:8500977
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5 others
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us-09-471-276-831_COPY_1_16 x BE108872
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Ratio:
                                                                                                                                                                                                                          AV272375 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus DNA clone 4931424020 y similar to AB023219 Homo sapiens musculus CNA clone 4031424020 y similar to AB023219 Homo sapiens musculus CNA clone 4031424000 y similar to AB023219 Homo sapiens muscus for KIAA1002 protein, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Program for Rat Gene Discovery and Mapping University of Lowa 451 Eckstein Medical Research Building Towa City, IA 52242, USA Tel: 19 335 9565 Fax: 119 335 9565
                        Eukaryota; Metazoa: Chordata; Cranlata; Vertebrata; Euteleostoni;
Mammalla; Eutherla: Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 222)
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
   Konno, H.,
                                                                                                     Mus musculus
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                                                                                                                                                                                                           AV272375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.ulowa.edu
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Bonaldo, M.F., Lenno
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/lab_bast" DHIDB (Life Technogies)*
/lab_bast" DHIDB (Life Technogies)*
/lab_bast" DHIDB (Life Technogies) with a modified follow. Wester: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eoo RI; The UI-R-RSI Library is dearled from 13 dpc whole embryo tissue. For a detailed description of the Library from which this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_SEQ:None found"
23 c 49 g
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/strain."Sprague-Davley"
/db_xref-"taxon:10116"
/clone-"U1-R-BS1-ayz-d-04-0-U1"
/clone_lib-"U1-R-BS1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.00
5.778
90.000
Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.
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Gaps: 0
Percent Identity: 80,000
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alignment_scores:
                   Percent Similarity:
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Email: geome-res@gsc.rikon.go.jp,

Dmail: geome-res@gsc.rikon.go.jp/
URL:http://geome-gsc.rikon.go.jp/
Ocawa.K., Tanaka.T.,
Sasaki.N., Itawa.N., Watcamaisu.M., Okazaki.Y. and
Matsuura.S., Carninci.P., Mucamaisu.M., Okazaki.Y. and
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                                                                                                                    Quality:
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                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                              47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Site_1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
project of Genome Exploration Research Group in Riken
                   52.00
5.200
90.909
                                                                                                                                                                                                                                                                                                                                                                                                    modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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/dev_stage-"adult"
/lab_host-"DH10B"
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/db_xref-"taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-reségec.riken.go.jp,
URL:http://genome.gec.riken.go.jp,
Carnincl.P., Nishiyama.Y., Westovor,A., Itoh,M., Nagaoka.S., Sasaki
N., Okazakiy., Muramatsu,M. and Hayashiaki,Y.
Thermostabilization.and thermoactivation.of thermolabile.enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Vokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                         High-efficiency full-length cDNA cloning. Methods Enzymol. 303
19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
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Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                trehalose and its application for the synthesis of full leconn. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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/note**Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike
                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="Al30018N12"
                                                                                    /dev_stage="16 days neonate"
/lab_host="DH10B"
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                                                                                                                                    /tissue_type="thymus"
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                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-559-81-6855
Email: ykohara@lab.
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae: Caenorhabditis.
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Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Kohara, Y., Shin-i, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, Mishigaki, A., McCohashi, T., Zeng, Q., Watanabe, H., Sugiyama, Y. and
                                                                                                                                                                                                                                                                                                                                Genome Biology Lab.
National Institute of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                        Expressed genes in C.elegans
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer (5'
/dev_stage="embryo"
1 70 c 79 g
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                                                                 hermaphrodite embryo"
                                                                                 /clone_lib="Yuji Kohara unpublished cDNA:Strain
                                                                                                             /clone="yk566e7"
                                                                                                                                /db_xref="taxon:6239"
                                                                                                                                                         /strain-"N2"
                                                                                                                                                                               /organism-"Caenorhabditis
                                                                                                                                                                                                                     Location/Qualifiers
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Percent Identity: 69.231
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This clone is available through: Genome Systems, inc. 4633 World
This clone is available through

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A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., E
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
R., Materston, R., and Wilson, R.,
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Bah69803.yl Gm-c1049 G196 max CDNA clone GENOME SYSTEMS CLONE
ID: Gm-c1049-3462 5' similar to TR.039540 039540 ASCORBATE OXIDASE
PROMOTER-BINDING PROTEIN ; mRNA sequence.
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Washington University School of Medicine
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Contact: Shoemaker R/Public Soybean EST Project
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314 286 1810
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                     'note-'Woctor pBluescript IJ SK+, Site_1: Rowh; Site_2: Xhoi: The Clark NIL was constructed and seed was provided by Dr. J. Specht; University of Nebraska (Shoemaker and Specht, 1953). The clowal library was constructed from mRNA isolated from whole seculings of 3 week old greenhousew grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a thoir restriction site and a 3 anchor. EcoRi adapters were ligated to the blunt-ended cDNA fragments followed by Xhoi digestion. The cDNA fragments were directionally cloned digestion. The cDNA fragments were directionally cloned
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4.000
81.250
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/dev_stage-"3 week old"
/lab_host-"DH108"
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/db_xrefo"taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G
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US-09-471-276-831_COPY_1_16 x BI425622/rev
3 MetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
                                               to reverse of:
                                                                                                                                                                                                                                                                                                                 vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

a 68 c 89 g 50 t
                                                                                                                                                               52.00
4.333
85.714
                                                                                                                                                           Percent Identity: 57.143
                                               from:
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Gaps:
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to:
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seq_name: gb_est2:BI053983

BI053983 423 bp mRNA EST 15-JUN-2001 PM3-GN0375-270101-002-g06 GN0375 Homo saptens cDNA, mRNA sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. BI053983.1 Homo sapiens (bases to 423) GI:14461513

Simpson, A.J. Nagal.M.A., da Silva,M. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Mucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., expressed

Shotgun sequencing of the human transcriptome with ORF sequence tags Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 am 4 andar, 01509-010, Sao Paulo-SP,

bmail: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-PM36t2-PM3-GN0375270101-002-g06st3-2001-01-276t4-1)
Seq.primer: puc 18 forward

Location/Qualifiers

/organism·"Homo sapiens" /db_xref·"taxon:9606" /clone_lib∘"GN0375"

'note-'Ocyan: placenta_normal; Vector: pucl8; Site_1: Smu
: Site_2: Smu!; A min!-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puC 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stilneency conditions." performed under low stringency conditions /dev_stage-"Adult" Site_1: Small

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alignment_block:
US-09-471-276-831_COPY_1_16 x BI053983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pleter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , DNA sequence.
A0975452
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RPCI-23-333I10.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_GSSs: RPCI-23-333I10.TJ
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
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                        /nob_bost="DHIOR"
/note-"Orden, Ekdney/Brain; Vector: pBACe3.5; Site_1:
/note-"Orden, Ekdney/Brain; Vector: pBACe3.5; Site_1:
/note-"Orden, Ekdney/Brain; Vector: pBACe3.5; Site_1
/note-"Orden, Ekdney/Brain; Vector: pBACe3.5; Site_1
/note-"Orden, Ekdney and EroRD archivlase; Site_1
/note-"Orden, Ekdney and EroRD archivlase; Site_2
/note-"Orden, Ekdney and France, Ekdney a
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4.727
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/clone="RPCI-23-333110"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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RPCI-23 Mus musculus genomic clone RPCI-23-333I10
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Ludwig Institute for Cancer Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
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Ratio:
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92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib-"GN0375"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soares, F., Brentani, R.R., Reis, L.F., de
                                                                                                                                                                                                            research poilis into the puc 18 vector Reverse retent transcription of tissue mRNA and coNA amplification were performed under low stringency conditions."

a 107 c 140 g 119 t
    52.00
4.727
78.571
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Gaps: 0
Percent Identity: 57.143
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US-09-471-276-831_COPY_1_16 x AQ977668
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LOCUS AQ977668
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Unpublished (1999)
Other_GSSs. RPCI-23-336KB.TJ
Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Confor Dr., Nockville, MD 20850, USA
7712 Medical Confor Dr., Nockville, MD 20850, USA
7712 Medical GO000
                                                                                                        Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               szhao@tigr.org
                                                                                                                                                                                                     Note-"Organ: Kidney/Brain: Vector: pBACe3.6; Site_1:
ECORI: Site_2: ECORI: Female C57BL/6I monse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR: and EcoR! Methylass. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

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/clone("RPCI-23-336K8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism∵"Mus musculus"
/strain∵"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                      /lab_host .. "DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                  /sex…"Female"
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                                               Length: 14
Gaps: 0
Percent Identity: 57.143
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                                                        alignment_block:
US-09-471-276-B31_COPY_1_16 x AZ097580
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                      Align seg 1/1 to: A2097580
                                                                                                                            Percent Similarity:
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Class: BAC ends.
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Department of Eukaryotic Genomics
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/clone_lib."RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex."Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain-"C57BL/6J"
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and Fraser,C.,M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_OSSS: RPCI-23-15C10.TV
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Tel: 301 838 0200
Fax: 301 838 0208
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                /note-Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; South Site_2: ECORI; Female C57BL/G3 mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The lightion products were transformed into
                                                                                                                                                                                                                                                                                                                ECORI sites. The ligation products were transformed DH10B electrocompetent cells (BRL Life Technologies).
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LOCUS BE967588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 52.00
Ratio: 4.727
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: BE967588 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
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                                                                                                                                                                                                                                 gb_est2:BE967588
BF222804 300 bp. mRNA EST 30-MAR-2001
7q23c11.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:3699092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE967588 1229 bp mRNA EST 04-OCT-2000 601648657F1 NIH_MGC_73 Homo sapiens cDNA clone IMAGE:3932438 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence start: 2
High quality sequence stop: 91.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: CLONETECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 1229)
NIH-MGC http://mgc.ncl.nih.gov/.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="NHE_MCC_73"
//ab.host="DHINB_(T] phage-resistant)"
//ab.host="DHINB_(T] phage-resistant)"
//ab.host="DHINB_(T] phage-resistant)"
//ab.host="Organ: brain; Vector: phNR-LIB (Clontech); Site_1:
//abc Organ: brain; Vector: phNR-LIB (Clontech); Site_1:
//abc Organ: brain; Vector: phNR-LIB (Clontech); Site_1:
//abc Organ: brain; Vector: Site_1:
//abc Organ: brain; Vector: Site_1:
//abc Organ: brain; Vector: brain;
//abc Organ: Abc Organ: Abc
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Alto, CA)."
1593 c 100 g 140 t
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/db_xref="taxon:9606"
/clone="IMAGE:3932438"
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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                     seq_name: gb_est2:BF591140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 333)
                                                                                                                                              BF591140.1 GI:11683464
                                                                                                                                                                      mRNA sequence.
BF591140
                                                                                                                                                                                                                      7h54c09.xl NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:3319792 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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1 (bases 1 to 300)
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                                                                       Homo sapiens
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DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: WCI-CGAP clone distribution information can be

Clone distribution: MCI-CGAP clone distribution information can be

Councilled through the I.M.A.G.E. Consortium/LLNL, send email to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 5,000 clones made from the same library (cloneIDs 1257096-123861), 1469064-1470983, and 147592-1476743). Subtraction by Bento Soste and M. Fatima Bonaldo. *a 66 c 48 g 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CRAP_CG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.50
4.682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:3699092"
/clone_lib="NCI_CGAP_GC6"
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US-09-471-276-831_COPY_1_16 x BF591140/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est2:BF390055
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                                                                  JOURNAL
MEDLINE
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Ratio:
                                                                                                                                                                                                        Raitus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria: Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                       BF99005: 433 bp mRAH EST 27-NOV-2000 UI-R-BS2-bdr-9-040-011.sl UI-R-BS2 Rattus norvegicus cDNA clone UI-R-BS2-bdr-9-04-0-UI 3', mRNA sequence.
University of Iowa
                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                      97044477
                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                               discovery
                                                                                                                                  1 (bases 1 to 433)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                 Norway rat
                                                                                                                                                                                                                                                                                                                           EST
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Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: NCI-CCAP clone distribution information can b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ph.D
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4.682
84.615
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/tissue_type~"colon tumor, RER+"
/lab_host~"DH10B"
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Gaps: 1
Percent Identity: 76.923
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AUTHORS
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LOCUS BE546037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est1:BE546037
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                                                                                                                                      TITLE
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                                                                                                        JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTCTTTTACTACTTTGGGGGGATAACTGGGTGGGGT 315
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Ratio:
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                          Tissue Procurement: ATCC
                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                        Unpublished (1999)
                                                                                                                           Eukaryota; Metazoa: Chordata: Caraliata: Vertebrata: Enteleostomi;
Mammalla: Eutheria: Primates: Catarrhini; Hominidae: Homo.
1 (bases | to 44)
MIH-MGC http://mgc.nci.nih.gov/
Mational institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BE546037
                                                                                                                                                                                                                                                                                                                                                                                                                               BE546037 443 bp mRNA EST 09-AUG-2000 601072427F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:3458310 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 Eckstein Medical Research Building Iowa City, 1A 52242, USA
Tel: 319 335 8550
Fax: 319 335 9565
                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                     Homo sapiens
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cDNA Library Preparation: Life Technologies, Inc.
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/lab_host-"DBHOB (Life Technologies)*
/lab_host-"DBHOB (Life Technologies)*
/note "Vector: pf773D-Pec (Pharmacla) with a modified polylinker; Site_1: Not I: Site_2: Eco RI; The UI-R-BS2 ibbrary is a subtracted library derived from 13 dpc whole embryo tissue. For a detailed description of the library from which this clone was derived, please visit our web site at retest.eng ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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TAG_TISSUE-embryo at 13 dpc
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/clone_lib."UI-R-BS2"
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/db_xref-"taxon:10116"
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                                                                                                                                                                                                                                                                                                                    Tymor Gone Index

Unpublished (1997)

Unpublished (1997)

Dontact: Robert Strausborg, Ph.D.

Damil: Compact Strausborg, Ph.D.

Damil: Compact Strausborg, Ph.D.

Damil: Compact Compac
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Ratio:
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1 (bases 1 to 467)
NCICGAP http://www.ncbi.nlm.nih.gov/ncicgap.
wallonal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Location/Qualifiers
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AI623983
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                                                                                                                                                                                                                                                            High quality sequence stop: 407 POLYA-NO.
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/db_xref="taxon:9606"
/ctone="IMAGE:2229597"
/ctone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
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/db_xref="taxon:9606"
/clone="IMAGE:3458310"
/clone_lib="NIH_MGC_12"
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/lab_host="DH10B"
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alignment_block:
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Ratio: 4.682
Percent Similarity: 84.615
                                                                                                                  US-09-471-276-831_COPY_1_16 x AI623983/rev
                                                                         Align seg 1/1 to reverse of: AI623983
235 GTTTCCTTTTACTACTTTGGGGGGATAACTGGGTGGGGG 197
                5 ValValPheLeuLeuLeuTrpGlyValThr...TrpGly 16
                                                                                                                                                                                                                                                                                                                  170 a
                                                                                                                                                                                                                                                                                                                                  /note-"Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NoI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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1 325 49.2 474 1 OMHULB 2 76 11.5 1327 2 TOMULB 3 76 11.6 1327 2 TOMULB 4 75.5 11.4 635 JCS896 5 74.5 11.3 680 2 JCS896 6 73 11.0 163 JCS896 7 72.5 11.0 192 2 S42994 8 71.5 10.7 848 2 JCS898 9 71 10.7 848 2 JCS898 10.4 192 2 S4298 11 69.5 10.4 192 2 S4298 11 69.5 10.4 192 2 S4298 11 68.5 10.4 192 2 S4298 11 68.5 10.4 2 JCS898 11 68.5 10.4 2 JCS898 11 68.1 10.4 192 2 S4298 11 68.1 10.4 192 2 S4298 11 68.1 10.3 192 2 S4298 11 68.1 10.3 192 2 S4298 11 68.1 10.3 192 2 S4299 11 68.1 10.3 192 2 S4299 12 67.5 10.2 142 2 TIVR8 13 67.1 10.1 192 2 S4299 14 67 10.1 192 2 S4299 15 67 10.1 192 2 S4299 16 67 10.1 192 2 S4299 16 67 10.1 192 2 S4299 17 10.1 192 2 S4299 18 67 10.1 192 2 S4299	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUNMARTES sult Query No. Score Match Length DB ID Description	tabase : PIR_60:* 1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*	nimum DB seq Length: 0 ximum DB seq length: 2000000000 st-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	arched: 219241 segs, 76174552 residues tal number of hits satisfying chosen parameters:	oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	quence: 1 MSMLVVFLLLMWGPVTELUELTGPKVLACSLALDGAS 126	n on: January 7, 2002, 16:48:23 ; Searc (wit) 496.	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd protein - protein search, using sw model
alpha-1-P-glycopro viral infectivity Immunoglobulin-ilk killer cell inhibi yora fectivity probable aldebyde Fc gamma (145) rec Fc gamma (145) rec Killer cell inhibi viral infectivity viral protes coronafacic acid s hypothetical prote beta-galactosidase viral infectivity	by chance to have a the result being printed, distribution. Description			219241		JELTGPKVLACSLALDGAS 126	Search time 19.35 Seconds (without alignments) 496.020 Million cell updates/sec	en itd.
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G75684 G75783 JHC289 JCC7713 JT14845 G84861 S48961 S48961 S43904 S43904 S43904 S43904 S43904 S43904 S43904 JF08864 JF0		T08302 CGHU4B S42991 S42968 S42973	T01669 JC7509 JH0290 T04462 D85383 B61228	\$42977 \$43001 \$42970 \$42992	S39747 B83834 S42942	T49369 G70764 B36916 WZBF20	T09442 S42998 S42959	T31441 S42997 S42975 S42975 S42954 S42972

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ACCOSE-TEGERENCES: GDB:119638; OMIM:138670
A:Map position: 19q-19q
C:Superfantly: alpha-118-glycoprotein; immunoglobulin homology
C:Superfantly: alpha-118-glycoprotein; plasma
F;21-74/Domain; immunoglobulin homology ciMMi>
F;111-163/Domain; immunoglobulin homology ciMMi>
F;211-74-75, alpha-11; immunoglobulin homology ciMMi>
F;212-74/Domain; immunoglobulin homology ciMMi>
F;221-255/Domain; immunoglobulin homology ciMMi>
F;227-355/Domain; immunoglobulin homology ciMMi>
F;237-155/Domain; immunoglobulin homology ciMMi>
F;237-155/Domain; immunoglobulin homology ciMMi>
F;237-158,342-350/Binding site; carbohydrate (Asn) (covalent) #status F;247-364/Ofisulfide bonds: #status prodicted
F;118-161,211-258,304-353/Disulfide bonds: #status experimental
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C:Date: 04-Dec-1986 #text_change 10-Sep-1999
C:Accession: A02113
G:Accession: A02113
Froc. Natl. Acad. Sci. U.S.A. 83, 2363-2367, 1986
A:Title: Anino acid sequence of human plasma alpha-1B-glycoprotein: homolog A:Beference number: A02113; MUID:86205955
A:Accession: A02113
                                                                                                                                                                                                                                                                                                                                       viral infectivity factor vif - human immunodeficiency virus type 1
C;Specles: human immunodeficiency virus type 1, HTV-1
C;Datc: 06-Jan-1995 *sequence_revision 06-Jan-1995 *Feext_change 20-Sep-1999
C;Accession: S42940
R;Metland, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, submitted to the EMBL Data Library, March 1994
A;Description: In vivo genetic variability of the HTV-1 gene.
A;Reference number; S42940
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S42940
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C;Superfamily: AIDS
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C; Comment: The function of
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A; Residues: 1-192 <WIE>
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A; Status: preliminary
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     QEWGAQEPVIILDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
                                           MIVWQVDRMRIRTWKSLVKHHIYISRKATGWFYRHHYESTHPRVSSEVHIPLGDARLVIT 67
                                                                               LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHQFLLTGDTQGRYRCRSGLSTGWTQLSKLLELTGPKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIFYETQXSLWAESEHXLKTLGQ----CDADVPGPPGDSRLPAVQEWGAQEPVHLDSPAI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                       nces: EMBL:230601; NID:g459446; PIDN:CAA83078.1; PID:g459447 AIDS v1f protein
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Pred. No. 3.7e-27;
- Mismatches 17;
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Pred.
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A;Accession: JC5896
A:Stration: JC5896
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A; Map position:
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C;Genetics:
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A:Accession: T09402
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inhibitory receptor p91B precursor .
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AlMolecule type: mRNA
A:Residues: 1-635 
A:Residues: 1-635 
A:Residues: 1-635 
A:Cross:references: GB:AF041036; NID:g2791693; PIDN:AAB96928.1; PID:g2791694
A:Cross:references: GB:AF041036; NID:g2791693; PIDN:AAB96928.1; PID:g2791694
A:Crosment: This protein function as ingibitory cell-surface molecule against cell act F:1-23/Domain: signal sequence setting predicted <SID: F:1-23/Domain: signal sequence setting predicted <SID: F:1-23/Domain: extracellular Ig-like #statu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryanashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matauda, Y.; Nishikawa,
J. Blochem, 123, 358-358, 1998
A;Title: Genomic structures and chromosomal location of p91, a novel murine regu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              killer cell inhibitory receptor p91C precursor - mouse c;Species; Mus musculus (house mouse) C;Datte: 18 Mar-1998 *text_change C;Datte: 18 Mar-1998 *text_change C;Accession: JC5896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin-like protein IGSEI - human
C:Species: Homo sapiens (man)
C:Date: 11-jun-1999 #sequence_revision 11-jun-1999 #text_change 21-jul-2000
C:Accession: T99402
Genomics 40, 175-162, 1996
A:Title: Cioning and expression of an immunoglobulin superfamily gene (IGSEI) in xq25
A:Title: Cioning and expression of an immunoglobulin superfamily gene (IGSEI) in xq25
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A;Molecule type: mRNA
A;Residues: 1-127 <MAZ>
                                                                    60 AVQEWGAQEPVHLDSPAIKHQFLLTGDTQ----GRYRCRSGLSTGWXQLSKLLEL 110
                                                                                                                                             VELLVSGNLOKPTIKAEPGSVIASKRAMTIWCQ------GNLDAEVYFLHNEGSQKTQ
                                                                                                                                                                                                                 VFLLLWGVTWGPVTEA----AIFYETQXSLWAESEHXLKTLGQCDADV--PGPPGDSRLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFYETOXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQEPVHLDS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOMTWIRPSHKTFOVSFLIGALTESNAGLYRCCYWKETGWSKPSKVLELEAP 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PAIKH---QFL---LTGDTQGRYRCRSGLSTGWXQLSKLLELTGP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: AF034198; NID: g2645889; PIDN: AAC52057.1; PID: g2645890
-LQQPGNKGRFF1PSVTQQHAGQYRCYCYSSAGWSQPSDTLEL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----PQAPWEN----ITLW-CRSPSRISSKFILLKDK 65
                                                                                                                                                                                                                                                                                                                       Score 75.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 76: I
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location of p91, a novel murine regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                     45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1327
                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-Nov-1999
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                      59
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mouse

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A:Cross-references. EMBL:00775. NID:4504475. PIDN:AAA1956.1. PID:5504476
A:Note: in the authors: translation 205-Asp is shown after residue 201 and, consequently c;Superfamily selatinase A; fibronectin type II repeat homology. Demogration repeat homology are repeat homology. The repeat homology is status atypical cMMP> (F.67-216,391-43)Domain: matrix metalloproteinase homology status atypical cMMP> (F.200-271)Commain: fibronectin type II repeat homology <2815- (F.200-271)Commain: homopexin repeat homology <2815- (F.200-271)Commain: homopexin repeat homology <2815- (F.200-271)Commain: homopexin repeat homology <2815- (F.200-271)Commain: status status predicted (Cys. His. His.) (inhibited) #status F.200-404-410/Binding site: zinc. catalytic (Cys. His. His.) (inhibited) #status F.200-404-410/Binding site: zinc. catalytic (Cys. His. His.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 7
R;11-23/Domain: signal sequence #status predicted <SIG>
F;24-118,119-220,221-315,316-418,419-517,518-618/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-680 <YAM>
A;Cross-references: GB:AF041035;
C;Comment: This protein function
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Hws musculus (house mouse)
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C:Accession: JC5895
R:Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishik
J. Biochem. 123, 589-368, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blochem. J. 300, 729-736, 1994
A;Title: Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from chicken embryo
A;Reference number: $46492; MUID:94280397
A;Accession: $46492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: JC5894; MUID:98218758
A; Accession: JC5895
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A; Residues: 1-663 <AIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Accession: $46492
R:Aimes, R.T.; French, D.L.; Quigley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :636-674/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                      Query Match
Best Local
   581
                                                                                                         530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 VELLVSGNLQKPTIKAEPGSVITSKRAMTIWCQ------GNLDAEV-----YFLHNE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 KSQKTQSTQTLQQPGNKGRFFIPSVTQQHAGQYRCYCYSSAGWSQPSDTLEL
                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 QEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQLSKLLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                   70 VHLDSPAIKHOFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACS 119
                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 VFLLLWGVTWGPVTEA----AIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                         PVTEAAIFYETOXSLWAESEHXLKTLGQCDADVPG-----PPGDSRLPAVQEWGAQEP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                      23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.3%;
                                                                                                         -AGNEYWYYTASNLDRGYPKKLTSLGLPPDVQRIDAAFNWGRN-- 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g2791691; PIDN:AAB96927.1; PID:g2791692 as inhibitory cell-surface molecule against cell active
                                                                                                                                                                                                                                      Score 73;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74.5; [
Pred. No. 4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
   -EEKKKMELATPKFIADS 612
                                                                                                                                                                                                                                                               DB 1; Length 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2:
                                                                                                                                                                                                                37;
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                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain PAO1
C;Genetics:
C;Gene: PA4899
C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; KOLGCULE type: DNA
A; Roseidues: 1-489 <STFO:
A; Cross-references: GB:AE004903; GB:AE004091; NID:g9951173; PIDN:AAG08284.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: A83033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
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A; Residues: 1-192 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, March 1994
A; pescription: In vivo genetic variability of the HIV-1 gene
A; Reference number: $42940
A; Accession: $42994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral infectivity factor vif - human immunodefictency virus type 1
C:Species: human immunodefictency virus type 1, HTV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
Fc gamma (IgG)
C;Species: Mus
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                                                                                                                                                                                                                                                                   밁
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A; Accession: A83033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \lambda; \text{Title: Complete genome sequence of Pseudomonas aeruginosa PA01, } A; Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable aldehyde dehydrogenase PA4899 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z30684; NID:g459605; PIDN:CAA83164.1; PID:g459606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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                                                      148471
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 QEWG---AQEPVHLDSPA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                             SFPARVHGRIVESDVPGKESRVYRSAIGVVGVISPWNFPLHLT-QRSIAPALALGNA 175
                                                                                                                                                                                                            --PAIKHOFLLTGDTOGR----YRCRSGLSTGWXQLSKLLELTGPKVLACSLALDGA 125
                                                                                                                                                                                                                                                                   GPSARAAVLYKAVEVFDRRHEEIVDWIIR------ESGSTRLKAEIEWGAARAITLESA 119
                                                                                                                                                                                                                                                                                                                  GPVTEAAIFYETQXSLWAESEHXLKTLGOCDADVPGPPGDSRLPAVQEWGAQEPVHLDS- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
   musculus (house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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25.6%;
                                                                                                                                                                                                                                                                                                                                                                                               10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwin, A.L.; Mizoguchi,
L.L.; Coulter, S.N.; Fo
                             affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                         16;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                               Score 71.5;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hi, S.D.; Warrener,
Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 489
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A ?

Hickey, M.J Larbig, K.;

opportunistic

Gaps

٠.

homology

Indels

9

Gaps

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A:Wolecule type: mRNA
R:Residuos: 1-404 <5EA>
R:Residuos: 1-404 <5EA>
A:Cross:references: GBM31314; NID:9200752; PIDN:AAA40056.1; PID:9200753
A:Cross:references: GBM31314; NID:9200752; PIDN:AAA40056.1; PID:9200753
C:Suppr:family: Fc gamma receptor: Iransmembrane protein
C:Suppr:family: Fc gamma receptor: Iransmembrane protein
C:Reywords: Immunoglobulin receptor: Iransmembrane protein
E:127-179/Domain: Immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Pittle: Wolcoular cloning and expression of the mouse high affinity Fc receptor for Igo A;Reference number: A43511; MUID:90111035 A;Recession: A43511 A3511 A;Recession: Polympianry preliminary preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Mote: Sequence extrated from NCBI backbone (NCBIN:85205, NCBIN:85208, R;Sears, D.W.; Osman, N.; Tate, B.; McKenzle, I.F.C.; Hogarth, P.M. J. Immunol. 144, 371-378, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.71tle: Structure and mapping of the gene encoding mouse high affinity Fc A;Reference number: A46480; MUID:92166399
A;Accession: A46480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FG gamma (19G) receptor high affinity - mouse
N.Alternate names: high affinity 1gG receptor
C:Species: Mus musculus (house mouse).
C:Date: 18 Jun-1993 issquence_revision 18-Nov-1994 #text_change
C:Accession: A46480; A43511
Kremnol. 148, NozA., McKenzie, I.F.; Hogarth, P.M.
Immunol. 148, 1570-1575, 1992
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A:Molecule type: mRNA
A:Residues: 1-336 <RES>
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C:Accession: 18471  
R:Pfins, J.B.: Todd, J.A.: Rodrigues, N.R.: Ghosh, S.: Hogarth, P.M.: Wicker, L.S.: Gaff Science 200, 695-588 1993  
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Iq A;Reference number: 148471; MID:93242399  
A;Reference number: 148471; MID:93242399
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A; Residues: 1.404 < OSM>
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              RESULT
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Best Local S
Matches 28
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                                                                                            59
                                                                                                                                         52 PPGDSRLPAVQEW----GAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLS
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                                                                                                                                                                                                                                                     4 LVVFLLLWGVTWGPVTEA------AIFYETQXSLWAESEHXLKTLGQCDADVPG 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PGDSS----TQWFINGTVVQTSTPSYSISVASFQDSGEYRCQIGSS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPGDSRLPAVQEWGAQEPVHLDSPATKHQFLLTGDTQGRYRCRSGLS 98
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                                                                                     -PGDSS----TOWFINGTAVQISTPSYSIPE---ASFQDSGEYRCQIGSS 100
                                                                                                                                                                                                 LLTTLLLWVPVGGEVVNATKAVITLQPPWVSIFQKENVTLWCEGPHL--
                                                                                                                                                                                                                                                                                                             Conservative
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Pred. No.
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Pred. No. 5.
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F:1-23/Domain: Signal sequence *status predicted <SIC>
F:1-23/Domain: Signal sequence *status predicted <PAT>
F:24-84/Product: Killer Cell inhibitory receptor p91A *status predicted <PAT>
F:24-119.119-220,221.315,316-418.419-517.519-618/Domain: extracellular Ig-like *statu F:656-674/Domain: transmembrane *status predicted <Ph>
F:656-674/Domain: cytoplasmic *status predicted <CYT>
viral infectivity factor vif - human immunodeficiency virus type
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Feb-1995 *sequence_revision 06-Feb-1995 *text_change ?
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C;Superfamily: AIDS vif protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: $42950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the FMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1
A:Reference number: $42940
A:Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viral infectivity factor vif - human immunodeficiency virus type C;Species: human immunodeficiency virus type 1, HTV-1 C;Date: 06:Feb-1995 #sequence_revision 06:Feb-1995 #text_change:
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S42950
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A;Status: nucleic acid sequence not
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R;Yamashita, Y; Fukta, D: Tsuji, A.; Nagabukuro, A.;
J. Biochem. 123, 358-368, 1998
A;Title: Genomic structures and chromosomal location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Killer cell inhibitory receptor p91A precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Wieland, U.; Hartmann, J.;
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A; Residues: 1-841 < YAM>
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Pred. No. 4.4;
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Pred. No. 22;
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   #text_change 20-Sep-1999
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S43967 viral infectivity factor vif - human immunodeficiency virus type 1 c;species: human immunodeficiency virus type 1. HTV-1 c;species: buman immunodeficiency virus type 1. HTV-1 c;species: buman immunodeficiency virus type 1. HTV-1 gene 20-Sep-1999 c;scoession: S42967 jsequence_revision 05-Feb-1995 *text_change 20-Sep-1999 c;accession: S42967 jsequence_revision 05-Feb-1995 *text_change 20-Sep-1999 c;accession: S42967 jsequence_revision set of the sequence control of the HTV-1 gene.

**Reference number: S4240
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A;Reference number: $42940
A;Accession: $42981
A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 <WIED:
A;Cross:references: DNED: $30642; NID: $459526; PIDN: CAAB3119.1; PID: $459527
C:Superfamily: AIDS vif protein
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C:Accession: S42981
Submitted to the EMBL Data Library, March 1994
A;Description: In vivo_genetic variability of the HIV-1 gene.
                                                                                                                    N;Alternate names: protein TSC23.80
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 30-Apr-1999 #sequence_revision 30-Apr-1999 #teo
C;Accession: T04212; S57524
R;Bevan, M; Hilbert, H; Braun, M; Holzer, E.: Brandt
submitted to the Protein Sequence Database, March 1999
A;Reference number: 215261
A;Reference number: 215261
A;Accession: T04212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-192 : WHED:
A;Cross-references: EMIED: A30628; NID:9459498; PIDN:CAA83105.1; PID:9459499
C;Superfamily: AIDS vif protein
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A;Cross-references: EMBL-A1049500
A;Experimental source: cultivar Columbia; BAC clone T5C23
R;Capelll, N.; Simon, P.; Diogon, T.; Greppin, H.
                                                                                                                                                                                                                                                                                                  osmotin precursor - Arabidopsis thaliana
N;Alternate names: protein T5C23.80
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                                                                              A; Molecule type: DNA
A; Residues: 1-244 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLWGV-----TWGPVTEAAIFYETOXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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Pred. No. 4.4;
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Pred. No. 4.4;
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                                                                                                                                                                                                                                               30-Apr-1999 #text_change 20-Aug-1999
                                                                                                                                                                                               E.; Brandt, A.; Duesterhoeft, A.;
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submitted to the EMBL Data Library, June 1995
A:Description: Isolation of an osmotin cDNA clone from Arabidopsis.
A:Reference number: 857524
A:Accession: 857524
A:Molocule type: mRNA
A:Residues: 1185, VV, 187-244 - CAP-
CGOSS-Teferences: EMBL:X89008; NID:9887389; PIDN:CAA61411.1; PID:
CGGnetics: 4
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F:1-72/Domain: signal sequence *status predicted <SIG>F:1-72/Domain: signal sequence *status predicted <MAT>
viral infectivity factor vif - human immunodeficiency virus type C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 2 C;Accession: $42996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Genome: nuclear
C; Superfamily: phytoene dehydrogenase
C; Keywords: mitochondrion
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C:Species: Mus musculus (house mouse)
C:Dato: 14-reb_1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
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A; Residues: 1-477 < TAK>
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A.ŢItle: Induction of terminal enzymes for heme biosynthesis during differentiation A;Title: Induction of terminal enzymes for heme biosynthesis during differentiation A;Reference number; S65629; MUID:95331315
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A; Note: T5C23.80
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                                                                                                                                                                                                                                                                                                                     69 --PVHLDSPAIKHQFLLTGDT-----QGRYRCRSGLSTG--WXQLSKLLE-----
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                                                                                                                                                                                                                                                                                                                                                                                                              16 GPVTEAAIFYETQXSL--WAE----SEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQE- 68
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27.3%; Pred. No. 14;
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#text_change 20-Sep-1999

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submitted to the BMBL Data Library, March 1994
A:Description in vivo genetic variability of the HIV-1 gene.
A:Reference numbor: $42940
A:Recission: $42947
A:Status: preliminary
A:Status: preliminary
A:Residues: 1712 - WIED-
A:Residues: 1712 - WIED-
A:Residues: 1712 - WIED-
A:Cross-references: BMBL:Z30610: NID:g459460; PIDN:CAA83087.1; PID:g459461; Suporfamily: AIDS vit protein
                                   A:Accession: $33981
A:Status: preliminary
A:Status: preliminary
A:Molecule type: mRNA
A:Rosituos: 1-192 <CARD
A:Rosituos: 1-192 <CARD
A:Gross-roforences: Embi.:211530: NID:g60192; PIDN:CAA77623.1; PID:g60195
C:Superfamily: AIDS vif protein
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$4247

Viral Infectivity factor vif - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Dato: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999

C:Accossion: 44247

Rivierand, U.; Hartmann, J.; Suhr, H.; Saliberger, B.; Eggers, H.J.; Kuehn,
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A;Description: In vivo genetic variability of the HIV-1 gene. A;Reference number: 942940
A;Recession: 84296
A;Scatus: preliminary
A;Sdatus: preliminary
A;Residues: 1-192 <WIE>
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Matches 22
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he EMBL Data Library, March 1994
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22.0%; Pred. No.
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Pred. No. 5.7;
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Best Local Similarity
Tatches 19; Conserv
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JC5748
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hypothetical protein SCE9.01 - Streptomyces C:Species: Streptomyces coelicolor
                                                                                                                                                                                                                                                                                               A;Gene: cfa4
C;Superfamily: Pseudomonas syringae coronafacic acid synthesis
                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-177 < PEN>
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A; Residues: 1-141 <OTT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number:
A; Accession: T14785
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                                        T36320
                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB;U56980; NID:g1655810; PID:g1655814
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CiSpecies: Homo sapiens (man)
CiPate: 20:Sep-1999 #sequence_revision 20:Sep-1999 #text_change 20:Sep-1999
CiAccession: TH/785
CiAccession: TH/785
R:Ottenwaelder, B.: Obermaier, B.: Newes, H.W.: Gassenhuber, J.: Wiemann, S.
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jun-2000 C;Accession: JC5748
                                            C; Species: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: adult uterus; clone DKFZp586N0723C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the Protein Sequence Database, August 1999 A; Reference number: 218184
                                                                  coronafacic acid synthetase component cfa4 [imported] - Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AL110265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein DKFZp586N0721.1 -
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Best Local Similarity
                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                 34 LHHSFYLTGDV-GRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVGSS 86
                                                                                                                                                                                                                           77 IKHQFLLTGDTQGRYRCR--SGLSTGWXQLSKLLE--LTGPKVLACSLALDGAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIVWQVDRMRIRTWISLVKHHIYISKKAKGWFYKHHYESTNPRISSEVHIPLGDARLVVT 67
                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 4.5;
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Pred. No.
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R:Penfold, C.N.; Bender, C.L.; Turner, J.G. Gene 183, 167-173, 1996
A;Title: Characterisation of genes involved A;Reference number: JC5745; MUID:97149295
A;Accession: JC5748 in biosynthesis of coronafacic acid, the

10.2%; Score 67.5; D Pred. No. 5.8; DB Length 177;

protein

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52 PPGDSRLPA----VQEWGAQEPVHLDSPAIKHQFLLTGDTQG----RYRC PPQDGLVPAALLAQDW-----Conservative -LDSGAASHYLVSTHDTDGTQHRVRC ω --Mismatches 13; Indels 165 93 13; Gaps

coelicolor (fragment)

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C:Accession: E84112
C:Accession: E84112
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hird Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A:Reference number: A83650; MUID:20263314
siz2999 ...
viral infectivity factor vif - human immunodeficiency virus type 1
c;Species: human immunodeficiency virus type 1, HIV-1
c;Species: 06-Feb-1995 #Sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
c;Accession: 84299
c;Accession: 84299
g;Merchiand, U; Hartmann, J; Suhr, H; Salzberger, B; Eggers, H.J.; Kuehn, submitted to the BMBL Data Library, March 1994
A;Bescription: In vivo genetic variability of the HIV-1 gene.
A;Reference number: $42940
s;Accession: $4299
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C:Spacies: Bacilius halodurans 
C:Date: 01-Dec_2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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E84112
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A;Reference number: Z21575
A;Accession: T36320
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C:Accession: T96320
R:Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandro
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A;Gene: BH3701
C;Superfamily: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA.
A;Residues: 1-672 <STO>-
A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07420.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A83650;
A;Accession: E84112
A;Status: preliminary
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C; Genetics:
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A; Residues: 1-436 <OLI>
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                                                                                                                                                                                                                                                                                                                                                                                      492 NEHDLYTLG------GYPGELR-DLLGIW--VEEIDALPPEEKNQIVITNDTGSLTGTY 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 26.8 nes 30; Conservative
                                                                                                                                                                                                                                                                                                                                           92 RCRSGLSTGWXQLSKLLELTGPKVLA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 PAVQEWG-AGEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLE 109
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26.8%; Pred. No. 17;
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Pred. No. 28;
                                                                                                                                                                                                                                                                                               559
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A;Accession: $42995
A;Status: preliminary
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                                                                                                                                                                                                                                                                R.Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, submitted to the EMBL Data Library, March 1994
A.Description: In vivo genetic variability of the HIV-1 gene.
A;Reference number: $42940
                                                                                                                                                                                                                                                                                                                                                          viral infectivity factor vif - human immunodeficiency virus type C:Species: human immunodeficiency virus type 1, HTV-1 C:Date: 06-Feb-1995 *sequence_revision 06-Feb-1995 *text_change :C:Accession: $42953
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submitted to the EMBL Data Library, March 1994
A; Description: In vivo genetic variability of the HIV-1 gene
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                                                                                                                                 A;Cross·references:
C;Superfamily: AIDS
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A; Residues: 1-192 <WIE>
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A; Residues: 1-192 <WIE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIVWQVDRMRIKTWNSLVKHHMYVSGKAKGWVYRHHYESTNPRISSEVHIPLGDARLIIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                              AIDS vif protein
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                                              10.1%;
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21.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LHTGERD--WHLGQGVSIEW
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Pred. No.
                                                                                                                                                       NID: 9459470;
                                                                Score 67;
                                              Pred. No.
                        Mismatches
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                                                                    DB 2;
                                                                                                                                                       PIDN:CAA83091.1; PID:g459471
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                                                                    Length 192;
                        Indels
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67

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24;

Gaps

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viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Dote: 06-Peb-1995 Heaquence_revision 06-Peb-1995 *text_change 20-Sep-1999
C:Accession: S4295
R:Miejand, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z30685; NID:g459607; PIDN:CAA83165.1; PID:g459608 C;Superfamily: AIDS vif protein
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                                                                                                                                                                                              Length 192
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              24;
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HIA-B-95401 - human
C:Species: Homo Saptens (man)
C:Species: Homo Saptens (man)
C:Date: 02-ui-1996 #sequence_revision 02-ui-1996 #text_change 21-Jan-2000
C:Accession: 156130
R:Hildebrand, W.H.; Madrigal, J.A.; Little, A.M.; Parham, P.
J. Immunol. 148, 1155-1162, 1992
A:Title: HIA-B-921: a family of molecules with identity to HIA-B7 in the alpha 1-A:Reference number: 156130; MUID:92148136
A:Residence: 156130
A:Scatus: preliminary; translated from GB/EMBL/DDBJ
A:Scatus: preliminary; translated from GB/EMBL/DDBJ
A:Ccoss: Texterences: CB:M7774; NID:g184116; PIDM:AAA03686.1; PID:g184117
C:Superfamily: class I histocompatibility antigen: immunoglobulin homology
F:220-285/Domain: immunoglobulin homology <IMM5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral infectivity factor wif - human immunodeficiency virus type 1
C:Species human immunodeficiency virus type 1, HVP (
C:Species human immunodeficiency virus type 1, HVP (
C:Dutc: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999 C:Dutc: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999 C:Accession: $4.244

R:Matland, V: Hertmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. aubmitted to the EMBL Data Library, March 1994

A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reforence number: $4.2940
A:Reforence number: $4.2940
A:Accession: $4.2940
A:Cross-references: EMBL-Z30609; NID:94.59462; PIDN:CAA83086.1; PID:94.59463
C:Superfamily: AIDS vif protein
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Best Local :
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113 PKVLACSLALDG
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mes 32; Conserv
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                                                                                                                         PGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTG 112
                                                                                                                                                                                                                          VFLLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLG------OCDADVPGP 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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                                                                                                                                                                             LLLLLWCALALTETWACSHSMRYFY-TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MVVWQVDRMRIRTWKSLVKHHMYISKKAKGWCYKHHYESTHPRISSEVHIPLGDAKLVIT 67
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                                                                            RGEPRAPWVEQEG---PEYWDRNTQIYKAQAQTDRESLRNLR-----GYYNQSEAGSHTW 119
                                                                                                                                                                                                                                                                              Conscrvative
                                                                                                                                                                                                                                                                                                   10.1%; Score 67;
24.2%; Pred. No.
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21.0%; Pred. No.
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                                                                                                                                                                                                                                                                              14; Mismatches
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                                                                                                                                                                                                                                                                                                                     A:Gene: hemA
C:Superfamily: glutamyl-tRNA reductase
C:Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Accession: T31441
R:Xiong, J.; Inoue, K.; Bauer, C.E.
R:Xiong, J.; Inoue, K.; Bauer, C.E.
A:Title: Tracking molecular evolution of photosynthesis
A:Pitle: Tracking molecular evolution of photosynthesis
A:Peterence number: Z21036; MUID:99061957
A:Accession: T31441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable glutamy1-tRNA reductase (EC 1.2.1.-) hemA - Heliobactilius mobilis 
C.Species: Heliobactilius mobilis 
C.Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
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A; Introns: 221/2
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A:Experimental source: strain 972h-: cosmid c323
c;Conetics:
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C;Accession: T38646
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Bothe, G.;
submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conserved hypothetical protein SPA(323.07c - fission yeast (Schizosaccharomyces pombe
C:Spacies: Schizosaccharomyces pombe
C:Date: 03-Dec:1999 #sequencc_revision 03-Dec-1999 #text_change 03-Dec-1999
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                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:AF080002; NID:g3820536; PID:g3820540; C;Genetics:
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A; Molecule type: DMA
A; Residues: 1-443 < XIO>
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T31441
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A; Residues: 1-533 <WOO>
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A; Accession: T38644
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Best Local Similarity
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                                                63
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74 LEWGQLQPQDFSKYFYVHTLYDAIRHLFRVASGLDSMVLGETQILGQVRTAYQKSCNEDC 133
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                                                                                                    VREKLSFTEAQLS---EALHKLQGMAGIEGCCILSTCNRTEIYGASTDMEKGMTAVKRFV 73
                                                                                                                                                 VTEAAIFYETQXSLWAESEHXLK-------TLGQCD-ADVPGPPGDSR--LPAVQ--- 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFSRQALKNLSPMLHFSFHGMLMIVTEWAAYEMTSLGAGYLGTAPLASQSILLTSTSLLF
                                                -EWGAQEP-----VIILDSPAIKHQF------LLTGDTQ--GRYR------C
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                                                                                                                                                                                                     Conservative
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22.9%; Pred. No.
                                                                                                                                                                                                                          10.1%; Score 66.5;
26.2%; Pred. No. 22;
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RESULT
S42997
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A; Description: In vivo genetic variability of the HTV-1 gene.
A.Reference number: 442940
A.Recession: 542997
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C.Species: human immunodefictency virus type 1, HIV-1
C.Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C.Paccession: $242997
R.Wieland, U.: Martmann, J.: Suhr, H.: Salzberger, B.: Eggers, H.J.: Kuehn,
viral infectivity factor vif - human immunodeficiency virus type 1 C:Species; human immunodeficiency virus type 1, HV-1 C;batc: 06-Pcb-1995 sequence_revision 06-Pcb-1995 *text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: In vivo genetic variability of the HIV-1 gene. A;Reference number: $42940 A;Accession: $42975 A;Accession: $42975 A;Acteus: preliminary A;Bateus: preliminary A;Malecule type: DNA A;Residues: 1-192 <MIED
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(;Species: human immunodeficiency virus type 1, HIV-1
C:Date: (05-peb-1995 #sequence_revision 06-peb-1995 #text_change 20-Sep-1999
C:Accession: S42975
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A; Residues: 1-192 <WIE>
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Best Local S
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                                                                                                                                                                                                                                                                                                8 LLLWGV-----TWGPVTEAAIFYETOXSLWAESEHXLKTLGOCDADVPGPPGDSRLPAV 61
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Pred. No.
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C;Accession: S42954
R;Mieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E. submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: 542940
A:Accession: S42954
                                                                                                                                                                                      viral infectivity factor vif human immunodeficiency virus type 1
c;Species: human immunodeficiency virus type 1. HTV-1
c;Decies: human immunodeficiency virus type 1. HTV-1
c;Dete: 06-Feb-1959 #sequence_revision 06-Feb-1959 #text_change 20-Sep-1999
c;Accession: 542972
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viral infectivity factor vif - human immunodeficiency virus type C;Species: human immunodeficiency virus type 1, HTV-1 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 2 C;Accession: $43006; $42948
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C;Superfamily: AIDS vif protein
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A;Molecule type: DNA
A;Residues: 1-192 <WIE>
A;Cross-references:
C;Superfamily: AIDS
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C;Superfamily: AIDS vif protein
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A; Accession: S43006
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                                                A; Molecule type: DNA
A; Residues: 1-192 <WIE>
                                                                                                                        A; Accession: S42972
                                                                                                                                                A; Description: In vivo genetic variability of A; Reference number: $42940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1994
                                                                                                A;Status: preliminary
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AIDS vif protein
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                        NID:g459508; PIDN:CAA83110.1;
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Pred. No.
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Pred. No.
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                        PID: g459509
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R:Anne, J.; van Wollaert, L.; Fiten, P.; Opdenakker, G.; Joris, B.; Eyssen, H. submitted to the EMBL Data Library, May 1993
A:Description: Nucleotide sequence analysis of the coding region containing the A:Reference number: $34241
A:Recession: $34245
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                                                                                                                                                                                                                             A:Gene: vif
C:Superfamily: AIDS vif protein
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                                                                                                                                                                                                                                                                                                                                                          R; Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, submitted to the EMBL Data Library, July 1996 A; Reference number: Z16673 A; Accession: T09442
                                                                                                                                                                                                                                                                                                                                                                                                                                      vif protein - human immunodefictency virus type 1 (strain JRFL)
C:Species: human immunodefictency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999
C:Accession: T09442
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C:Spaceles: actinophage VMB
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-192 < PAN>
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hes 22; Conserv
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                    62 QEWGAQEPVHLDSPAJKHQFLLTGDTQGRYRCRSGLSTGW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 DVEAPPRSGRGSGIDAWRSFLADHEINVDADASREDMIAAAEQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 DVPGPPGDSRLPAVQEWG---AQEPVHLDSPAIKHQFLLTGDTQG
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                                                                                           8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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                                                      MIVWQVDRMRIRTWKSLVKHHMYTSGKAKGWIYRHHYESTHPRISSEVHIPLGDARLVIT 67
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Pred. No.
                                                                                                                                                    Score 65;
Pred. No.
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12;
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                                 L-ascorbate peroxidase (EC 1.11.1.11) - leaf mustard C:Species: Brassica juncea (leaf mustard) C:Datc: 21-May-1999 #sequence_revision 21-May-1999 #:C:Accession: T08071
submitted to the
                  R; Tay, E.; Pua, E.C
                                                                                                                T08071
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EMBL

Data Library, December 1997

21-May-1559 #text_change 19-May-2000

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C;Superfamily: AIDS vif
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A;Molecule type: DNA
A;Residues: 1-192 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral infectivity factor vif - human immunodeficiency virus type
C:Spacies: human immunodeficiency virus type I, HTVI
C:Dato: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change
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A;Molecule type: DNA
A;Residues: 1-192 <WIE>
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A:Description: In vivo genetic variability of the HTV-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1 HTV-1
C;hate: 06-Feb-1995 #sequence_revision 05-Feb-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S42959
                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S42940
                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: In vivo genetic variability of the HIV-1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
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A; Accession: S42998
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Best Local Similarity
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                                          62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
                                                                                                                                                                                      Local Similarity
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                                                                                                                          8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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                                                                                     MIVWQVDRMRIRTWKSLVKYHMYKSGKAEKWFYRHHYESTHPRISSEVHIPLGDARLVIT 67
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-LHTGERD--WHLGQGVSIEW
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                                                                                                                                                                                   Score 65;
Pred. No.
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Pred. No.
                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                       Length 192;
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                                                                                                                                                                  Indels
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C;Superfamily: cytochrome-c peroxidase
C;Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase
C;Keywords: Chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;162/Rcitve site: His (distal axial ligand) #status predicted
F;163/Binding site: heme iron (His) (proximal axial ligand) #status predicted
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C:Species: Neurospora crassa
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000
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A; Residues: 1-250 < TAY>
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A;Accession: T08071
A;Status: translated from GB/EMBL/DDBJ
Rajandream, M.A.: Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Mature 393, 537-544, 1998
A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, J.; Sulston, A.; Whitehead, S.; Barrell, B.G. A.Authors: Squares, R.; Sulston, A.; Whitehead, S.; Barrell, B.G. Authors: Squares, R.; Sulston, A.; Suls
                                                                                                                                                                           R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Hamlin, N.; Hc; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
                                                                                                                                                                                                                                                              probable blaC - Mycobacterium tuberculosis (strain H37RV)
C;speclas: Mycobacterium tuberculosis
C:bate: 17-ul-1988 #text_change 20-Jun-2000
C:bate: 17-ul-1988 #text_change 20-Jun-2000
C:bate: 17-ul-1988 #text_change 20-Jun-2000
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C; Superfamily: Neurosp
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A; Map position: 6
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A; Experimental source:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 WKVVL 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGWXQLSKLLE-----LTGPKVLACSLALDGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV----QEWG---AQEPVHLDSPAIK 78
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ilarity 29.8%;
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Pred. No. 16;
5; Mismatches
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                                                                                                                                                                                 Holroyd,
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                                                                                                                                                                                                                     Gordon,
                                                                                                                                                                                 ωÌ
                                                                                                                                                                                                                                                                                                                                           gene 20 protein - 1numan herpesvirus 3
c:species: human herpesvirus 3, variceila-zoster virus
c:pacte: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 16-Jul-1999
c:Accession: B27343
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A;Reference number: A36916; MUID:93259953
A:Accession: B86916
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       site-specific recombinase Int - Streptomyces lividans
C;Species: Streptomyces lividans
C;Date: 07-Apr-1994 sequence_revision 18-Nov-1994 *text_change 18-Nov-1994
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A.Molecule type: DNA
A.Rosidues: 1-483 -CDNy
A;Cross-references: EMBL:X04370; NID:g59989; PIDN:CAA27903.1; PID:g60009
                                                                                                                                  R.Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1815, 1986
A;71tle: The complete DNA sequence of varicella-zoster virus
A;Reference number: A27345; MUID:86306657
A;Accession: B27343
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A; Residues: 1-455 <BI
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Pred. No.
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Pred. No.
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Willternate names: hypothetical protein ipa-92r

N:Alternate names: hypothetical protein ipa-92r

C:Species: Bacillus subtills

C:Species: Bacillus subtills

C:Accession: S39747; P70056

C:Accession: S39747; P70056

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A:Gene: 20
C:Superfamily: varicella-zoster virus gene 20 protein
C:Keywords: capsid assembly: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                   A.Crods-references: GB:299123; GB:AL009126; NID:g2636240; PIDN:CAB15789.1; PID:g2636298
A:Experimental source: strain 168
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C;Superfamily: hypothetical protein ylbo
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A;Note: The nucleotide sequence was submitted to the EMBL blat Library, June 1993
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1993
R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.K; Alloni, C; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ebriich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
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A: Residues: 1-258 < KUN>
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                                                                                                                                                                                                                                               Watch 9.8%; Score 64.5; Local Similarity 29.1%; Pred. No. 19;
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                                                 62 QEWGAQEPVHLDSPAIKH-QFLLTGD 86
                                                                                                                                                               12 GVTWGPVTEAAIFYETQXSL-WAESEHXLKTLGQCDADVPGPPGDSRL----PAV----- 61
                                                                                                      GFRWNAVVRHQ--YEKALQLAKKQRKQRMRALGN-----GQPAKKRLLYQPPAVDPEII 10:
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Pred. No. 35;
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Search completed: January 7, 2002, 16:52:06 Job time: 223 sec

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Result
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Maximum DB seq
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and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2000
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ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/135,782
CURRENT PILING DATE: 1998-08-18
NUMBER OF SED ID NOS: 10
SED THAR: 4 SUBMITH 10
SED ID NOS: 10
SED IN SER THE 244
TYPE: PRT
OTHER: NO. 6027929ccc sp.
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US-09-345-468-12
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В
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICAMT: XL. Shuang-yong
APPLICAMT: XL. Shuang-yong
TITLE OF INVENTION: Method For Cloning And Producing The NspI Restriction
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The
TITLE OF INVENTION: Recombinant NspI Restriction Endonuclease
FILE REFERENCE: MEB-143
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APPLICANT: Valinchenker, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
TILE REFERENCE: 7853-147
CURRENT APLICATION MUMBER: US/09/345.466
CURRENT FILING DATE: 1999-06-30
NUMBER OF SEO LO NOS: 24
SOPTMARE: FastSEQ for Windows Version 3.0
SEO UD NO 12
LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09135782 Patent No. 6027929
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                                                                                               Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
132 DHRFP-MERWGASEPPHLTSMNDNEIKRKFQLLKKDTSGNHNLLKSRSCERCIKTG 186
                        55 DSRLPAVQEWGAQEPVHLDS---PAIKHQF-LLTGDTQGRYR-----CRSGLSTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 Match 21.2%; Score 87.5; DB 4: Length 631; Local Similarity 27.5%; pred No. 0,0078; Local Similarity 27.5%; pred No. 0,0078; Indels 5 ses 38; Conservative 11; Mismatches 38; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 CHYYSSAGWSEPSDPLEL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 CRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 VISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLDRNNPLEPKNKARFSIPSMTEHHAGRYR 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 VQEWG------AQE------PVHLD-----SPAIKHQFLLTGDTQ---GRYR 92
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                                                                                                                       39.38;
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                                                                                               Score 75.5; DB 3; Length 244; Pred. No. 0.076; Indels 1
                                                                                               Caps
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                 Sequence 4, Application US/09193191 Patent No. 6130078 GENERAL INFORMATION:
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APPLICANT: XIAO, JIAN-PING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY, AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFRERVEL/DOCKET NUMBER: DX05
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
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APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
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APPLICATION NUMBER: US 61
FILING DATE: 16-DEC-1996
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APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
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APPLICATION NUMBER: US
FILING DATE: 05-DEC-19
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                    109 ESSUPLEL 116
                                                                                                                                                                                                          103 QLSKLLEL 110
                                                                                                                                                                                                                                                         52
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 901 Califo
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                61 VQE-----WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                               1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                                                      GOETQEYRLYREKKTAPWITRIPQEL---VKKGQFPIPSITWEHAGRYRCYYGSDTAGRS 108
                                                                                                                                                                                                                                                                                                                                         MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVI-----TQGSPVTLRCQG 51
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05-DEC-1997
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Best Local Similarity 37.5%;
Matches 21; Conservative
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LENGTH: 244
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CURRENT FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: No. 6130078toc sp.
                                                         TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: LUNGFE
CLONE: 1232054
                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: VIRAL RECEPTOR PROTEIN
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 DSRLPAVQEWGAQEPVHLDSPA---IKHQF-LLTGDTQGRYR-----CRSGLSTG-100
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FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                  TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                     LENGTH:
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                                                                            LUNGFET 03
                                                                                                                 linear
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US-08-464-523B-27
Sequence 27, Application US/08464523B; Patent No. 5723761
GENERAL INFORMATION:
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US-09-113-750A-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 24.6 Matches 29; Conservative
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                                                                                                                                                                       Query Match 10.1%; Score 67; DB 4; Length 254; Best Local Similarity 29.9%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Recombinant Raccoonpox virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 APALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAOCNVTLEVSTGPGAAVVAGAVVG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 HSIKTL-ELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFF 198
121 OFHPEIFGIGNVSKVYVD---IKHQFI 144
                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 422523
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/113,750A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 HXLKTLGOCDADVPGPPGDSRLPAVQEWGAQEPVHLDS----PAIKHQF------- 81
                                   65 -----GAQEPVHLDSPAIKHQFL 82
                                                                           63 AAEIYEPGRSLWCRIGH--DRCGEDDHDELGFMVPPGLSSEGHLTSVYAWLAFLSFSYTA 120
                                                                                                              21 AAIFYETQXSLWAESEHXLKTLGQCDADVPG---PPG---DSRLPAVQEW------ 64
                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212)262-0400
TELEFAX: (212)664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                              254 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David E. Junker and Mark D. Cochran
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                        DNA (genomic)
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Pred. No. 1.2;
                                                                                                                                                    Mismatches
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Toni A. Voelker

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US-08-999-774A-10
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                                                                                     Sequence 10, Application US/08999774A Patent No. 6274312
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/152.00
EILING DATE: 10.00V-1993
PRIOR APPLICATION DATA: 30.08/261,69
PRIOR APPLICATION UNMBER: 08/261,69
ETILING DATE: 16-2UN-1994
ATTORNEY/ACENT IMFORMATION:
NAME: DODAD & SOBEREY
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (916) 753-151 INFORMATION FOR SEQ ID NO:
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APPLICANT:
               APPLICANT: Gish, Kurt C. APPLICANT: Scghezzi, Wolfgang APPLICANT: Shanahan, Frances
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/L
FILING DATE: 10-NOV-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Plant Acyl ACP Thioesterase TITLE OF INVENTION: Sequences
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APPLICANT:
                                                                                                                                                                                                    328 SMPTEVLETQELCSLALE 345
                                                                                                                                                                                                                                        110 LTGPKVL----ACSLALD 123
                                                                                                                                                                                                                                                                           273 PLFVDSPVIEDSDLKVHKFKVKTGDS-----IQKGLTPGWNDLDVNQHVSNVKYIGWILE 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
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REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1920
CITY: Davis
                                                                                                                                                                                                                                                                                                              69 PVHLDSPAIK-----HQF-LLTGDTQGRYRCRSGLSTGWXQLSK-------LLE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Calgene, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                  24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 415 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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  Lees, Emma M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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02-JUN-1995
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NO: 27:
                                                                                                                                                                                                                                                                                                                                                                 10.0%; Score 66; DB 1; Length 415; 30.8%; Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                    APPLICANT: RUVKUM: GATY
APPLICANT: RUTKUM: ASTRICT
APPLICANT: Patcerson, Garth
APPLICANT: Patcerson, Garth
APPLICANT: Patcelson, Garth
APPLICANT: Patch
APPLICANT: Tissenbaum, Heidi
APPLICANT: Moreta, Jason
APPLICANT: More
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102, Application US/08857076C Patent No. 6225120
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TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CURRENT APPLICATION NUMBER: US/08/857,076C
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APPLICATION NUMBER: US 60/032,818
FILING DATE: 11-DEC-1996
FILING DATE: 11-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           165 GLQAPGPLPAPAGDKGDLLLQAYQQSCLADHLLTASWGA-DPVPTKAPGEGQEGLPLTGA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 10-DEC-1997
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87 TOGRYRCRSGLSTGW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 ------GDSRLPAVQE--------WGAQEPVHLDSPAIKHQFL-LTGD 86
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: NUMBER OF SED ID NOS: 114
: SOPTWARE: FRSENSED for Windows Version 4.0
: SED ID NO 102
: LENGTH: 501
: ORANISH: Homo sapiens
US:-08-857-076-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1997-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acid
                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Goli, Surya K. APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                  TOPOLOGY: line
IMMEDIATE SOURCE
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          383 ---DPILSQAPTL----LLLGGLPS----SSKLATGVGLCPKPLEARGPSSLVPTLSM 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 GVT-GPLHTYSSSLFSPAEGPLSAGEGCFSSSQALEAL--LTSDTPPPPADVLMTQV--- 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 GAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GVTWGPV--TEAAIFYETQXSLWA-----ESEHXLKTLGQCDADVPGPPGDSRLPAVQEW 64
    LIBRARY:
                                                    STRANDEDNESS:
                                                                                                                                                                                                               NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
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                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94304
                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                685 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Corley, Neil C.
Guegler, Karl G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillman, Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 65; DB 28.0%; Pred. No. 4.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16; Mismatches 45; Indels
                                                                                                                                                                                                   PF-0321 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 501;
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US-09-136-282-2
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                                                                                                                                   ; MOLECULE TYPE: protein US-09-136-282-2
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Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6063609
                                                    Matches
                                                                  Best Local Similarity
                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ for UCURRENT APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 20-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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40 KTLGQ-CDAD-----VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQF----
                                                                                                                                                                                                                                                                      TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box 91
CITY: Valley Forge
                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                   TYPE:
                                                                                                                                                                                                                                                                 TELEX: 846169
                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                  NAME: Prestia, Paul F
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
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                                                                                                                                                                                                                 685 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOUZYK, MARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSHAK, AMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HANSBURY, MICHAEL NERURKAR, SANDHYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANDERSON, KAREN
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                     linear
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                                                                                                                                                                              single
                                                                  9.8%;
26.7%;
                                                  14; Mismatches
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Sequence 2, Application US/09136282
                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 IIVDPTTGKRYCRGKVLGKGGFAKCYEMTDLTNNKVYAAKI 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratner & Prestia
O. Box 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.8%; Score 65; DB 2; Length 685; 26.7%; Pred. No. 7.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   60/056,112
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Score 65; I
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                GH-70231
                   DB 3;
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                   Length 685
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32; Indels

28; Gaps

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TOPOLOGY: lines;
IMMEDIATE SOURCE;
ITHBARY: HUVENC;
CLONE; 39043
US-09-272-796-1
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Patent No.
                                                                                                                                     Matches 27;
                                                                                                                                                     Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Shah, PUTVÍ
TITLE OF INVENTION: DISEASE ASSOCIATED PHOTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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    72
                                                                  20
                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                82 LLTGDTQGRYRCRSGL--STGWXQLSKLLELTGPKVLACSL 120
                                                                                                  40 KTLGQ-CDAD-----VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQF------ 81
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 IIVDPTTGKRYCRGKVLGKGGFAKCYEMTDLTNNKVYAAKI 112
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                                                                  QALCKGCGADSKKKRPPOPPEESOPPOSO---AQVP-----PAAPHHHHHHSHSGPEISR 71
ITVDPTTGKRYCRGKVLGKGGFAKCYEMTDLTNNKVYAAK1 112
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                                                                                                                                                                                                                                                                                                                    amino acid
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Shah, Purvi
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                                                                                                                                   Conservative
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Corley, Neil C.
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                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                     9.8%;
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                                                                                                                                   14;
                                                                                                                                Score 65; DB 4;
Pred. No. 7.5;
14; Mismatches
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                                                                                                                                   32; Indels
                                                                                                                                   28;
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9.7%;
Best Local Similarity 33.3%;
Matches 23; Conservative

Score 64; DB Pred. No. 2.5; Mismatches DB 4;

34; Indels Length 249

Gaps

51 GPPGDS---RLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLL 108

30 GPPGVDLYRLEKLSSSRYQDQAVLFIPAMKRSL-----AGRYRCSYQNGSLWSLPSDQL 83

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109 ELTGPKVLA 117

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FILE REFERENCE: GH-70231-D1
CURRENT APPLICATION NUMBER: US/09/505,744
CURRENT FILING DATE: 2000-02-16
EARLIER APPLICATION NUMBER: 09/216,282
EARLIER FILING DATE: 1998-08-20
EARLIER APPLICATION NUMBER: 60/056,112
EARLIER APPLICATION NUMBER: 60/056,112
EARLIER FILING DATE: 1997-08-20
NUMBER 0F SBQ ID NOS: 3
SOFTWARE: FASTSEQ for Windows Version 3.0
SBQ ID NO 2
; ORGANISM: Homo sapiens
US-09-345-468-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: HOMO SAPIENS US-09-505-744-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-345-468-9
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                                                                                                    NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WISfield, S.
APPLICANT: Villeval, J.
APPLICANT: Vindroherrus, M.
APPLICANT: Vaindfor-Perrus, M.
APPLICANT: Vaindfor-Perrus, M.
APPLICANT: WINCHILD (JYCOPROTEIN VI AND USES THERBOF
FILE REPERRANCE: 7833-147
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/09345468 Patent No. 6245527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mark M. Bouzyk
APPLICANT: Michael J. Hansbury
APPLICANT: Jeffrey R. Jackson
APPLICANT: Sandhya S. Nerurkar
APPLICANT: Amy K. Roshak
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                                                                                                                                                                                     CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/345,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: HUMAN SERUM INDUCTBLE KINASE (SNK)
                                                       TYPE: PRT
                                                                             LENGTH: 249
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26.7%; Pred. No. 7.5;
ative 14; Mismatches 32; Indels
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US-09-345-468-3
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Best Local S
Matches 23
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Patent No. 624527
GENERAL INFORMATION:
APPLICANT: Busfield, S.
APPLICANT: Villeval, J.
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 339
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SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local
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APPLICANT: Villeval, J.
APPLICANT: Andadrot-Pertus, M.
APPLICANT: Valnohenker, M.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REPERENCE: 753-147
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                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/345,468 CURRENT FILING DATE: 1999-06-30
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             TYPE: PRT
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104 ELVATGVFA 112
                                      109 ELTGPKVLA 117
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                                                                                                                                                        Local Similarity
nes 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GPPGDS--RLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLL 108
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                                                                                                               51 GPPGDS--RLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                            GPPGVDLYRLEKLSSSRYQDQAVLFIPAMKRSL-----AGRYRCSYQNGSLWSLPSDQL 103
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                                                                                                                                                                        9.78;
                                                                                                                                                     Score 64; DB 4; Length 339; Pred. No. 3.8; 4; Mismatches 34; Indels
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Pred. No. 3.5;
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                                                                          us-08-985-950-20
                Sequence 20, Applicat Patent No. 6140076 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
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APPLICATION NUMBER: U
FILING DATE: 21-MARCH
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US,
FILING DATE: 05-DEC-19
CLASSIFICATION: 435
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TITLE OF INVENTION: Isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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  APPLICANT:
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                                                                                                                                                                                             108 LELTG--PK 114
                                                                                                                                                     132 LVMTGAYPK, 140
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FILING DATE: 06-DEC
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                   53 PGDSRLPAVQE---WGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSK--L 107
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                                                                                                                                                                                                                             74 -- EYRLYREKKSASWITRIRPELVKNGQFHIPSITWEHTGRYGCQYYSRARWSELSDPLV 131
                                                                                                                                                                                                                                                                                                        18 MTPIVTVLICLGLSLGPRTHVQTGTIPKPTLWAEPDSVITQGSPVTLSCQGSLEAQ---- 73
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                                                                                                                                                                                                                                                                                                                                                1 MSMLVVFLLLWGVTWGPVTEAAIFYETOXSLWAE-----SEHXLKTLGQCDADVPGP 52
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                                                        Application US/08985950
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901 California Avenue
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Adema, Gosse Jan
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SYSTEM: PC-DOS/MS-DOS
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06-DEC-1996
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25.6%; Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                        4; Length 431;
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US-08-985-950-16
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Patent No. 6
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Best Local (
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                                                                                                                                                     GENERAL INFORMATION:
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FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 06-DEC-1996
ATTORNEY/ACENT INFORMATION:
NAME: CTION, EMAIN P.
REGISTRATION NUMBER: 34.09/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650)496-1204
NFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         CORRESPONDENCE ADDRESS
                                                                                            TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes; NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 60/041,279
EILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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                                                                                                                                     APPLICANT: Adema, Gosse Jan
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                                                                                                                                                                                                                                                                                                                                                                                                               53 PGDSRLPAVQE---WGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSK--L 107
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                STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                         ADDRESSEE: DNAX Research Institute
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%; Score 63.5; D
25.6%; Pred. No. 6.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               us 60/032,252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
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MOLECULE TYPE: protein
us-08-985-950-16
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                                                                                                                                                                                                                                                                                          Sequence 18, Application US/08985950 Patent No. 6140076 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/03
FILING DATE: 16-DEC-1996
PRIOR APPLICATION NUMBER: US 60/03
APPLICATION NUMBER: US 60/03
FILING DATE: 06-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                       APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                     132 LVMTGAYPK 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 LELTG -- PK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 05-DEC CLASSIFICATION: 439
                                                                                               COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 615 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                     California
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PRIOR APPLICATION NUMBER: US 60/041,279
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                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC:DOS/MS:DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                         ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 -- EYRLYREKKSASWITRIRPELVKNGQFHIPSITWEHTGRYGCQYYSRARWSELSDPLV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 MTPIVTVLICLGLSLGPRTHVQTGTIPKPTLWAEPDSVITQGSPVTLSCQGSLEAQ---- 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 PGDSRLPAVQE---WGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSK--L 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDADVPGP 52
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06-DEC-1996
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25.6%; Pred. No. 10;
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-985-950-18
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Best Local Similarity 25.6%; Pred. No. 10;
Matches 33; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6271343
GENERAL INFORMATION:
                                                                                                                                                                                                                       APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
APPLICANT: Foster, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19,
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TELEPHONE: (550)852-9196
TELEFAX: (550)496-1204
INFORMATION FOR SEQ ID NO: 18:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 615 amino acids
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APPLICATION NUMBER: US 60
FILING DATE: 06-DEC.1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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PRIOR APPLICATION DATA:
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 LVMTGAYPK 140
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        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                         ADDRESSEE: 2ymogenector
STREET: 1201 Eastlake Ave East
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                                                                                                                                     COUNTRY:
                                                                                                                                                      STATE: WA
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                                                                                                                     98102
                                                                                                                                                                      Seattle
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                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                 Lok, Si
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; MOLECULE TYPE: protein
US-09-071-224-19
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Best Local Similarity
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                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                    CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FOSTER, Donald C.
APPLICANT: Addms, Robyn L.
APPLICANT: Lehner, Joyce M.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
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NAME: Lunn, Paul G
               ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                            SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                                                                                            STREET: 11.
STREET: 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 TYGPHSCHIPKDLALF - TPYEIWVEATURLGSARSDYLTLDYLDYVTTDPPPDYHYSRY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 GGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVED--SVDWKVVDDVSNQT----SCRLA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 200 - 16678
                                                                                                                           APPLICATION NUMBER: US/09/071,224 FILING DATE:
                                                                                                                                                                                             COMPUTER: 1BM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 QEWGAQEPVHLDSPAIKHOFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 TWGPVT----EAAIFYETQXSLWAESEHXL-----KTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
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                                                     FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
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            Lunn,
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Jelmberg, Anna C.
Gilbert, Teresa
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                                                                                                                                                                                                                                                                                                                                                               Zymogenetics
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26.7%; Pred. No. 7.
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RESULT 24
US-09-120-601-2
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Best Local Similarity 26.7
Matches 32; Conservative
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SEQ ID NO 2
LENGTH: 405
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APPLICANT: Maslakowski, Piotr
TITLE OF INVENTION: No. 6060276e1 Orphan Receptors
FILE REFERENCE: RBG 630
                                                                                                                                                                                                    Sequence 2, Application US/09120601 Patent No. 6207413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09012072 Patent No. 6060276
               APPLICANY: MASIANOWSKI, PLOTT
TITLE OF INVENTION: 0. 6207413el Orphan Receptors
FILE REFERENCE: REG 530
CUMRENT APPLICATION NUMBER: US/09/120,601
CURRENT FILING DATE: 1998-07-22
EARLIER APPLICATION NUMBER: 09/012,072
EARLIER APPLICATION NUMBER: 09/012,072
EARLIER PILING DATE: 1998-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/012,072
CURRENT FILING DATE: 1998-01-22
NUMBER OF SEO ID NOS: 4
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NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                        230 GGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVED--SVDWKVVDDVSNQT-----SCRLA 282
                                                                                                                                                                                                                                                                                                                                                                                                                               172 TYGPHSCHIPKDLALF--TPYEIWYEATNRLGSARSDYLTLDYLDYVTTDPPPDYHYSRV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 GGLEDQLSVRWYSPPALKDFLFQAKYQIRYRVED--SVDWKVVDDVSNQT-----SCRLA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 TYGPHSCHIPKDLALF - TPYEIWYEATHRIGSARSDYLTLDYLDYYTTDPPPDYHYSRY 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 TWGPVT----EAAIFYETQXSLWAESEHXL-----KTLGQCDADVPGPPGDSRLPAV 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 amino acids
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26.7%; Prod. No. 7.
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; MOLECULE TYPE:
; FRAGMENT TYPE:
US-09-071-224-6
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Best Local Similarity
Matches 32; Conser
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                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LAID, PAUL
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                            INFORMATION FOR SEQ ID NO:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: 1BM Compatible
OPERATING SYSTEM, DOS
SOFTWARE: POSISBO FOR WINDOWS VERSION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FOSTER, Donald C.
APPLICANT: Adams, Robyn L.
APPLICANT: Lehner, Joyce M.
APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                      TOPOLOGY:
                                                                  TYPE: amino & STRANDEDNESS:
                                                                                                                                                             TELEX:
                                                                                                                                                                              TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 98102
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                                                                                                       LENGTH:
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                                                                                     amino acid
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1201 Eastlake Ave East
                                                                                                       425 amino acids
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                                                      linear
                 protein
internal
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                                                                    single
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26.7%; Pred. No. 7.7;
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US-09-071-224-23
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US-09-111-730-2
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                                                                                                                                                                                                                 RESULT
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CURRENT FILIG DATE: 1998-07-08

NUMBER OF SEO LD NOS: 9

SOFTWARE: PICENTIN Ver. 2.0

SEO LD NO 2

SEO LD NO 2
                                                                                                                                                           Sequence 23, Appli
Patent No. 6271343
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Toshimasa Shinki
APPLICANT: Tatsuo Suda
APPLICANT: Yuzuru Ishimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TAKAO SATUTA
APPLICANT: H1romichi Suzuki
APPLICANT: H1romichi Suzuki
TITLE DE INVENTION: 25-HYDROXYVITAMIN D3-1a-HYDROXYLASE AND DNA ENCODING THE HYDROXYI
PILE REFERENCE: 1074
                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Matsuhiko Hayashi
APPLICANT: Toshiaki Monkawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hideharu Anazawa
APPLICANT: Hiroko Shimada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                   APPLICANT:
APPLICANT:
                                                                                                     APPLICANT:
TITLE OF INVENTION:
                   APPLICANT:
                                     APPLICANT:
                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                     123 ACGLITAEGEEWQRLRSLL 141
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                                                                                                                                                                                                                                                                                                     96 -- GLSTG----WXQLSKLL 108
                                                                                                                                                                                                                                                                                                                                                                        61 VQ-----LTGDTQGRYRCRS- 95
                                                                                                                                                                                                                                                                                                                                                                                                             15 VRWAPELGASLGYR-----EYHSARRSL----ADIPGPSTPSFLAELFCKGGLSRLHE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                13 VTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tadashi Yoshida
                                                                                                                                                                            Application US/09071224
                                              Presnell, Scott R.
Jelmberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
              Lehner, Joyce
                                Adams, Robyn L.
                                                                                                                           Š,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 62.5;
24.5%; Pred. No. 10;
MAMMALIAN ZCYTOR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.5%; Score 62.5; DB 4; Length 425; 26.7%; Pred. No. 8.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35;
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Best Local Similarity
"" hes 32; Conserva
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Sequence 22, App. ...
8271343
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TOPOLOGY: lin
MOLECULE TYPE:
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LENGTH: 303 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
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APPLICATION NUMBER: US/09/071,224
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           APPLICANT: Lok, Si
APPLICANT: Presnell, Scott R.
APPLICANT: Jelmberg, Anna C.
APPLICANT: Gilbert, Teresa
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                                                                                                                      CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                         APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOR5
                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 TVGPHSCHIPKDLALF--TPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 209
                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 TWGPVT-----EAAIFYETQXSLWAESEHXL-----KTLGQCDADVPGPPGDSRLPAV 61
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                                COUNTRY:
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                                                                                      STREET:
                                                                                                     ADDRESSEE:
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1201 Eastlake Ave East
                                                                                      1201 Eastlake
                                  USA
                                                                                                                                                                                              Adams, Robyn L.
                                                                                                                                                                                                          Foster, Donald C.
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                                                                                                       Zymogenetics
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26.7%; Pred. No. 6.9;
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APPLICANT: Lok, S
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SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acid
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Presnell Scott R.
APPLICANT Schaberg, Anna C.
APPLICANT Gilbert, Toreas
APPLICANT Gilbert, Toreas
APPLICANT Adams, Robyn L.
APPLICANT Lehner Joyce M.
APPLICANT: Lehner Joyce M.
TITLE OF INVENTION: MAMAALIAN ZCYTORS
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                   STATE: WA
COUNTRY: US
ZIP: 98102
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                                                                                                                                                                                                                                      STREET: 1201 E
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COMPUTER: IBM CON
OPERATING SYSTEM:
CLASSIFICATION:
                                                                                                                                                                                                                                                               ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121
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REGISTRATION NUMBER: 32,743
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                      FILING DATE
                                       APPLICATION NUMBER:
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FastSEQ for Windows Version 2.0
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26.7%; Pred. No. 9.8;
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                                       US/09/071,224
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US-09-071-224-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOK, S!
APPLICANT: PTESSEE!, SCOTT R.
APPLICANT: Jelmbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Golder, Donald C.
APPLICANT: Koster, Donald C.
APPLICANT: Lehner, Joyce M.
APPLICANT: Lehner, JOYCE M.
APPLICANT: Lehner, JOYCE M.
APPLICANT: Lehner, JOYCE M.
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Best Local Similarity 26.7%; Pred. No. 9.8;
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                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FASTSEG for Windows Version
CURRENT APPLICATION NOWAE
APPLICATION NUMBER: US/09/071,224
                 REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
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MEDIUM TYPE: Diskette
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TELEPHONE: 205-442-6627
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CITY: Seattle
STATE: WA
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                                                      NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
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STREET: 1201 Eastlake Ave East
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TELEPHONE:
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206-442-6627
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US-09-071-224-27
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; MOLECULE TYPE: protein US-09-071-224-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                              INFORMATION FOR SEQ ID NO:
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LENGTH: 389 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTMARE: PASTERO FOR WINDOWS VERSION 2.0
CURRENT APPLICATION DATA: US/09/071,224
APPLICATION NUMBER: US/09/071,224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jelmberg, Anna C.
APPLICANT Foster, Teresa
APPLICANT Foster, Donald C.
APPLICANT Lehner, Robyn L.
APPLICANT Lehner, Joyce M.
TITLE OF INVENTION: MANHALIAN ZCYTOR5
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
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MEDIUM TYPE: Diskette
                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
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Local Similarity 26.7%; Pred. No. 9.8;
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                        STRANDEDNESS:
TOPOLOGY: 11
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                                                                                                                                                                                       TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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STREET: 1201 Eastlake Ave East
                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98102
                                                                                 amino acid
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                                        linear
                                                             single
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                                                                       Query Match 9.3%; Score 61.5; D: Best Local Similarity 26.7%; Pred. No. 9.9; Matches 32; Conservative 10; Mismatches
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Best Local Similarity
Matches 32; Conserv
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION: •
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
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STREET: 1201 Ea
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Foster, Donald C. APPLICANT: Adams, Robyn L.
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155 TYGPHSCHIPKDLALF--TPYEIWVEATNRLGSARSDVLTLDILDVVTTDPPPDVHVSRV 212
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
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                                      14 TWGPVT-----EAAIFYETQXSLWAESEHXL-----KTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                       amino acid
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Gilbert, Teresa
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26.7%; Pred. No. 9.8;
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213 GGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVED--SVDWKVVDDVSNQT-----SCRLA 265

QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121

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; FRAGMENT TYPE:
US-09-071-224-4
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US-08-348-353-17
                  RESULT
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 425 amino acid
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MEDIUM TIPE: DISACETE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FOSCESO FOR WINDOWS VETSION 2.0
CURRENT APPLICATION DATA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
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ATTORNEY/AGENT INFORMATION:
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APPLICANT Gliberg Anna C.
APPLICANT Glibert, Teresa
APPLICANT Soster, Donald C.
APPLICANT HAMBER ADDNA L.
APPLICANT LEHNER, BODYN L.
APPLICANT: LEHNER, JÖYCE M.
TITLE OF THEMETION: MAMMALIAN ZCYTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1201 EXCITY: Seattle STATE: WA COUNTRY: USA
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                                                                        246 GGLEDQLSVRWVSPPALKDFLFQAKYQIRYRVED--SVDWKVVDDVSNQT-----SCRLA 298
                                                                                                                                                  188 TVGPHSCH1PKDLALF -- TPYEIWVEATURLGSARSDVLTLDILDVVTTDPPPDVHVSRV 245
                                                                                                          62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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TELEFAX: 206-442-6678
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REGISTRATION NUMBER: 32,743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/071,224 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             425 amino acids
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1201 Eastlake Ave East
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                                                                                                                                                                                                                                                9.3%; Score 61.5;
26.7%; Pred. No. 11;
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                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                     DB 4; Length 425;
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US-08-465-965-17
: Sequence 17, Application US/08465965
; Patent No. 5968512
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                                                                                                                                                                                                                                                                                                                                                                            RESULT
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INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,353
FILING DATE: 30-NOV-1994
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                            APPLICANT: Tuomanen, Elaine
APPLICANT: Wasure, Robert
TITLE OF INVENTION: Actibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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LENGTH: 1248 amino acids
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TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT: Masure,
                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   939 IENTAKLSGEVQ 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Belance
                                                                             STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                    CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
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TELEPHONE: 201-40.
TELEPHONE: 201-10.
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COMPUTER: IF
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CITY: Hackensack
STATE: New Jerse
                                                                                                                                       STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 IKHQFLLTGDTQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 ETQXSLWAESEHXLK--TLGQCDADVPGPPGDSRLPA----VQEWG---AQEPVHLDSPA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 30.6
les 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Jackson, David
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                               07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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                                                                                                                                                          Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibody Recognizing Endothelial Cell
Ligand for Leukocyte CR3
38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 61.5; D
Pred. No. 49;
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28;
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                                                                                                                                                                                                                                                                                                                                                                    US-08-465-966-17
                                                                                                                                                                                                                                                                                                                                                                                      RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08465966 Patent No. 6015560
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 201-343-1684 PRINCIPLE TO THE TELEFAX: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03725
FILING DATE: 04-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 23-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                      APPLICANT: Masure, Robert
TITLE OF INVENTION: Antibody Recognizing Endothelial Cell
TITLE OF INVENTION: Ligand for Leukocyte CR3
NUMBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                            APPLICANT:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                        939 IENTAKLSGEVQ 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  879 EANALLWAAGELTVKAQNITNKRAALIEAGGNARLTAAVALLNKLGRIRAGEDMHLDAPR 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson, David
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 06-JUL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 IKHQFLLTGDTQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 ETQXSLWAESEHXLK--TLGQCDADVPGPPGDSRLPA----VQEWG----AQEPVHLDSPA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-MAY-1991
                                                                                                          COUNTRY:
                                                                                                                              STATE:
                                                                                                                                                               STREET:
                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                           07601
                                                                                                                                                Hackensack
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                                                                                                                           New Jersey
                                                                                                                                                               411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1248 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.3%; Score 61.5; ilarity 30.6%; Pred. No. 49; Conservative 13; Mismatches
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                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                           Tuomanen,
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                                                                                                                                                                                                                                                                                             Elaine
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Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 61.5; Best Local Similarity 30.6%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION: Katz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 04-MAY-1992
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 07/695,613
FILING DATE: 03-MAY-1991
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/348,353
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
                                                                                                                                                                                                                                                   APPLICANT: Donadio, S
APPLICANT: Mccalpine, J B
TITLE OF INVENTION: Erythromycin Analogs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1248 amino acids
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TELEPHONE: 201-487-5800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson, David
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APPLICATION NUMBER: PCT/US92/03725
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                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             939 IENTAKLSGEVQ 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     879 EANALLWAAGELTYKAQNITNKRAALIEAGGNARLTAAVALLNKLGRIRAGEDMHLDAPR 938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
COMPUTER: IRM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                               STREET: Abbott I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 IKHQFLLTGDTQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 ETOXSLWAESEHXLK--TLGQCDADVPGPPGDSRLPA----VQEWG---AQEPVHLDSPA 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-NOV-1994
                                                                                                                              CITY: Abbott Park
STATE: IL
                                                                                           ZIP:
                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                     5824513
                                                                                           60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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23-MAY-1994
                                                                                                                                                                                                                                                                          Recombinant DNA Method for Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26,742
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  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3;
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ATTORNEY/AGENT INFORMATION: NAME: Danckers, Andreas

Danckers, Andreas M

CLASSIFICATION: 435 APPLICATION NUMBER: FILING DATE: 17-JAN

17-JAN-91

US/07/642,734C

CURRENT APPLICATION DATA:

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Patent No. 6004787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 31; Conservative 10; Mismatches 59; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: JEM PC compatible
OPERATING SYSTEM: DC-TOS5/MS-DOS
SOFTMARE: PULGEITH Release #1.0, Version #1.25
                                                                                                                            TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mcalpine, J B
TITLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1180 SAVVCAQDAAALREAL--GDEPVTALVHAGTLTNFGSISEVAPEEFAETIAAKTAL 1233
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3567 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 491
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-9396
MOLECULE TYPE:
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                        NAME: Casuto, Dianne REGISTRATION NUMBER: 40,943
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/439,009A FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 QEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACSLAL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 TWGP-----VTEAAIFYETQXSLWA--ESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                    TOPOLOGY:
                                      TYPE: amino acid
                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donadio, S
                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven F. Weinstock
protein
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Matches

32;

Conservative

10; Mismatches

57; Indels 21; Gaps

S

14 TWGPVT-----EAAIFYETQXSLMAESEHXL------KTLGQCDADVPGPPGDSRLPAV 61

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; MOLECULE TYPE: protein 
US-09-071-224-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Appli
Patent No. 6271343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.2%;
Best Local Similarity 26.7%;
                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1180 SAVVCAQDAAALREAL--GDEPVTALVHAGTLTNFGSISEVAPEEFAETIAAKTAL 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1127 SWTPHGTVLVTGAASPVGDQLVRWLADRGAERLVLAGAC------PGDDLLAAVBEAGA 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
                                                                                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FITLE OF INVENTION: MAMMALIAN ZCYTOR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: V
y Match 9.2%;
Local Similarity 26.7%;
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                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/071, 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                     TOPOLOGY:
                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                    amino acid
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                                                                                                                                                  389 amino acids
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                                                                                                                                                                                                                         206-442-6678
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Gilbert, Teresa
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                                                                                                     linear
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                                                                                                                                                                                                                                                                         96-22
Score 60.5;
Pred. No. 13;
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                DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3567;
              Length 389;
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US-08-702-367A-19
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                                                                                                                                       Sequence 19, Application US/08702367A Patent No. 5981246
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Best Local Similarity
                                                                                                                    GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: EPH-LIKe
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
                                                              APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                        NUMBER OF SEQUENCES: 4
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                                                                                                                                                                                                                                                            957 TAEDLTQMGITLPG 970
                                                                                                                                                                                                                                                                                                  111 TGPKVLACSLALDG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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FILING DATE:
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        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 984 amino acids
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                                                                                                                                                                                                                                                                                                                                                                           PGDSRLP--AVOEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVTEAAIFYETQXSLWA-----PGP 52
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1840 Dehavilland Drive
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     Amgen Patent Operations/RBW
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23.1%; Pred. No. 48;
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                                                                              EPH-Like Receptor Protein Tyrosine
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Best Local Similarity 23.1%; Pred. No. 48;
Matches 31; Conservative 13; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: WINTER: ROBERT B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                       COMPUTER REDABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PECENTIA MELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: EPH-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fox, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 TGPKVLACSLALDG 124
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STREET: 1840 Dehavil
CITY: Thousand Oaks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/702,367A
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                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                       FILING DATE
                                                                                                                                       APPLICATION NUMBER: PCT/US95/04681
                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                                                                                                                                                                                                                                                                  California
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1840 Dehavilland Drive
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856 PVDCPAPLYELMKNCWAYDRARRPHFQKLQAHLEQLLANPHSLRTIANFDPRVTLRLPSL 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
                                        17 PVTEAAIFYETQXSLWA-----PGP 52
                                                                              13; Mismatches
                                                                                                                       DB 2;
                                                                                    45
                                                                                                                         Length 984;
                                                                                 Indels
                                                                                 45:
                                                                                 Gaps
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US-08-667-939A-2
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  Query Match

Best Local Similarity

Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY 1995
ATTORNEY/AGENT INFORMATION:
NAME: BROMDY, NOSOT L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION UNHEER: US/O8/667,939A
FILING DATE: 24-UN-1396
PRIOR APPLICATION LATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE PROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LUO, Shu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             916 SGSDGIPYRTVSEW------LESIRMKRYIL------HFHSAGLDT----MECVLEL 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                856 PVDCPAPLYELMKNCWAYDRARRPHFQKLQAHLEQLLANPHSLRTIANFDPRVTLRLPSL 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 TGPKVLACSLALDG 124
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                                                                                                                              TOPOLOGY:
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                      TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 PGDSRLP--AVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLEL 110
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mes 31; Conserv
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                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                254 amino acids
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9.1%; Score 60; DB 2
28.3%; Pred. No. 8.5;
ative 13; Mismatches
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23.1%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                             LUO 2A
                                       DB 2; Length 254;
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    43; Indels
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    30;
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RESULT 45

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Best Local Similarity 23.7%; Pred. No.
Matches 40; Conservative 14; Mismatc
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
COOTMARE: PSTONS/MS-F-DOS
COOTMARE: PSTONS/MS-F-DOS
CURRENT APPLICATION NUMBER: US/08/750 for
FILING DATE: US/08/750 for
CLASSIEUT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Altmann, Scott W. APPLICANT: Rock, Fernando L. APPLICANT: Bazan, J. Fernand APPLICANT: Kastelein, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS NUMBER OF SEQUENCES: 11
                      119 VERGRDVKYSYQQNKLNLEVTALIEKPDIHLSGPLESGLWRPTRLSCSL 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/008,574
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                                                           93 CRSGLSTGWX-QLSKL-LELTG------PKVLACSL 120
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                                                                                                     59 WFRDGEIPYYAEVVATNNPDRRVKPETQGRFRLLGDVQKKNCSLSIGDARMEDTGSYFFR 118
                                                                                                                                         54 -- GDSRLPAVQEWGA-QEPVHLDSPAIKHQFLLTGDTQGR------YR 92
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                                                                                                                                                                                   3 LLLLPLLWG---GSLQEKPV-YELQVQKSVTVQEGLCVLVPCSFSYPWRSWYSSPPLYVY 58
                                                                                                                                                                                                                           4 LVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVP-----GPP---- 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bazan, J. Fernando
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                                                                                                                                                                                                                                                                                                                                                                                                                             single
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17;
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US-07-683-957B-3
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NAME: GOLdstein, JOTGE A.

REGISTRATION NUMBER: 29,021

REFERENCE_POCKET NUMBER: 0609,3060000

TELECOMMUNICATION INFORMATION:

INFORMATION FOR SEQ ID NO. 3:
                                                                                                                                                                                                            Query Match 9.1% Score 60; DB 1; Length 553;
Best Local Similarity 27.8%; Pred. No. 25;
Matches 32; Conservative 9; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application Patent No. 5310880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Donaboe, Patricia X.
APPLICANT: Magin, Ribbard C.
APPLICANT: MacLaughlin, David T.
TITLE OF INVENTION: Durification of M lierian inhibiting
NUMBER OF INVENTION: Substance
NUMBER OF SEQUENCES: Substance
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seerie Xessler, Goldstein 6 Fox
STREET: 1100 New York Avenue, N.H.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
130 HLAEVIWEPQLLLKFQEP-----PPGGASRWEQALLVLYPGPGPQVTVTGAGLQG 179
                                                                                                    | DEANFLEAVOESRIGEPOD--LATFGWCSTD-----SQTTLPALORLGAWLGETGEQQLL,VL, 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/683,957B FILING DATE: 19910412 CLASSIFICATION: 530
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ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 New
CITY: Washington
STATE: D.C.
                                        71 HLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQ-LSKLLELTGPKVLACSLALDG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/07683957B
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Search completed: January 7, 2002, 16:49:55 Job time: 282 sec

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Leukocyte immunogl

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Result
No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  139.5
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92.5
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90.5
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1.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{geneseq}/\text{An1980}.DAT:*

2.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{geneseq}/\text{An1981}.DAT:*

3.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{geneseq}/\text{An1981}.DAT:*

4.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{An1981}.DAT:*

5.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{An1981}.DAT:*

5.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1981}.DAT:*

6.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1981}.DAT:*

7.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1981}.DAT:*

9.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1981}.DAT:*

9.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1981}.DAT:*

10.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

11.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

12.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

13.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

14.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

15.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

16.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

17.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

20.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

21.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

22.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

23.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\text{An1991}.DAT:*

24.\(\frac{\text{SIDS2}/\text{Gyothat}\text{Gyeneseq}/\text{Gyeneseq}/\
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length: 2000000000
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Match
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Maximum Match 100%
Listing first 100:
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Copyright (c) 1993 - 2000 Compugen
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regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, a well as stability of maka. The ESTs are also useful as probes for chromosome mapping, and to obtain full length cONA clones. The ESTs can also be used in forensic procedures to identify individuals, or in diagnostic procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used gone therapy protocols. The nucleic acids encoding signal peptides can gene therapy protocols.
                                                                                                      ARA42265 to ARA43075 represent novel 5' exprossed sequence tag (EST) sequences corresponding to human secreted proteins ARA46651 to ARA45649 represent the EST-related proteins corresponding to ARA42365 ARA454052. The 'EST's can be used for producing secreted human general ARA43052. They can be used to identify and isolate 5' untranslated products. They can be used to identify and isolate 5' untranslated
                                                                                                                                                                                       Claim 3; Page 603; 837pp; English
                                                                                                                                                                                                               Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
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forensic; location; development; protein synthesis; stability;
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directing extracellular secretion of a polypeptide

or.

growth hormone (GH) activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method involves correlating the level of expression of certain specific genes with the level of GH activity in the liver, or with an expected change in the condition of the liver as the result of GH activity. Excessive GH

The invention relates to a method of diagnosing abnormal levels of

Claim

Page

53; 65pp;

English

Diagnosing abnormal levels of growth hormone activity in liver comprising assaying growth transcriptional activity and protein expression level of hormone-regulatable liver genes, as diagnostic markers of liver pathology

N-PSDB;

2001-007239/01.

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Kopchick JJ, Tiong

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Best Local Similarity 100.
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insertion of a polypeptide into a membrane, or importing a polypeptidi into a cell. The proteins encoded by the EST sequences may be useful into a cell. The proteins encoded by the EST sequences may be useful treating a variety of human conditions. Secreted proteins he therapeutic value, and the identification of new secreted proteins is valuable. ANZ42249 to ANZ42264 and ANZ46464 to ANZ4650 represent
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See Indirecting protein, partoconese 3 sytuchrome P45011A,

See Indirecting protein, partoconese Indirecting Group General P45011A,

See Indirecting Group Group Group General P45011A,

See Indirecting Group G
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                                                                                                                                                                                                                                                                                                                                                       acquired immunodeficiency syndrome; infiammatrory disorders, sociasis, AIDS; embryonic disorder; brain; cerebral coedema; ischaemia; tumour; prostate; cerebrovaṣcular disease; picultary; Cushing's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    liver genes and proteins are useful as diagnostic markers of liver pathology. Assays for the expression of these genes is useful for the diagnosts of liver pathologies associated with gigantism or acromegaly or with diabetes, as other causative agents may act directly or indirectly
                                                         Misc-difference
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                    neurodegenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; MANGO 511; transmembrane protein; diagnostic; asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MANGO 511, variant #3 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU01393 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunological disorder; arthritis; graft rejection; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 LSKLLELTGPKVLACSLA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vfeliqngwflsgvrletgvlsyrfslgaitsnnsgiyrcrcgveppvdihlpalnkwtm 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLPAVQEWGAQEPVHLDSPAIKHQFLL---TGDTQGRYRCRSGLS-----TGWXQ 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           msllatvlllwgftlgpgntlmldsgsepklwaepqsllepwan1tlvcavdlp----tk 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQ-----CDADVPGPPGDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                         Location/Qualifiers
/note= "Encoded by agt"
                                                                                                                                                                                                                                                                                                                    disease; Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21.1%; 29.0%;
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Pred. No. 4.4e-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    variant #3 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunological disorders, infiammatory disorders (e.g. psoriasis and astima), renal disorders, embryonal disorders, brain-related disorders (e.g. cerebral dedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-related disorders, pituitary-related disorders (e.g. castate-related disorders, pituitary-related disorders (e.g. castate-related disorders, pituitary-related disorders (e.g. castate).
                                                               immunological disorder; arthritis: graft rejection: renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psoriasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease;
                                                                                                                                                                                                                                                                              AAU01394 standard; Protein; 299 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents the amino acid sequence of human MANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 299-300; 362pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
disease -
                                                neurodegenerative disease; Parkinson's
                                                                                                                                      Human; MANGO 511; transmembrane protein; diagnostic; asthma
                                                                                                                                                                          Human MANGO 511, variant #4 amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                      sdplel 133
                                                                                                                                                                                                                                                                                                                                                                                                     SKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0039;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-211461/21.
N-PSDB; AAS02105.
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12-MAY-2000; 2000WO-US13228.
                                     16-NOV-2000
                                                                        WO200068383-A2
                                                                                                                                            Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human.
                                                                                                                                                                                                    Leukocyte immunoglobulin like receptor LIR-9sl.
                                                                                                                                                                                                                                            11-APR-2001
                                                                                                                                                                                                                                                                               AAB04182;
                                                                                                                                                                                                                                                                                                                  AAB04182 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vspalmvllciglsigpkthvqagniskatiwaepgsvisrgnsvtircqgtleaqeyri 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDAD---- 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharp JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barnes T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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N-PSDB; AAA54608.
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                                                                                                                           12-MAY-1999;
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Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                               Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or instificient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 111; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAAS4610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-687645/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1999;
1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDAD----
                                                                                                                                                                                                                      and disease states with suppressed immune function.
                                                   Conservative
                                                                                                                                                                             265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0310463
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                                                                        13.8%; Score 91.5;
26.2%; Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borges L;
                                                   18;
                                                   Mismatches
                                                                        DB 21;
                                                   Indels
                                                                                                 Length 265;
                                                27;
                                                Gaps
   48
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128 sdple1 133
                                                                     105 SKLLEL 110
                                                                                                                                79 vkegsp----
                                                                                                                                                                                                 49 -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHOFLLTGDTO---GRYRCRSGLSTGWXQL 104
                                                                                                                                                                                                                                                             19 vspalmvllclglslgprthvqagnlskatlwaepgsvlsrgnsvtlrcqgtleaqeyrl 78
                                                                                                                                epwdtgnpl---epknkarfsipsmtehhagryrcyyyspagwsep 127
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11-APR-2001 (first entry) AAB04180 standard; Protein; 299 Leukocyte immunoglobulin like receptor; LIR; gene therapy; Leukocyte immunoglobulin like receptor LTR-9ml. ⋛

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12-MAY-2000; 2000WO-US13228
                                             16-NOV-2000
                                                                                   WO200068383-A2
                                                                                                                                                                   autoimmunity; autoimmune disorders;
                                                                                                                           Homo sapiens
                                                                                                                                                                   immune system; human.
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Cosman DJ, (IMMV) IMMUNEX CORP Anderson DM, Borges ŗ

99US-0310463

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RESULT
AAU01330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human: MANGO 511; transmembrane protein; diagnostic; asthmatic immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorder; psoriasis; AIDS; embryonic disorder; brain, cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushiny's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or Indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 106; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MANGO 511 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2001
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                          Modified-site
                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disease; Parkinson's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vspalmvllclglslgprthvqagnlskatlwaepgsvisrgnsvtircqgtleaqeyrl 78
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                      /note-
69..74
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64..66
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60..65
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54..59
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43..46
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                                                 *Protein kinase C phosphorylation
"N-myristylation site"
                                                                                                      "Immunoglobulin (Ig)-like
                                                                                                                                                               "N-myristylation site"
                                                                                                                                                                                                                     "N-myristylation site"
                                                                                                                                                                                                                                                                          "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                               "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                    "Mature MANGO 511"
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Signal peptide"
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Pred. No. 0.012;
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                                                                                                          domain"
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transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunological syndrome), inflammatory disorders (e.g. psoriasis and astima), renail disorders, inflammatory orders, ferrin-related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischemia), tumours, prostate-related disorders, pitultary-related disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's disease).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
Sequence
                                                                                                                       The sequence represents the amino acid sequence of human MANGO 511
                                                                                                                                               Claim 8; Fig 7; 362pp;
                                                                                                                                                                                   New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 151, TANGO 519 or TANGO 509 secreted or transmembrane protein useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                          Kirst SJ,
                                                                                                                                                                                                                                                                                                (MILL+) MILLENNIUM PHARM INC
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DB; AAS02065.
                                                                                                                                                                                                                                                                        Sharp JD,
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AA;
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289..2
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285..299
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238..2
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207..2
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193..198
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ote- "Casein kinase II
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                                                                                                                                                                                                                                                                        Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Asn
                                                                                                                                               English
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                                                                                                                                                                                                                                                                        Barnes T,
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                                                                                                                                          Query Match
Best Local
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                                                                                                     1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDAD----
   SKLLEL 110
                          vkegsp-----
                                                    -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQL 104
                                                                             vspalmvllclglslgprthvqagnlskatlwaepgsvisrgnsvtircqgtleaqeyrl
                                                                                                                                          Similarity
                                                                                                                              Conservative
                          epwdtqnpl---epknkarfsipsmtehhagryrcyyyspagwsep
                                                                                                                                          13.8%;
                                                                                                                              18;
                                                                                                                                          Score 91.5; DB Pred. No. 0.012;
                                                                                                                              Mismatches
                                                                                                                                                       DB 22;
                                                                                                                              48;
                                                                                                                              Indels
                                                                                                                                                       Length
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sdplel 133

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RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                            The sequence represents the amino acid sequence of human MANGO 511 warinst #1 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the disgnosis, prognosis and treatment of immunological disorders (c.g. arthritis, graft rejection and acquired immunodeficiency syndrome). Inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders
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                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 295-296; 362pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding IMTERCEPT 307, MANGO 511, TANGO 351, TANGO 353, TANGO 359 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MANGO 511, variant #1 amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-SEP-1999;
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                                                                                                                                                                                                                                                                                                                (e.g. cerebral ocdema), cerebrovascular diseases (e.g. ischemia),
tumours, prostate-related disorders, pitultary-related disorders (e.g.
cushing's disease) and meurodegencrative diseases (e.g. Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative disease; Parkinson's
128
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sdplel 133
                              SKLLEL 110
                                                             vkegsp----
                                                                                                                        vspalmvllclglslgprthvqagnlskatlwaepgsvlsrgnsvtircqgtleaqeyrl
                                                                                                                                                         MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-211461/21.
DB; AAS02102.
                                                                                         -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQL 104
                                                                                                                                                                                                                                                                      299
                                                                                                                                                                                          Conservative
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                                                             epwdtgnpl---epknkarfsipsmtehhagryrcyyyspagwsep 127
                                                                                                                                                                                                     13.8%; Score 91.5; DB 22; 26.2%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser
                                                                                                                                                                                       18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnes T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease.
                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kingsbury
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                      Length
                                                                                                                                                                                          27;
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                 RESULT
AAU01392
ID AAU
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                                                                                                                                                                                                         Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                            The sequence represents the amino acid sequence of human MANGO 511 variant #2 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome), inflammatory disorders (e.g. psortasis and asthma), renal disorders, embryonic disorders, brain-related disorders (e.g. screbtor), cerebrovascular diseases (e.g. ischemia), tempors, prostate related disorders, pituitary-related disorders (e.g. cushors), prostate related disorders, pituitary-related disorders (e.g. cushors).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acquired immunodeficiency syndrome: inflammatory disorders: psortasis: ALDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease; neurodegenerative disease; Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU01392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361. TANGO 499 or YANGO DUP SCLEENING THE FIRST STATES AND TREATMENT OF ARTHRITIS, disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mucheic acid encoding IMTERCEPT 307, MANCO 511, TANGO 351, TANGO 490 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-211461/21.
N-PSDB; AAS02103.
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 297-298; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2000; 2000WO-US25982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; MANGO 511; transmembrane protein; diagnostic; asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human MANGO 511, variant #2 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU01392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunological disorder; arthritis; graft rejection; renal disorder;
  128
                                 105
                                                                     79
                                                                                                       49
                                                                                                                                        19
                                                                                                                                                                          1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
sdplel 133
                                                                   vkegsp----
                                 SKLLEL 110
                                                                                                    -VPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQL 104
                                                                                                                                      vspalmvllclglslgprthvqagnlskatlwaepgsvisrgnsvtircqgtleaqeyrl 78
                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                299 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sharp JD,
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 299
                                                                   epwdtgnpl---epknkarfsipsmtehhagryrcyyyspagwsep 127
                                                                                                                                                                                                                          13.8%; Score 91.5; DB 26.2%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser CC,
                                                                                                                                                                                                            18;
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                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnes T,
                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kingsbury
                                                                                                                                                                                                                                           Length 299;
                                                                                                                                                                                                            Indels
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RESULT
AAW69233
                                                                                 Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                          allergy, colorectal or breast cancer. Jymphöma; leukaemia, infection by intracellular pathogens etc). The antagonists are also useful as immunomodulators and inhibitors of viral (e.g. human immune deficiency or dengue viruses) entry into cells. The proteins may also be used to screen for aspecific binding agents, i.e. (antisygonists, for raising antibodies (Ab), and for identification of particular cells or tissues. The Ab can be used therapentically as antagonists, as assay reagents for dispositic determination of the proteins. The DNA and its fragments are affinity purification of the proteins. The DNA and its fragments are sectul as hybridisation probbes or primers for isolating related gence, in any pridisation cromosome mapping) and dispositically to measure
                                                                                                                                                                                                                                                                                                                                                           This sequence is the Fc receptor like III protein (FCR-III) of the invention cells containing the DNA are used to express the recombinant protein, and to screen for specific (ant)agonists. The proteins are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding Fo receptor-like polypeptides or their fragments - and related vectors, transformed cells and antibodies useful for treating and diagnosing diseases of the haematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For receptor-like protein; phagocytosis inducer; rheumatoid arthritis; immune complex related disease; systemic lupus eryhematosus; allergy, hemolytic anaemia; thrombocytopaenia; anaphylaxis; cancer; lupuboma; leukaemia; infection; immunomodulator; viral entry inhibitor; therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW69233 standard;
                                                                                                                                                                                                                                                                                                         to induce phagocytosis, and their (ant)agonists are used to treat immune complex related diseases (e.g. rhemmatoid arthritis, systemic lupus erythematosus, haemolytic anaemia, thrombocytopaenia, anaphylaxis,
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 23; Fig 3A; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAV44826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9831806-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCR-III protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW69233;
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               immune systems
                                                                                                                 expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy M,
                                                                                 623
    Conservative
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970S-0034205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
               13.7%; Score 90.5; DB 28.3%; Pred. No. 0.04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ni J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "mature FcR-III"
  10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               À
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
                               DB 19;
  38;
                               Length 623;
  Indels
51;
Gaps
  6
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Claim 4; Page 89-91; 112pp; English

suppressed

inmune

function

This sequence represents a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-pmb17. This sequence can be administered

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AAW82552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic; treatment; disorder; ITIM; MRC class I receptor; inhibito cyroplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; LIR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW82552;
Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                       N-PSDB; AAV69338
                                                                         WPI; 1998-609990/51
                                                                                                              Cosman
                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                          24-APR-1997;
                                                                                                                                                                                                                               23-APR-1998;
                                                                                                                                                                                                                                                                    29-OCT-1998
                                                                                                                                                                                                                                                                                                   W09848017-A1.
                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reg ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIR-pbm17; immunoregulator; leukocyte immunoglobulin-like receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human LIR-pbm17 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
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                                                                                                                                                                                        97US-0842248
                                                                                                                                                                                                                               98WO-US08244
                                                                                                                                                                                                                                                                                                                                                             /note-
625..62
                                                                                                                                                                                                                                                                                                                                                                                                  /note= "ITIM YxxL/V motif"
595..598
                                                                                                                                                                                                                                                                                                                                                                                                                                         543..546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= extracellular_domain
17..631
                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          444..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- LIR-pmb17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein; 631
                                                                                                                                                                                                                                                                                                                                                                . 628
                                                                                                                                                                                                                                                                                                                                           "ITIM YxxL/V motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "ITIM YxxL/V motif"
                                                                                                                                                                                                                                                                                                                                                                                "ITIM YXXL/V motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --PVHLD----SPAIKHQFLLTGDTQ---GRYR 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inhibitor;
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     having TTMs are inhibitory receptors mediating negative signalling, whilst those lacking ITTMs are activatory receptors. Fallure of a receptor that mediates negative signalling could result in autoimmune diseases, whilst fallure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to produce probes for detecting LIR nucleic acids or isolating LIR DNA from the problem of the problem of the problem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amounts of LIR polypeptide. LIR-P3G2 and certain other LIR family members contain cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (ITIMS), whilst other LIR family members lack ITIMS. By analogy with the structure and function of known MHC Class I receptor molecules, LIRs
                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORF
                                                                                                                                                                                                                                                                                       12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB04177 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other species.
                                                                        Example 9;
                                                                                                              Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                              12-MAY-1999;
                                                                                                                                                                                                                                                                                                                     16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                 W0200068383-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukocyte immunoglobulin like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapeutically to treat disorders associated with insufficient/defective
                                                                                                                                                                                                                                                                                                                                                                                                                     Leukocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chyyssagwsepsdplel
                                                                                                                                                                                                       DJ,
                                                                                                                                                             AAA54601.
                                                                                                                                                                                                                                                                                                                                                                                                        lmmunoglobulin
lty; autoimmune
                                                                      Page 95-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                         2000WO-US13228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein: 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%;
                                                                                                                                                                                                     ₽,
                                                                      117pp;
                                                                                                                                                                                                                                                                                                                                                                                                        like recept
disorders;
                                                                                                                                                                                                     Borges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                      English
                                                                                                                                                                                                                                                                                                                                                                                                                    receptor; LIR; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor pbm17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVHLD----SPAIKHQFLLTGDTQ---GRYR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.5;
No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                        immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s----s
                                                                                                                                                                                                                                                                                                                                                                                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isolating LIR DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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CCCCXXXXPPTXXX

immunological disorders

Fig

227pp;

English

New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, the and diagnosing hemorrhagic disorders, thrombotic diseases and

treating

N-PSDB Qian

2001-080877/09 DB; AAF29472.

Busfield

SJ, Kingsbury

Villelal J,

Jandrot-Perrus

ĭ

Vainchencker

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G111

DS;

G

(MILL-) MILLENNIUM PHARM INC

The present sequence is given in a specification relating to an isolate nucleic acid molecule encoding a platelet mombrane glycoprotein recepto glycoprotein vi (GPVI), also called TANGO 268. The GPVI polynucleotides

polypeptides and

their modulators,

e.g.

nucleic

acids

receptor isolated 30-JUN-1999; 06-DEC-1999; 14-FEB-2000;

99US-0454824. 2000US-0503387. 2000WO-US18152

9905-0345468

04-JAN-2001

30-JUN-2000;

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AAB61263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
                                                                                                                                                                                                                              Human: monocyte inhibitory receptor precursor; famso 268 cardian cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarterioscierotic; hemmostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; hemmorrhagic disorder; ischaemia; cardiovascular disease; immunological disease; liver o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune discases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                          04-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                      WO200100810-A3
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                       Californ
                                                                                                                                                                                                                                                                                                                  Human monocyte inhibitory receptor precursor
                                                                                                                                                                                                                                                                                                                                                                   AAB61263
                                                                                                                                                                                                                                                                                                                                                                                           AAB61263 standard; Protein; 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    chyyssagwsepsdple1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viswgspvtiwcqgsleaqeyqldkegspepldrnnplepknkarfsipsmtqhhagryr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQEWG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mtpaltallclglslgprtrvqagpfpkptlwae-----s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----AQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PVHLD----SPAIKHQFLLTGDTQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                            cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                                                                             stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW69234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPYT These disorders include bleeding disorders (e.g. thromboxic disorders (e.g. thromboxic contents) blood vessel injury, thromboxic disorders (e.g. thromboxic colusion of the coronary arguments (e.g. stroke a fixed stroke a st
                                  WPI: 1998-414105/35.
N-PSDB; AAV44827.
                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For receptor-like protein; phagocytosis inducer; rheumatoid arthritis; immune complex related disease; systemic lupus erythematosus; allergy; hemolytic anaemia; thrombocytopaenia; anaphylaxis; cancer; lupuboma; leukaemia; infection; immunomodulator; viral entry inhibitor; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity
Nucleic acid encoding Fc receptor-like polypeptides or their
                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                            18-JUN-1997;
21-JAN-1997;
                                                                                                                                                                                                                20-JAN-1998;
                                                                                                                                                                                                                                                     23-JUL-1998
                                                                                                                                                                                                                                                                                     WO9831806-A2
                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FcR-IV protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW69234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW69234 standard; Protein; 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chyyssagwsepsdplel 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          viswgspvtiwcqgsleaqeyrldkegspepldrnnplepknkarfsipsmtehhagryr 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VQEWG-----AQE-----PVHLD-----SPAIKHQFLLTGDTQ---GRYR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mtpaltallclglslgprtrvqagpfpkptlwae------pg----s 37
                                                                                      Murphy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                            97US-0049872
97US-0034205
                                                                                                                                                                                                                98WO-US01184.
                                                                                                                                                                                                                                                                                                                                         /note-
17..47:
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         .472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.2%;
                                                                                      Z.
                                                                                                                                                                                                                                                                                                                                                        "signal peptide"
                                                                                                                                                                                                                                                                                                                        "mature FcR-IV"
                                                                                      ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 87.5; DB Pred. No. 0.093;
                                                                                      01sen
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                                                                                      ,SH
                                                                                      Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stroke and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myocardial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
AAW82551
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  Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                    Doma in
                                                                                                                                                                             Key
                   Domain
                                                                                      Protein
                                                                                                                         Domain
                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                            AAW82551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 el 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 EL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA
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fragments - and related vectors, transformed cells and antibodies, useful for treating and diagnosing diseases of the haematopoietic
                                                                                   and immune systems
23; Fig 4A; l41pp; English
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minis sequence is the Fo receptor-like V protein (FRF-IV) of the invention. Cells containing the DNA are used to express the recombinant protein and to screen for specific (ant)sayonists. The proteins are used to induce phagocytosis, and their (ant)sayonists are used to treat immune complex related diseases (e.g., rheumatosid arrhritis, systemic lupus carpine to the protein of the protein and protein by allery, colorectal or breast cencer, lymphoma, leukaemia, infection by allery, colorectal or breast cencer, lymphoma, leukaemia, infection by allery, colorectal or breast cencer, lymphoma, leukaemia, infection by cintracellular pathogens etc). The antagonists are also useful as complex relations and inhibitors of viral (e.g., human immune deliciency or dengue viruses) entry into cells. The proteins may also be used to screen complex conditions and interpretation of particular cells or tissues. The Ab can be used therapeutically as antagonists, sa assay reagents for diagnostic condition of the levels of expression of the proteins and for a fitner with protein and the frameworks. affinity purification of the proteins. The DNA and its fragments are useful as hybridisation probes or primers for isolating related genes, situ hybridisation (chromosome mapping) and diagnostically to measure mRNA expression. 'n

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8 LLLWGVTWGPVTEAAIFYETOXSLWAE-----SEHXLKTLGQCDA------DVPG 51
                                       8 llclglslgpsthmqagplpkptlwaepgsviswgnsvtiwcqgtleareyrldkeespa 67
PPGDSRLPAVQEWGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                                                                      Conservative
                                                                                                                                          12.9%;
                                                                                                                      11; Mismatches
                                                                                                                                          Score 85.5; DB
Pred. No. 0.11;
                                                                                                                                                           DB 19; Length 472;
                                                                                                                         44; Indels
                                                                                                                         33;
                                                                                                                   Gaps
                                                                                                                         S
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p.....q
-wdrqnpl---epknkarfsipsmtedyagryrcyyrspvgwsqpsdpl 113
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LIR-pbm2; immunoregullator; leukocyte immunoglobulin-like receptor;
therapeutic; treatment; disorder; ITIM; MIRC class I receptor; inhibito
cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW82551 standard; Protein; 448 AA
                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             09-FEB-1999
                                                                                                                                                            negative signalling; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
Location/Qualifiers
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inhibitor;

260.

280

/label- LIR-pmbhh

/label- signal

/label= transmembrane_domain /label= extracellular_domain 17..448

/label- cytoplasmic_domain

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                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                 ₽
                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having TTMMs are inhibitory receptors mediating negative signalling, whilst those lacking TTMMs are activatory receptors. Failure of a receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to produce probes for detecting LIR nucleic acids or isolating LIR DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amounts of LIR polypeptide. LIR-P3G2 and certain other LIR family members contain cytopiasmic immunoreceptor tyrosine-based inhibitory motifs (ITINS), whilst other LIR family members lack TIIMS. By analogy with the structure and function of known MHC class I receptor molecules, LIRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-pmb2. This sequence can be administered therepoutleally to treat disorders associated with insufficient/defective
                                          Human gp49 HM18 polypeptide
                                                                          17-JUL-1998
                                                                                                       AAW53463;
                                                                                                                                     AAW53463 standard; Protein; 448 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 85-86; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with suppressed immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV69337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-609990/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reg ion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                               114 el 115
                                                                                                                                                                                                                                            109 EL 110
                                                                                                                                                                                                                                                                        68 p-----wdrqnpl---epknkarfs1psmtedyagryrcyyrspvgwsqpsdpl 113
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                     52 PPGDSRLPAVQEWGAQEPVHLDSPAIKHQF ·-- LLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                                                                                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                                                                                                                                                 B LLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDA------DVPG 51
                                                                                                                                                                                                                                                                                                                                   llclglslgprthmqagplpkptlwaepgsviswgnsvtiwcqgtleareyrldkeespa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 AA
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-0842248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "ITIM motif"
442..445
                                                                                                                                                                                                                                                                                                                                                                                                               12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "IT'IM motif"
                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 84.5; DB
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                              44;
                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 448;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          members
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bone marrow; Human; gp49;

cell-surface member; FceRI

HM18; HM43; immunoglobulin; immune response; mast cell;

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PXX PXX SXX XXX DXX
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                                                                                                                                                                                                                                                                     AAB04176
                                                                                                                                                                                                                                                                                    RESULT 17
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents human 9949 polypeptide HM18. The present invention also describes: (1) a fusion polypeptide comprising a human 9949 component and Foest or a detectable marker; (2) a recombinant nucleic acid encoding human 9949 or a human 9949-Foest [siston as above; (3) a cell or vector comprising the recombinant nucleic acid as in (2), and (4) an antibody which selectively binds to 9949. Manmallan 9949 or its related DMA can be used to treat an undestred immune response, especially a mast cell-related disease.
                                                           WO200068383-A2
                                                                                                                     autoimmunity;
                                                                                                                                                                                             11-APR-2001
                                                                                                                                                                                                                            AAB04176;
                                                                                                                                                                                                                                                       AAB04176 standard; Protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 1A-B; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful to treat undesired immune responses, especially mast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell-surface member of immunoglobulin super-family,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-193318/17.
12-MAY-2000; 2000WO-US13228.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-SEP-1997;
                              16-NOV-2000
                                                                                                                   Leukocyte immunoglobulin like receptor; LIR; gene thorapy; autoimmunity; autoimmune disorders; immune system; human.
                                                                                                                                                                Leukocyte immunoglobulin like receptor pbm2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                 114 el 115
                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LLLWGVTWGPVTEAA1FYETQXSLWAE-----SEHXLKTLGQCDA------DVPG 51
                                                                                                                                                                                                                                                                                                                                                            EL 110
                                                                                                                                                                                                                                                                                                                                                                                         p----q
                                                                                                                                                                                                                                                                                                                                                                                                                     PPGDSRLPAVQEWGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                  llclglslgprthmgagplpkptlwaepgsviswgnsvtiwcqgtleareyrldkeespa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV23273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Austen KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         wdrqnpl---epknkarfsipsmtedyagryrcyyrspvgwsqpsdpl 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castells MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 84.5; DB 19;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Katz HR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33,
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RESULT 18
AAW82553
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                                                                                                                                            LIR-phonew; immunorequilator; leukocyte immunoqulobulin like receptor; therapeutic; treatment; disorder; TTM; MRC class I receptor inhibito cytoplasmic immunoreceptor tyrosine-based inhibitory mortif; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Most cells transformed with a vector which are capable of expressing a lewkcyter immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoLimnunc glaspesses and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosman DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAY-1999;
                  Domain
                                    Domain
                                                                        Domain
                                                                                                                                                                                  Human LIR-pbmnew protein.
                                                                                                                                                                                                    09-FEB-1999
                                                                                                                                                                                                                                       AAW82553 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 9; Page 91-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                       Protein
                                                                                                                    Homo sapiens.
                                                                                         Peptide
                                                                                                                                                                                                                                                                                   114 el 115
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                                                                                                                                                                                                                                                                                                                                                         llclglslgprthmqagplpkptlwaepgsviswgnsvtiwcqgtleareyrldkeespa 67
                                                                                                                                                                                                                                                                                                                                                                            LLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDA-----DVPG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-687645/67
                                                                                                                                                                                                                                                                                                                       p------
                                                                                                                                                                                                                                                                                                                                       PPGDSRLPAVQEWGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                                                                                                                                                                                                                                                                                                                                                    n 12.8%;
Similarity 27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA54600
                                                                                                                                    signalling; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                          448 AA;
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                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-0310463.
                  580..
                                    /label-
457..579
/label- cytoplasmic_domain 554..557
                                                      /label= extracellular_domain
17..590
                                                                               /label- signal
                           /label≖ transmembrane_domain
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                       wdrqnpl---epknkarfsipsmtedyagryrcyyrspvgwsqpsdpl 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DM.
                  . 590
                                     . 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117pp; English
                                            LIR-pmbnew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Borges
                                                                                                                                                                                                                                                                                                                                                                                              11; Mismatches
                                                                                                                                                                                                                                        590
                                                                                                                                                                                                                                                                                                                                                                                                    Score 84.5; DB
Pred. No. 0.13;
                                                                                                                                   disease; suppressor;
                                                                                                                                                                                                                                        ⋛
                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                              44:
                                                                                                                                                                                                                                                                                                                                                                                                             Length 448;
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                                                                                                                                      LIR
                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                      inhibitor;
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 XEEXEXTXC
                                                                                                 AAB04178
                                                                                                                                                                                                                                                Matches
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                                                                        AAB04178;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                        61
                                                                                                          19
                                                                                                                                                                                           48
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This sequence represents a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-pubbrew. This sequence can be administered therapeutically to treat disorders associated with insufficently defective amounts of LIR polypeptide. LIR-p302 and certain other LIR family members contain cytoplasmic liminoreceptor tyrosine-based inhibitory motifs (ITIHS). Whilse other LIR family members lack KINHS. By analogy with the structure and function of known MHC Class I receptor molecules, LIRs
                                                                                                         diseases, whilst failure of a receptor mediating activatory signaling could result in suppressed immune function. They are also useful to produce probes for detecting LIR nucleic acids or isolating LIR DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 94-96; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV69339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-609990/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-APR-1997;
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                                                                             other species.
                                                                                                                                                                                                                                        receptor that mediates negative signalling could result in autoimmune
                                                                                                                                                                                                                                                                          having ITIMs are inhibitory receptors mediating negative signalling, whilst those lacking ITIMs are activatory receptors. Failure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with suppressed immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating autoimmune diseases or disease states associated
590 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0842248
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                                                                                                                    isolating LIR DNA from
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Best Local Similarity
autoimmunity; autoimmune disorders; immune system; human
                     Leukocyte immunoglobulin like receptor; LIR; gene therapy,
                                                                 Leukocyte immunoglobulin like receptor pbmnew.
                                                                                                                11-APR-2001
                                                                                                                                                                                                     AAB04178 standard; Protein; 590 AA
                                                                                                                                                                                                                                                                                                                   113 lelvatgfyaeptlla 128
                                                                                                                                                                                                                                                                                                                                                              108 LEL--TG----PKVLA 117
                                                                                                                                                                                                                                                                                                                                                                                                       dkeglpwarkrqnplepgakakfhipstvy-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mtltlsvliclglsvgprtcvqagtlpkptlwaepasvlargkpvtlwcqqpleteeyrl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLK-----TL---GQCDA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                             (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.3%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                       -dsagryrcyyetpagwsepsdp 112
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Region

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Best Local :
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                                                                       LIR-18A3; immunorogulator; leukocyte immunoglobulin-like receptor; LIR; therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhibitor cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be
          Doma in
                                                                                                                                         09-FEB-1999
                                                                                                                                                                            AAW82545 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 100-101; 117pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687645/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                       Homo sapiens
                                                                                                                      Human LIR-18A3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leukocyte
                            Peptide
                                                                                                                                                                                                                          113
                                                                                                                                                                                                                                           108 LEL--TG----PKVLA 117
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                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                               mtltlsvliclglsvgprtcvqagtlpkptlwaepasviargkpvtlwcqgpleteeyrl 60
                                                                                                                                                                                                                         lelvatgfyaeptila 128
                                                                                                                                                                                                                                                             dkeglpwarkrqnplepgakakfhlpstvy-----dsagryrcyyetpagwsepsdp 112
                                                                                                                                                                                                                                                                               DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                                                                                                                                                                                   MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLK----
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                                                                                                                                                                                                                                                                                                                                                                                                                            the gene therapy of disorders mediated directly or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e immunoglobulin-like receptor (LIR) nucleic acids, useful for autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                  and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                  590 AA;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9908-0310463
 /label- extracellular_domain
                   /label- signal
                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            12.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Borges
                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                             652
                                                                                                                                                                                                                                                                                                                                              Score 81.5;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                              . 44;
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                                                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                       590;
                                                                                                                                                                                                                                                                                                                                      27:
                                                                                           inhibitor;
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                                                                                                             В
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  AAB04170
                                                                                                                                                 Query Match
Best Local S
Matches 41
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                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-609990/51.
N-PSDB; AAV69329.
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                         produce probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09848017-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                       103
                                                                                           61
                                                                                                                                                 Local Similarity
nes 41; Conser
          21
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                                                       QLSKLLELT ----
                                                                                                                                                                                               652 AA;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0842248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US08244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             646..649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      485..652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460..484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17..652
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                                                                                                                                                          11.9%;
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contain cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (ITIMS), whilst other LIR family members lack ITIMS. By analogy with the structure and function of known MHC Class I receptor molecules, LIRs having ITIMS are inhibitory receptors mediating negative signalling, whilst those lacking ITIMS are activatory receptors. Failure of a receptor that mediates negative signalling could result in autoimune diseases, whilst follure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful,
e.g. for treating autoimmune diseases or disease states associated
with suppressed immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel leukocyte immunoglobulin-like receptor (This polypeptide LIR-18A3. This sequence can be administered therappeutically to treat disorders associated with insufficient/defective amounts of LIR polypeptide. LIR-P3G2 and certain other LIR family members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 59-61; 112pp; English
109 essdplelvvtgayikptlsaqpspvvnsggnvilgcdsqvafdgfs 155
                                                                                                                                                                                                                                                                                                                                                                 1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                           ggetgeyrlyrekktalwitripgel----vkkgqfpipsitwehagryrcyygsdtagrs
                                                                                                                                                                                                                     VQE------WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                                           mtpiltvliclglslgprthvqaghlpkptlwaepgsvi-----tqgspvtlrcqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note: "ITIM motif"
616..619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note: "ITIM motif" 564..567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting LIR nucleic acids or isolating LIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "ITIM motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "ITIM motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytoplasmic_domain
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                                                                               -----GPKVLAC--SLALDGAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 78.5; DI
Pred. No. 1.1;
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 652;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA from
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                                                                                                                                                                                                                                                                                                                                                                                                                  Host cells transformed with a vector which are capable of expressing a leukocyte imminoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of discorders mediated directly or indirectly by defective or insufficient amounts of anyof the LIR polypeptides can be used to treat autoimmine of seases and disease states with suppressed immune incretion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human.
                            Nostoc NspI restriction endonuclease (NspIR).
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687645/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cosman DJ, Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte immunoglobulin like receptor (LIR) 18A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB04170 standard; Protein; 652 AA
 NspI restriction endonuclease; NspIR; Nostoc; NspI methylase; NspIm
                                                       13-JUN-2000
                                                                                                        AAY57323 standard; Protein; 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 66-68; 117pp; English.
                                                                                                                                                                     109 essdplelvvtgayikptlsaqpspvvnsggnvilqcdsqvafdgfs 155
                                                                                                                                                                                                103 QLSKLLELT----
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                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                             _
                                                                                                                                                                                                                                                                                                  1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                       ggetgeyrlyrekktalwitripgel---vkkggfpipsitwehagryrcyygsdtagrs 108
                                                                                                                                                                                                                                                  VQE-----WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                         mtpiltvliclglslgprthvqaghlpkptlwaepgsvi-----tqgspvtlrcqg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA54592
                                                                                                                                                                                                                                                                                                                                                                                              652 AA;
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                        11.9%; Score 78.5;
24.6%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                            16; Mismatches
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                                                                                                                                                                                                -GPKVLAC -- SLALDGAS 126
                                                                                                                                                                                                                                                                                                                                                       DB 21;
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                                                                                                                                                                                                                                                                                                                                                       652;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a Napi restriction endonuclease (NapiR), obtained from Nostoc sp. The NapiR is recombinantly obtained using a Napi methylase (NapiR) promodified E. colik strain RigammabE3). The endonuclease and methylase are useful for creating recombinant DNA molecules. The present sequence represents a Nostoo NapiR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated DNA encoding the NspI endonuclease and methylase, useful for creating recombinant DNA molecules - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US6027929-A
Claim 2; Page 20-21; 30pp; Japanese
                          New peptide - useful for inhibiting dephosphorylase
                                                     N-PSDB; AAX88978
                                                                WPI; 1999-422622/36
                                                                                                                    12-DEC-1997;
                                                                                                                                             12-DEC-1997;
                                                                                                                                                                       29-JUN-1999
                                                                                                                                                                                                JP11169184-A
                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                           Dephosphorylase inhibiting protein; p91; tyrosine phosphatase SHP-1; SHP-2; inositol-5-phosphate SHIP: phosphating tyrosine;
                                                                                                                                                                                                                                                                                                  Mouse dephosphorylase inhibiting p91-like protein #4
                                                                                                                                                                                                                                                                                                                             16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                        AAY24321;
                                                                                                                                                                                                                                                                                                                                                                                AAY24321 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 3; 14pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-AUG-1998;
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                                                                                           (UYOK-) UNIV OKAYAMA
                                                                                                                                                                                                                                                  immunoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                             132 dhrfp-merwgasepphltsmndneikrkfqllkkdtsgnhnllksrscerciktg
                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 DSRLPAVQEWGAQEPVHLDS---PAIKHQF-LLTGDTQGRYR-----CRSGLSTG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                    97JP-0362285
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                                                                                                                                             97JP-0362285
                                                                                                                                                                                                                                                  immunomodulatory agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.4%;
                                                                                                                                                                                                                                                                                                                                                                                635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75.5; DB Pred. No. 0.72; S; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
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RESULT 2
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Best Local S
Matches 33
of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                            The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes new proteins for inhibiting dephosphorylase. The proteins can be combined with tyrosine phosphatase SHP-1, SHP-2 or inositol-5-phosphatase SHIP by phosphating tyrosine. The present invention also describes an immunoreceptor comprising one the above proteins, and DNA coding the above proteins. The new proteins can be used as an immunomodulatory agent. The present sequence
                                                                                                                                      Claim 8;
                                                                                                                                                                                 and/or diagnosis of the
                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                        Ota T,
                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST
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02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human protein sequence SEQ ID NO:11629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001
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                                                                                                                                                                             Primar sets for synthesizing polynucleotides, particularly the 5602 full-longth coMas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000;
                                                                                                                                                                   tull-length cDNAs -
                                                                                                                                                                                                                                                                        Ishii S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VFLLLWGVTWGPVTEA----AIFYETQXSLWAESEHXLKTLGQCDADV--PGPPGDSRLP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVQEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQLSKLLEL 110
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32; Conser
                                                                                                                                                                                                                                                                                      Isogai T,
                                                                                                                                    SEQ ID 11629; 2537pp +
                                                                                                                                                                                                                                                                      Suglyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a protein
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2000JP-0183767.
2000JP-0241899.
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99JP-0300253
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T, Wakamatsu
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Pred. No. 2.5;
12; Mismatches
                                                                                                                                    CD ROM; English
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   in gone therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs The primers are also useful for the detection and/or diagnosis of the shootmality of the price accorded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs are primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH0324 represent human cDNAs sequences: AAH03246 to AAH0324 consistent could sequences; and AAH03629 to AAH0362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                             of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                             represent oligonucleotides, all of which are used in the exemplification
                                                                   33
                                                                                                                                                                 Local Similarity
                                                                   AESEHXLKTLGQCDADVPGPPG------DSRLPAVQEWGAQEPVHLDSP-AIKHQ
addeavlnliaecewdlgrppgstsfsqkgreadsr...-gsqesrhllspqlvqyq
                                                                                                                                                                                                                                                                                                   458 AA;
                                                                                                                                  Conservative
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                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                Score 75;
                                                                                                                                  Mismatches
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                                                                                                                                  23;
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81

FLLTGDT -- QGRYRCRSGL-----STGWXQL 104

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RESULT
AAG64131
ID AAG
                                                                       AAG64131 standard; Protein; 647
Leucine
                        25-SEP-2001
                                                AAG64131
multi-repeating
                       (first entry)
sequence
71
polypeptide
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antiinflammatory; Leucine multi-repeating sequence 71; cancer; haemopathy; human immunodeficiency virus; HTV; infection; immunopatha inflammatory disease; cytostatic; virucidal; immunomodulatory; haemostatic.

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Unidentified
                            15-JAN-2001;
                                  WO200155374-A1
                            2001WO-CN00045
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Mao Y,
                                                 (BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
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2001-476206/51.

26-JAN-2000; 2000CN-0111505

HIV infection, Leucine multi-repeating sequence 71 and encoded polynuclootide applicable in diagnosis and treatment of malignant tumor, hemop N-PSDB; AAH48534. immunological diseases treatment of malignant tumor, hemopathy, and various inflammations

Claim Page 30-32; Chinese

The invention relates to an isolated polypeptide of leucine multi-repeating sequence 71 comprising a sequence of 647 amino acids, or its fragment, analogue or derivative. The polypeptide and the polynucleotide encoding it are useful in the diagnosis and treatment

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RESULT
NAY24322
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Best Local
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                                                                                                                                                                                                                                                                                                                                    The present invention describes new proteins for inhibiting dephosphorylase. The proteins can be combined with tyrosine phosphatase SHP-1, SHP-2 or inositol-5-phosphatase SHIP by phosphating tyrosine. The present invention also describes an immunoeceptor comprising one the above proteins, and DNA coding the above proteins. The new proteins can be used as an immunomodulatory agent. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dephosphorylase inhibiting protein; 991: tyrosine phosphatase SHP-2, inositol-5-phosphate SHIP; phosphating tyrosine; immunoreceptor; immunomodulatory agent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 22-24; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP11169184-A
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                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide - useful for inhibiting dephosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX88979
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                                                                                                                                                                                                                                                                                                                   represents a protein from the present invention.
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                                              215 vellvsgnlqkptikaepgsvitskramtiwcq-----gnldaev-----yflhne 260
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les 29; Conservative
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   62 QEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                       Local Similarity
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                                                                                                 VFLLLWGVTWGPVTEA----AIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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Pred. No.
                                                                                                                                                                   Score 74.5;
Pred. No. 3
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                                                                                                                                                                                                                                                                        RESULT
LIR-pbm8; immunoregulator; leukocyte immunoglobulin-like receptor; LIR; therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhibitor;
                                                                            Human LIR-pbm36-2 protein
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RESULT 2
AAY24320
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Best Local Similarity
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                                               AAW82548;
                                                                                     AAW82548 standard; Protein; 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                            215 vellvsgnlqkptikaepgsvitskramtiwcq-----gnldaev-----yflhne 260
                                                                                                                                                                                                   261 ksqktqstqtlqqpgnkgrffipsvtqqhagqyrcycyssagwsqpsdtlel 312
                                                                                                                                                                                                                                               62 QEWGAQEPVHLDSPAIKHQFLLTGDTQ---GRYRCRSGLSTGWXQLSKLLEL 110
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                                                                                                                                                                                                                                                                                                                                                                                       32;
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(first entry)
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Pred. No. 3.6;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                       receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 73-74; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV69334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor.
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                           other species.
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                                101 WXQLSKLLEL 110
107 wsepsdple1 116
                                                                      60
                                                                                                    48
                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                     1 MSMLVVELLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQ-----CDA-----
                                                                                                                                  mtpiltvliclglslgprthvqagtlpkptlwaepgsvi-tggspvtlwcggiletqeyr 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              suppressed immune function
                                                                   lyrekktapwitrip-----
                                                                                                  ---DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-G 100
                                                                                                                                                                                                                                                                                          289 AA;
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0842248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label extracellular_domain 17..289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label-_transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- LIR-pmb36-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ∕label∽ signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         detecting LIR nucleic acids or isolating LIR DNA from
                                                                                                                                                                                                                         11.2%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280
                                                                                                                                                                                                        15;
                                                                 qeivk-----kgqfplpsitwehtgryrcfygshtag 106
                                                                                                                                                                                                                    Score 74;
Pred. No.
                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                       DB 19;
                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                    Length 289;
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                        34..
                                                                                                                                                                                                      Gaps
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DEX P
                                                                                                                                                                  AAW82544
                                                                                                                                                                                             RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Human LIR-P3G2 protein
                                                 09-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human;
                                                                                                AAW82544;
                                                                                                                                           AAW82544 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB04173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB04173 standard; Protein; 289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Host cells transformed with a vector which are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 79-80; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-687645/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2000; 2000WO-US13228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200068383-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nomo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte immunoglobulin like receptor pbm36-2.
                                                                                                                                                                                                                                                                   107 wsepsdplel 116
                                                                                                                                                                                                                                                                                                                 101 WXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQ-----CDA----- 47
                                                                                                                                                                                                                                                                                                                                                            lyrekktapwitrip-----qelvk-----kgqfplps1twehtgryrcfygshtag
                                                                                                                                                                                                                                                                                                                                                                                                              ---DVPGPPGDSRLPAVQEWGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                             mtpiltvliclglslgprthvqagtlpkptlwaepgsvi-tqgspvtlwcqgiletqeyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0310463
                                                                                                                                              Protein; 650 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.2%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45;
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This sequence represents a novel leukocyte immunoglobulin like receptor (LIR) pollypeptide LIR-PGG. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective amounts of LIR pollypeptide. LIR-PGG and cortain other LIR family members contain cytopiasmic immunoreceptor tyrosine-based inhiptory powers (TTMs), whilst other LIR family members lack TTMS, analogy with the structure and function of known MMC class I receptor molecules, LIRs maring TTMS are activation; receptors signalling, whilst those lacking ITMs are activation; receptors. Failure of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIR-9362; immunoregulator; leukocyte immunoglobulin-like receptor; LIRs therapeutic; treatment; disorder; TTM, HMC class I receptor; inhibitor cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doma in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                negative
                                                  receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to
                                                                                                                                                                                                                                 Claim 4; Page 53-55; 112pp; English.
                                                                                                                                                                                                                                                                                                             N-PSDB; AAV69328
                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                          other species
                                         produce probes for detecting LIR nucleic acids or
                                                                                                                                                                                                                                                                    Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                             (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9848017-A1
                                                                                                                                                                                                                                                                                                                           1998-609990/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              signalling; autoimmune disease; suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                         97US-0842248
                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US08244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "immunoglobulin-like domain II" 221..318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- extracellular_domain 17..650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 644 . . 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            614..617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533..536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /labe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319..419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "immunoglobulin-like domain I"
119..220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= LIR-P3G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "ITIM motif"
                                                                                                                                                                                                                                                           function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "ITIM motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "ITIM motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "ITIM motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytoplasmic_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain III*
                                         isolating LIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibitor;
                                         DNA from
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Sequence

650 AA

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34

Conservative

14;

Mismatches

50;

Indels

30;

Gaps

5

60

mtpiltvliclglslgprthvqaghlpkptlwaepgsvi-----tqgspvtlrcqg 51

MSMLVVFLLLINGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA

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RESULT :
                                                                   Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can bused to produce the LIR polypeptide. LIR coding sequences may be
                                                                                                                                                                                                                                                                                                                            Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB04169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB04169 standard; Protein; 650
                                                                   Sequence
                                                                                            used in the gene therapy of disorders mediated directly or undirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                     Example 3;
                                                                                                                                                                                                                                             Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200068383-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte immunoglobulin like receptor; LIR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Leukocyte immunoglobulin like receptor (LIR) P3G2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 essdplel 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 QLSKLLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 mtpiltvlic1gls1gprthvqagh1pkpt1waepgsvi-----tqgspvt1rcqg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MSMLVVFLLLMGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ggetgeyrlyrekktapwitripgel---vkkgqfpipsitwehagryrcyygsdtagrs 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VQE--
                                                                                                                                                                                                                                                                                                   2000-687645/67
                                                                                                                                                                                                                                                                                      AAA54591
                                                                   650 AA;
                                                                                                                                                                                                       Page 60-62; 117pp; English
                                                                                                                                                                                                                                                                                                                              Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmune disorders; immune system; human
                                                                                                                                                                                                                                                                                                                                                                                  9908-0310463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.2%;
               11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WGAQEPVHLDSPAIKHQF----LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                                                                              Borges L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
               Score 74;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 74; DB
Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
               3.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                            21;
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                          Length 650
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                                                                                                                                                               can be
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AAW62782
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Best Loc
Matches
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1996;
09-DEC-1996;
16-DEC-1996;
                                                                                                                                                                                                                                                                                  AMA62779-88 are encoded by human moncyte genes, collectively designated KF03. The genes are found in activated moncytes. The specification also describes other proteins encoded by activated monceytes, which are designated FF03 and YEQI. The genes function in controlling development, differentiation, and/or physiology of the mammalian immune system. The products can be used for treating shormal proliferation, regeneration, degeneration or attophy. They can be used
                                                                                                                                 Sequence
                                                                                                                                                                                                    for treating e.g. cancerous conditions, degenerative conditions, anto-immune responses, transplantation rejection, graft versus ho discuss, or inflammatory conditions. The products can also be used in the products of the products of the conditions of the products of the products of the conditions of the products of the products of the conditions of the products of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Maolated activated monocyte cell gene(s) - used to develop
products for treating e.g. cancer, degenerative conditions,
autoimmune responses, transplant rejection or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degenerative condition; autoimmune response; transplantation rejection; graft versus host disease; inflammatory condition; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW62782 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDF03: activated monocyte; YE01; KTE03; control; development; differentiation; mammalian immune system; treatment; cancerous condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by human monocyte gene designated KLM67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-333325/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phillips JH, Zurawski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adema GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-1998
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                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gqetqeyrlyrekktapwitripqcl---vkkgqfpipsitwehagryrcyygsdtagrs 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VQE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type I transmembrane protein; immunoglobulin-like doma activated monocyte; YEO1; KTEO3; control; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pages 98-100; 104pp; English
                                                                                                                                                                                  diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gorman DM,
                                                                                                                                 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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96US-0762187.
96US-0033181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                      11.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lanier LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ier LL, McClanahan TK,
Zurawski SM;
                      Score 74;
Pred. No.
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                         DB 19;
3.9;
                                                Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meyaard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domain;
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                       aniagonists can also be used to treat restenosis caused by migration of smooth muscle cells following angiphlasty and to reduce blood supply to selected tissues. The antagonists particularly inhibit neovascularisation where this is induced by cytokinos, e.g. transforming growth factor alpha, epidemail growth factor or especially vascular endothein factor alpha, epidemail growth factor or especially vascular endothein factor.
                                                                                                                                                             metalloprotease 2 (MMP-2) protein (ANM41227). The present peptide is derived from anno acids 516-537. The peptides are able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a vitronectin receptor inhibitors of alpha-v-beta-5 can inhibit angiogenesis. The specification describes a novel labelled package that contains an inhibitor of angiogenesis i.e. an alpha-v-beta-5 antagonising polypeptide that binds to integria alpha-v-beta-5 and includes a part of the C-terminal domain of MMP-2. The antagonists are used to inhibit angiogenesis in inflamed tissue. In solid tumours or metastases, and an a vide range of coular disorders (e.g. diabetic or other forms of retinopathy, necessicular
                                                                                                                                glaucoma, or corneal transplants). They are particularly used to induce regression or to inhibit growth of tumours. The alpha-v-beta-5
                                                                                                                                                                                                                                                                                                                                                                             Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               Packaging material containing polypeptide antagonist of alphav, beta5 integrin - used for inhibition of and one and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1996;
31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW41238 standard;
              created using
                                                                                                                                                                                                                                                                                                                                         Peptides AAW41234-39 are derived from the chicken matrix
                                                                                                                                                                                                                                                                                                                                                                                                              treating tumours, inflammation, eye diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-041758/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCRI ) SCRIPPS RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matrix metalloprotease-2; MMP-2; alpha-v-beta-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW41238
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                                                                                                                                                                                                                                                                                                                                                                           Page -; 117pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheresh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor; inhibition;
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              information
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96US-0015869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedlander
           provided
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                                                                    contribution of comprises anino acid residues 445-597 of chicken be mature matrix metalloptotelnase 2 (chMMP-2, see AMM4111). It can be produced by recombinant methods such as FCR amplification (see AMV12502) of chMMP-2 coding sequence (see AMV3995) and cloning into a region person of the coding sequence (see AMV3995) and cloning into coding sequence (see AMV393-94) of human or codicted mather 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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ocular disorders such as diabetic retinopathy or macular degeneration (all claimed). They can also be used to treat restencis caused by migration of smooth muscle cells following angioplasty and to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Packaging material containing polypeptide antegonist of alphav
beta3 integrin - used for inhibition of angiogenesis, and for
treating tumours, inflammation, eye diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2: Page 158-159; 234pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-1996;
31-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diabetic retinopathy; macular degeneration; restenosis; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPG------PPGDSRLPAVQEWGAQEP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0018733
96US-0015869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US09158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --agneywvytasnldrgypkkltslglppdvgridaafnwgrn--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%;
23.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 19: Length 122;
0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8×86888
Query Match
Best Local S
Matches 26
                                                                                                                          Peptides ANAI124-39 are derived from the chicken matrix metalloprotess-2 (MMP-2) protein (ANAI127). The present peptide is metalloprotess-2 (MMP-2) protein (ANAI127). The present peptide is derived from amino acids 44-537. The peptides are able to acc as alpha v-beta-5 antegonists. Alpha-v-beta-5 is a vitrometin receptor. Inhibitors of alpha-v-beta-5 can inhibit angiogeness in the peptide that binds and open concellabel and people that contains an inhibitor of the period of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         blood supply to selected tissues (claimed). The new antagonists are highly selective for analogonesis. Only mew blood vessels express alpha-v beta-3, so mature vessels are unaffected, and the antagonists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     should be of low toxicity.
                   tissue, in solid tumours or metastases, and in a wide range of ocular disorders (e.g. diabetic or other forms of retinopathy, meovascular glaucoma, or corneal transplants). They are particularly used to induce regression or to inhibit growth of tumours. The alpha-v-beta-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating tumours, inflammation, eye diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Packaging material containing polypeptide antagonist of alphav, beta5 integrin - used for inhibition of anglogenesis, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-041758/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brooks P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SCRI ) SCRIPPS RES INST
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31-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vitronectin receptor; inhibition; angiogenesis; tumour growth,
restenosis; neovascularisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW41235 standard; protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pqdekavff----agneywvytasnldrgypkkltslglppdvqridaafnwgrn--
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                                                                                                                                                                                                                                                                                                                                                                                                                           2; Page -; 117pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheresh DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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96US-0015869
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                                                                                                                                                                                                                                                                                                                                                                                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Friedlander M:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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                                                   to induce
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antagonists can also be used to treat restenosis caused by migration of

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AAW41089
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Best Local s
Matches 26
                            meturic matrix metalloprotocianse 2 (chwwb-2 see Anwilli) it can be produced by recombinant methods such as PCR amplification (see Anvi2501) of chwwh-2 coding sequence (see Anvi2503) and cloning into a post of the compression in E. coll as a fixeion protein with glutchione-g-transferses. The invention relates to the classification in E. coll as a fixeion protein discovery that angiogenesis is mediated by the specific vitronectin comport alpha v beta-3 and that limitation of alpha v beta-3 function inhibits angiogenesis. Claimed antagonists of alpha v beta-3 except conditions angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smooth muscle cells following angioplasty and to reduce blood supply to selected tissues. The antaquonists particularly inhibit necovascularisation where this is induced by cytokines, e.g. transforming growth factor alpha. epidermal growth factor or especially vascular andotholial growth factor; note: this sequence does not appear in the specification; it was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Callus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diabetic retinopathy; macular degeneration; restenosis; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       created using information provided.
                                                                                                                                                                                                                                                                        Packaging material containing polypeptide antagonist of alphave beta3 integrin • used for inhibition of angiogenesis, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW41089 standard;
                  chicken MMP-2
                                                                                                                                                                                        This polypeptide comprises amino acid residues 410-637 of chicken
                                                                                                                                                                                                                                                          treating tumours, inflammation, eye diseases etc.
                                                                                                                                                                                                                                                                                                                            WPT; 1998-032334/03.
                                                                                                                                                                                                                                                                                                                                                                                               (SCRI ) SCRIPPS RES INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenesis; inhibitor; antagonist: integrin alpha-v beta-3;
vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLACS 119
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                                                                                                                                                                                                                       Page 157-158; 234pp;
  AAW41098-110),
                                                                                                                                                                                                                                                                                                                                                              Cheresh DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         metalloproteinase chmmP-2 (aa410-637).
              fusion polypeptides, cyclic or linear polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                96us-0015869
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derivatised polypeptides, a monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 73;
Pred. No.
                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chicken;
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                                                                                                                                                                     It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody or organic mimetic compound. The antagonists are used to inhibit angiopenesis in inflammed tissue for treatment of arthritis or rheumatoid arthritis; solid cumours or metastases particularly to induce tumour regression or inhibit growth of tumours; and in occitar disorders such as diabetic retinopathy or macular degeneration
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31-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                    (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                     30-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                        restenosis; neovascularisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matrix metalloprotease-2; MMP-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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96US-0015869
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                                                                                                                                                                                                          DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.0%; Score 73;
23.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibition;
                                                                                                                                                                                                          Friedlander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-v-beta-5 antagonist; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis;
                                                                                                                                                                                                            3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour growth:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Peptides AAW1234-39 are derived from the chicken matrix metalloprotease-2 (MMP-2) protein (AAW1227). The present peptide is derived from amino acids 410-637. The peptides are able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a virromectin receptor inhibitors of alpha-v-beta-5 can inhibit maylogenesis. The specificate describes a novel labelled package that contains an inhibitor of

an alpha-v-beta-5 antagonising

polypeptide that binds

The specification

Claim 2;

Page -; 117pp; English

treating tumours, inflammation, eye diseases etc

Packaging material containing polypeptide antagonist of alphav, beta5 integrin - used for inhibition of anglogenesis, and for

WPI; 1998-041758/04.

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RESULT 38
AAW41111
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenesis: inhibitor; antagonist; integrin alpha-v beta-3; virrometin receptor; rheumatoid arthritis; tumour; metastasis; diabetic retinopathy; macular degeneration; restenosis; therapy
                         Disclosure; Page 163-167; 234pp; English
                                                                                  Packaging material containing polypeptide antagonist of alphav.
beta3 integrin - used for inhibition of angiogenesis, and for
treating tumours, inflammation, eye diseases etc.
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                                                                                                                                                                                                                    N-PSDB; AAV03995
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                                                                                                                                                                                                                                              1998-032334/03
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1..26
/label= Sig_peptide
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Pred. No.
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vitronectin receptor; inhibition; angiogenesis; integrin; tumour growt
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                                                                                                                                                                    treating tumours, inflammation, eye diseases etc.
                                                                                                                                                                                            Packaging material containing polypeptide antagonist of alphav, beta5 integrin - used for inhibition of angiogenesis, and for
                                                                                                                                                                                                                                                                         WPI; 1998-041758/04.
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31-MAY-1996;
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96US-0015869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%;
23.6%;
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                                                                                                                                                                                                                                                                                                                          Friedlander M;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Length 663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumour growth;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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The present sequence represents the chicken matrix metalloprotease-2 (wMP-2) protein sequence. Fragments of this protein (AAW41234-39) are able to act as alpha-v-beta-5 atagopoists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of alpha-v-beta-5 can inhibit

Disclosure; Fig 15A-B; 117pp; English.

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AAH29926
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contains an inhibitor of anglogenesis i.e. an alpha-v-beta-5 untagonising polypeptide that binds to integrin alpha-v-beta-5 and includes a part of the C-terminal domain of MMP. The antagonists are used to inhibit anglogenesis in inflamed tissue, in solid tumours or
                             The present invention relates to the coding and protein sequences for i Mostco Maphi restriction endonucleuse and methylase enzymes. Both of those enzymes are components of the bacterial restriction-modification system. They can be used in the laboratory to create recombinant
                                                                                                                                                                                                                                           New recombinant DNA encoding for NapHI restriction endonuclease methylase enzymes useful for creating recombinant molecules and producing these enzymes in large quantities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6130078-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nostoc sp restriction endonuclease NspHIR protein sequence
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                                                                                                                                                                                    Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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    molecules,
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAC64949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 -NOV - 1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pqdekavff-----agneywvytasnldrgypkkltslglppdvqr1daafnwgrn-- 580
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and to produce strains which overproduce these enzymes, making
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  663 AA;
                                                                                                                                                                                    column 13-16; 13pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
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RESULT 41
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                        expressing a leukocyte immunoglobulin like receptor (LTR), can be used to produce the LTR polypeptide. LTR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LTR polypeptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 113-114; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin like receptor; LIR; gene therapy autoimmunity; autoimmune disorders; immune system; human.
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                                                                                                                                                                                                                                                                                           Host cells transformed with a vector which are capable of
                                                                                                                                                                                                                                                                                                                                                 treating autoimmune diseases function
                                                                                                                                                                                                                                                                                                                                                             Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for 
treating autoimmune diseases and disease states with suppressed immune
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 82
                           74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 DSRLPAVQEWGAQEPVHLDSPA---IKHQF-LLTGDTQGRYR-----CRSGLSTG 100
epknkarfsipsmtehhagryrcyyyspagwsepsdplel
                           SPAIKHQFLLTGDTQ----GRYRCRSGLSTGWXQLSKLLEL
                                                      skatlwaepgsvisrgnsvtircqgtleageyrlvkegsp
                                                                                   TQXSLWAE-----SEHXLKTLGQCDAD-----VPGPPGDSRLPAVQEWGAQEPVHLD
                                                                                                                                                                                                                                                                                                                                                                                                       AAA54611
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                                                                                                              Conservative
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                                                                                                                         Score 72.5;
Pred. No. 1
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Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor LIR-9s2
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RESULT 42
AAB04181
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Best Local Similarity
                                                                                                                                                                                                                                                                             Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (IIR), can be used to produce the LIR polypoptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or the LIR polypoptides can be used to treat autoimmune polypoptides. The LIR polypoptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
Interferon regulatory factor; IRP; chimeric protein; serine; threonine; carboxy terminus; amino terminal domain; aspartic acid; phosphorylation; post-translational modification; sendai virus; cancer treatment; herpes;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leukocyte immunoglobulin like receptor LIR-9m2
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                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 108-109; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                   Chimeric protein IRF-7(1-246)/IRF-3(132-427).
                                                     25-JAN-2000
                                                                                           AAY15104 standard;
                                                                                                                                                                                                                                                                                                                                                                                Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
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                                                                                                                                                        SPAIKHOFLLTGDTO---GRYRCRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                         skatlwaepgsvisrgnsvtircqgtleaqeyrlvkegsp-
                                                                                                                                                                                            TQXSLWAE----SEHXLKTLGQCDAD-----VPGPPGDSRLPAVQEWGAQEPVHLD 73
                                                                                                                                                                                                                                                                                                                                                                                                             AAA54609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin like receptor; LIR; gene therapy;
lty; autoimmune disorders; immune system; human.
                                                                                                                                                                                                                                                              287
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                                                                                                                                                                                                              Conservative
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                                                                                           Protein;
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                                                                                                                                                                                                                       11.0%; Score 72.5;
26.0%; Pred. No. 2;
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PRDI/PRDIII; promoter: ISRE regulatory element; stimulation; activate; activate; binding; transcriptional activity; viral infection; proteasome mediated degradation; influenza; HIV infection; cytokine gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type
Misc-difference 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Wild type
Misc-difference 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Claim 11; Fig 13; 93pp;
                                    Carboxy-terminus modified highly active forms of interferon regulatory factor proteins used for the treatment of viral infections
                                                                                                                                                  Hiscott J,
                                                                                                                                                                                                                             07-APR-1998;
                                                                                                                                                                                                                                                              07-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        target cell.
                                                                                            N-PSDB; AAX90994
                                                                                                                                                                                      (DAVI-) DAVIS-JEWISH GEN HOSPITAL MORTIMER
                                                                                                                                                                                                                                                                                                     14-OCT-1999.
                                                                                                                                                                                                                                                                                                                                      W09951737-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                              1999-620201/53.
                                                                                                                                                  Lin R;
                                                                                                                                                                                                                          98CA-2234588
                                                                                                                                                                                                                                                              99WO-CA00314
                                                                                                                                                                                                                                                                                                                                                                                             /note=
520
                                                                                                                                                                                                                                                                                                                                                                                                                                 /note*
519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Corresponds to modified amino-terminal domain
of IRF-7 protein"
                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "Corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247..542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRF-3 protein'
                                                                                                                                                                                                                                                                                                                                                                        "Wild type Ser replaced with Asp"
                                                                                                                                                                                                                                                                                                                                                                                                               "Wild type Ser
English
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to modified carboxy-terminus
                                                                                                                                                                                                                                                                                                                                                                                                            replaced with Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           replaced with Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                   replaced with Asp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replaced with Asp'
                                                                                                                                                                                         B
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The present sequence is the chimeric protein comprising, residues 1-246 from the modified aminor-terminal domain of interferon regulatory factor, IRE-7 and 132-427 residues from the carboxy-terminus of modified IRE-3 (5D) protein. The scrime and throntine residues are post-translationally modified By phosphorylation, following sendal virus infection. The modified By substituted with aspartic actid, inections as a strong activator, of promoters containing ISRE and PROI/PROILI caulatory
                                                                                                                                                                                                                                                                                                                                                               elements, stimulation of DNA binding and transcriptional activity and protessome mediated degradation. The modified IRE sequences are used for the treatment of viral infections like, influenza, horpes or HIV infection. They may also be used to activate a cytokine gene, in cancer treatment or to modify a target cell of an organism.
                                                                                                                                                                                                                                                                                                               Sequence
                                                   105
54
                                                                                                           7 FLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVP----GPP-----
------GDSRLPAVQE------WGAQEPVHLDSPAIKHQFL-LTGD
                                               fvmlrdnsgdpadphkvyalsrelcwregpgtdqteaeapaavpppqggppgpflahtha
                                                                                                                                                                       40;
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                               542
                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                               10.98;
                                                                                                                                                                       14;
                                                                                                                                                                                               Score 72;
Pred. No.
                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                       56;
                                                                                                                                                                                                                           Length 542;
                                                                                                                                                                       Indels
                                                                                                                                                                       52;
                                                                                                                                                                   Gaps
98
                                                       164
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glqapgplpapagdkgdlllqavqqscladhlltaswga-dpvptkapgegqeglpltga

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RESULT 44
AAM25575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1999;
21-JAN-2000;
25-APR-2000;
            antiparkinsonian, and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antisponists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rehumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal intentions, autoimmunity, genetic diseases, hacmatopoletic disorders, intentions, autoimmunity, genetic diseases, hacmatopoletic disorders.
                                                                                                                                                                                            cells they are expressed in, such as antiinflammatory; antirheumatic; antianthritic; immunosuppressive; antiantental; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutegen; cardiovascular; antianaemic; antiagregant; haemostatic; vulnerary; antiulocr; osteopathic dermatological; antiallorgic; antiasthmatic; antidiotric; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dormatiological; antiallergic; antiaslumatic; artidiabetic; gytostatic; neuroprotective; antidepressant; nouropic; antiparkinsonian; infection; neuroprotective; antidepressant; nouropic; antiparkinsonian; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; poncreatitis; cardiac dysfunction; neuropathology; cardiac anaphylatis; autoimmnity; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 20; Page 220; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and {\sf HIV} infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antlinflammatory; antirheumatic; antiarthritic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM25575 standard;
                                                                                                                                                                                                                                                                                                                                   AAH99166 to AAH99904 encode the human proteins given in AAM25225 to AAM25963. The proteins can have activities based on the tissues and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-2000: 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153455-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurological disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 caggpglpagelygwavettpsptsdtgedildellgnmvla 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-457603/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TQGRYRCRSGLSTGW------XQLSKLLELTGPKVLA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH99516
platelet disorders, thrombocytopaenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0488725.
2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0471275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrine; cardiant; central nervous system; virucide
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wounds, burns,
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RESULT 45
AAR12427
 SXCCCCCCCX PTT TXX
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BXDXDXDX
BXDXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                  This chimeric sequence is one example of a hybrid Fc receptor of the invention. The hybrid Fc receptor retains the Iq binding functions of the constituent receptor types. It can be used for regulating antibody production in vivo and in plasmaphoresis to
Sequence
                          remove immune complexes or pathological antibodies. Rabbit IgG
bound to cells transfected with the chimeric Fc(gamma) receptor
See also AAO12079.
                                                                                                                                     Claim 10; fig 3A; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR12427 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis, severe combined immunodeficiency, eczema, allergic rininitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                             control auto-immune diseases
                                                                                                                                                                                                                       N-PSDB; AAQ12078
                                                                                                                                                                                                                                                              Hogarth PM, Hulett MD,
                                                                                                                                                                                                                                                                                                                                                                        16-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hybrid Fc(gamma)RI/RII receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR12427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                          New immunoglobulin binding hybrid Fc receptor molecules
                                                                                                                                                                                                                                    WPI; 1991-164135/22.
                                                                                                                                                                                                                                                                                         (UYME-) UNIV MELBOURNE
                                                                                                                                                                                                                                                                                                                     25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                               25-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                    W09106570-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin-binding molecule; Fc(gamma)RI; Fc(gamma)RII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qvptsm---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QEPVHLDSPAIKHQFLLTGDTQGRYRC---RSGLS---TGWXQLSKLLELTGP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 AA;
 324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                     89AU-0007045
                                                                                                                                                                                                                                                                                                                                             90WO-AU00513
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Domains D1 and D2 of Fc(gamma)RI
196..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 324 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----lgxffcifsregispcwpgwsqtpkvlhlprp
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fc(gamma)RII transmembrane and cytoplasmic
                                                                                                                                                                                                                                                              lerino FL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 71.5; DB
Pred. No. 0.59;
6; Mismatches
                                                                                                                                                                             and allergic reactions and
                                                                                                                                                                                                                                                              McKenzie IFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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Query Match

10.7%;

Score 71;

DB 12;

Length 324;

	Search completed: January 7, 2002, 16:49:15 Job time: 307 sec	Best Local Similarity 25.5%; Prod. No. 3.6; Matches 28; Conservative 9; Mismatches 37; Indels 36; Gaps 5; Oy 4 LVVFLLLMGVTWGPVTEAAIFYETOXSLWAESEHXLKTLGOCDADVPG 51



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G992_6/ptodata/3/16/68_COM8_seq;

G992_6/ptodata/3/16/gtoda/68_COM8_seq;

G992_6/ptodata/3/16/gtoda/68_COM8_seq;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Cgn2_6/ptcodata/2/1na/6B_COMB.secj.u/
/ Cgn2_6/ptcodata/2/1na/6A_COMB.secj.u/
/ Cgn2_6/ptcodata/2/1na/6A_COMB.secj.u/
/ Cgn2_6/ptcodata/2/1na/6A_COMB.secj.u/
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Database length: 113238999
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Query: US-09-471-276-831_COPY_1_16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MODEL-frame+_p2n.model -DEV-x1h
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equences: 351203
                                                                                                                                                                                                                                                                                                              3-311-517 + 42-50 109.87 180.78
3-318-4 + 42-50 101.08 557.62
3-10318-9 + 42-50 97.07 933.62
3-10318-11 + 42-50 96.47 1.0ee+3
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46.00 112.52
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; Sequence 2, Application

Application US/09402002

GENERAL INFORMATION:
APPLICANT: Ueyama
APPLICANT: Abe, K

APPLICANT: Keshi, I APPLICANT: Matsuhil TITLE OF INVENTION: TITLE OF INVENTION:

Ueyama, Hiroshi Abe, Kanako Keshi, Hiroyuki Matsuhisa, Akio WENTION: PROBES:

FOR THE DIAGNOSIS OF INFECTIONS BY KLEBSIELLA PNEUMONIAE

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-402-002-2

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seq_documentation_block:
    Sequence 3, Application US/09027064
    Patent No. 6133006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blignment_block:
US-09-471-276-831_COPY_1_16 x US-09-402-002-2/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-09-402-002-2 from: 1 to: 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cavley, Jr., Thomas A.
REGISTRATION NUMBER: 40,944
REFERENCE/DOCKET NUMBER: 19036,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300;
TELEPHONE: (312) 474-6448
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1747 base pairs
TYPE: Nucleic acid
                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    1392 ATGG 1389
                                                                                                                                                                                                                                                                                                                                                                              1442 GTGACAATATTGATATTATTCCTGCTGGTTGCAATGACCTGGGGAACCAC 1393
               APPLICANT: SHABON, USMAN
APPLICANT: BERGSMA, DERK
TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               14 rTrp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 233 Sc
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                               1 MetSerMetLeuValValPheLeuLeuLeu......TrpGlyValTh 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Klebsiella pneumoniae
STRAIN: Clinical Isolate KP-85-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-271-815-3
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                                                                                   SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09271815 Patent No. 6297036
                                                                                                                        EARLIER APPLICATION NUMBER: 09/027.064
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 60/053,924
EARLIER FILING DATE: 1997-07-28
NUMBER of SEQ ID NOS: 6
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/271,815
CURRENT FILING DATE: 1999-03-18
                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33 FILE REFERENCE: GH-70172-1
                                                                                                                                                                                                                                                                                                                  APPLICANT: BERGSMA, DERK APPLICANT: SHABON, USMAN
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                                                               LENGTH: 1338
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LENGTH: 1338 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845 TCCCGCCTCCTGATGACCCCTGCCACTCTGGGGCCCTCACCTGG 886
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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STREET: P.O. BOX 980
CITY: VALLEY FORGE
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/053,924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 20-FEB-1998
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4.182
78.571
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Percent Identity: 57.143
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-027-064-1
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Align seg 1/1 to: US-09-027-064-1 from: 1 to: 2394
                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                               NAME: PRESTIA, PAUL F
RECISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
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                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: cDN
                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/0
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                            LENGTH: 2394 base pairs
TYPE: nucleic acid
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Gaps: 0
Percent Identity: 57.143
                                                                                   Length: 14
Gaps: 0
Percent Identity: 57.143
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-271-815-1
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: SHABON, USHAN
TITLE OF INVENTION: A YMX-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
FILE REFERENCE: GH-70172-1
CURRENT APPLICATION UNBER: US/09/271,815
CURRENT FILING DATE: 1999-03-18
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5874241thrup, Thomas E
                                                                                                   CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Takahashi, Joseph
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawrence H
                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Clock Gene and Gene Product NUMBER OF SEQUENCES: 53
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CITY: Chicago
STATE: Illinois
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                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                         60601
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                                                                                                                                                                                                                                                                                                USA
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78.571
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Percent Identity: 57.143
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; LENGTH: 7498
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-885-291-1
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; Sequence 1, Application US/08885291A
; Patent No. 6057125
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US-09-471-276-831_COPY_1_16 x US-08-816-693A-1
; Sequence 1, Application US/09496672
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US-09-471-276-831_COPY_1_16 x US-08-885-291-1
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Quality:
                     seq_documentation_block:
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                                                             seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-496-672-1
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Ratio: 5.111
Percent Similarity: 100.000
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Ratio: 5.111
Percent Similarity: 100.000
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CURRENT FILING DATE: 1997-06-30
EARLIER APPLICATION NUMBER: 08/816,693
EARLIER FILING DATE: 197-03-13
UNMER OF SED ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Takahashi, Joseph S. APPLICANT: Turek, Fred W. APPLICANT: Pinto, Lawrence H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT FILE REFERENCE: 0290-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5598 CTGCTTCTGTATGGGGTCACTTGGGGT 5624
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NFORMATION FOR SEQ ID NO: 1:
                                                                                                           5598 CIGCITCIGIATGGGGTGACTIGGGGT 5624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 7498 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 LeuLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                      LeuLeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
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389..2954
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                                                                                                                                                                                                                                                                                                        Percent Identity: 88.889
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SEQ ITWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 7498
TYPE: DNA
GRGANIZM: AUS musculus
US-09-496-672-1
                                alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-172-108-48
                                                                                                                                                                                                                                   ; OTHER INFORMATION: 700607235H1 US-09-172-108-48
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Ratio: 5.111
Percent Similarity: 100.000
Align seg 1/1 to: US-09-172-108-48 from: 1 to: 285
                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-496-672-1 from: 1
                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/172,108
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEO 10 NOS: 56
SOPTWARE: PERL Program
SEO 10 NO 48
LENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Cunnigham, Mary Jane
APPLICANT: Zweiger, Gary B.
APPLICANT: Zweiger, Gary B.
APPLICANT: Seilhamer, Jeiffrey J.
APPLICANT: Seilhamer, Jeiffrey J.
TITLE OF INVENTION: MAKKENS FOR PEROXISOMAL PROLIFERATORS
FILE REPERANCE: PA-1012 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Application US/09172108 Patent No. 6160104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1997-INUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CLOCK GENE AND GENE PRODUCT FILE REFERENCE: 0290-5 CURRENT APLICATION NUMBER: US/09/496,672 CURRENT FILING DATE: 2000-02-03 PRIOR APPLICATION UNBERE: 08/885,291 PRIOR APPLICATION UNBERE: 08/885,291 PRIOR FILING DATE: 1997-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Takahashi, Jos
APPLICANT: Turek, Fred W
APPLICANT: Pinto, Lawren
                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5598 CTGCTTCTGTATGGGGTGACTTGGGGT 5624
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                                                                                                                           Quality:
Ratio:
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                                                                                                       45.00
3.750
75.000
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Percent Identity: 88.889
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                                                                                              Length: 16
Gaps: 0
Percent Identity: 56.250
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-172-711-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: 700607235H1 US-09-172-711-45
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SEQ ID NO 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09172711
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CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cunnigham, Mary Jane
APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott Re,
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: MONITORING TOXICOLOGICAL RESPONSES
FILE REFERENCE: PA-0011 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE: -
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TYPE: DNA
ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A.
                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NUTT, Stephen TITLE OF INVENTION: AMPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                            APPLICATION NUMBER: US 07/896,611 FILING DATE: 10-JUN-1992
                                                                                                                                         FILING DATE:
                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                  E: Foley & Lardner
1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAMBOJ, Rajender
ELIOTT, Candace
                                                                                                                                      06-JUN-1994
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75.000
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                                                                                                                                                               US/08/254,573
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-254-573-1/rev
                         alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-264-419C-3
                                                                                                                               alignment_scores:
                                                                                                                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(840)
US-09-264-419C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION:
US-08-254-573-1
                                                                                                                                                                                                                                                                               SOFTWARE: Pat
SEQ ID NO 3
LENGTH: 840
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Align seg 1/1 to: US-09-264-419C-3 from: 1 to: 840
                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09264419C Patent No. 6174682
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/264,419C CURRENT FILING DATE: 1999-03-08
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2875 CTTTCTATTTTGTTGTTGTTTTTGGCACTGAAGGGTTTGGGATGGGGC 2828
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REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: [703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3220 base pairs
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LOCATION:
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                                                                                               Quality:
Ratio:
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AVENTION: No. 6174682el Thioredoxin Family Active Site Molecules and
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62..2782
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116..2782
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62..115
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81.250
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76.923
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FR: 16777/179 ALLE
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Gaps: 0
Percent Identity: 50.000
                                                                               Percent Identity:
                                                                                                               Length:
                                                                                               Gaps:
                                                                             13
0
53.846
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seq_documentation_block:
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09264419C
Patent No. 6174682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/264,419C
CURRENT FILING DATE: 1999-03-08
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Rhodadoust, Mehran
TITLE OF INVENTION: No. 6174682el Thioradoxin Family Active Site Molecules and Uses
TITLE OF INVENTION: Therefor
FILE REFERENCE: MNI-076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (74)...(913)
OTHER INFORMATION: AT POSITION 1050 N-ANY NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 CTGCCAGTCCTGCTGCTGTTGCGTTGCGGTGCTCCCTGG 142
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Little, Andrew
                                                                                                                                                                                                                               STREET: 755 PAGE
CITY: PALO ALTO
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3
                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 MetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
                                                                                               SOFTWARE:
                   CLASSIFICATION:
                                        FILING DATE:
                                                                                                                                                                                                 ZIP: 94304-1018
                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                          ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MetLeuValValPheLeuLeuTeuTrpGlyValThrTrp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCAGTCCTGGTGCTGTTGCTTTGGGGTGCTCCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09033428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: US-09-264-419C-1
                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                            Henderson, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                Lamparski, Henry
                                                                                                                                                                                                                                                                                                                                                                                                               Schuur, Eric
                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.00
4.400
76.923
                                                                                                                                                                                                                                                                                                                                                      EXPRESSING
                                                                                                                                                                                                                                                                                                                                      23
                                                         US/09/033,428
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Gaps: 0
Percent Identity: 53.846
                                                                                                                                                                                                                                                                                                                                                 VECTORS SPECIFIC FOR CELLS
APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 1207
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-033-428-1/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-931-608A-1
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Percent Similarity: 93.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
                                                                                                                INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    737 AACCTTTTGTTGGTATATCTGTTACTTTATGGTATTTCCTTAGGT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 34
TELECOMMUNICATION INFORMATION:
HYPOTHETICAL:
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lobel, Peter APPLICANT: Sleat, David
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGly 16
                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                      STRANDEDNESS:
                                                                                                                                                       TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Hackensack
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                                                                                              LENGTH:
                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NE: (415) 494-0792
706141 MRSNFOERS SFO
706141 MRSNFOERS SFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3E: David A. Jackson, Esq.
411 Hackensack Ave, Continental Plaza, 4th Floor
                                                                                              3487 base pairs
                                                                                                                                                       201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                       linear
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                                                                                                                                                                       201-487-5800
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                                                         double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOVEL HUMAN LYSOSOMAL PROTEIN AND METHODS OF ITS USE
                                                                                                                                                                                                                                                                                                                          US/08/931,608A
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Gaps: 0
Percent Identity: 46.667
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-931-608A-1/rev
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                                                                                          alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-033-428-2/rev
                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear US-09-033-428-2
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                                                         Align seg 1/1 to reverse of: US-09-033-428-2 from: 1 to: 5224
                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6254862
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                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPARTIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOSTMARE: PALENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/033,421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 5224 base pairs
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TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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4.778
81.818
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3.071
93.333
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Gaps: 0
Percent Identity: 54.545
                                                                                                                     Gaps: 0
Percent Identity: 46.667
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US-09-471-276-831_COPY_1_16 x US-08-676-169-1
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                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-981-459-1
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Percent Similarity: 100.000
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GENERAL INFORMATION:
                                                                       GENERAL INFORMATION:
APPLICANT: CHIRNSIDE
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                          Sequence 1, Application US/08981459
Patent No. 6090390
                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                11132 TTATCTATGATTGTATTGCTATTCTTGCTTTGGGGT 11167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 31-JUL-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
        CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PLLC
STREET: 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chirnside, Evan Douglas
TITLE OF INVENTION: BOUNIE ARTERITIS VIRUS PEPTIDES; ANTIBODIES
TITLE OF INVENTION: AND THEIR USE IN A DIAGNOSTIC TEST
                                                                                                                                                                                                                                                                                                                                   1 MetSerMetLeuValValPheLeuLeuTeuTrpGly 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crawford, Arthur R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08676169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: NIXON & VANDERHYE P.C.
1100 No. 5773235th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12687 base pairs
                                                                                                                                      CHIRNSIDE, Ewan Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.00
                                                                                                Diagnostic Test For Equine Arteritis Virus Mediated Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 58.333
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#lignment_block:
US-09-471-276-831_COPY_1_16 x US-08-981-459-1
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; Sequence 517, Application US/09328111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-328-111-517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
                                      NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                              APPLICANT: LOWIS, MATCIA E.
APPLICANT: MONARD, JOHN E.
APPLICANT: MONARD, JOHN E.
APPLICANT: SCHLEGEI, ROBERT
TITLE OF INVENTION: MOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION UNDER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION UNDER: US/09/088,801
EARLIER APPLICATION UNDER: US/09/088,801
EARLIER APPLICATION UNDER: US/09/088,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11132 TTATCTATGATTGTATTGCTATTCTTGCTTTGGGGT 11167
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carroll III, Eddie APPLICANT: Carino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                     APPLICANT: Dert1, Adnan APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Endege, Wilson O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202-393-5350
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TYPE: DNA
                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 202-638-6666
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NAME: HOLMAN, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetSerMetLeuValValPheLeuLeuLeuTrpGly 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
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TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
FILING DATE: 19-FEB-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
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3.583
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Percent Identity: 58.333
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NAME/KEY: misc_feature
LOCATION: (1)...(611)
OTHER INFORMATION: n ·· A,T,C
US-09-328-111-517
                                                      alignment_scores:
                                                                                                                  US-08-583-318-4
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us-09-471-276-831_COPY_1_16 x us-09-328-111-517
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  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Staunton, Dona
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytop
TITLE OF INVENTION: Bindi
                                                                                                                                                                                                                                                                                                         TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,318
                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                    LOCATION:
                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
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                                                                                                                                                                                                                                                                    ENGTH:
                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60606
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                                                                                                                                                                                                                                               nucleic acid
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                    Ratio:
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                                                                                                                                                                                                                                                                    1631 base pairs
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  42.50
3.542
80.000
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80.000
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Percent Identity: 66.667
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-583-318-4
seq_documentation_block:
                                          seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-699-103B-11
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                                                                                                                                                                          Align seg 1/1 to: US-08-699-103B-9
                                                                                                                                                                                                                    US-09-471-276-831_COPY_1_16 x US-08-699-103B-9
                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6107462
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/854-0875
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                     1599 ATGCTCGTTGGCTTCCTCTTGGACTGGGTCTCAACCACCTGGGGA 1643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 2200 Sand Hill Road, Suite 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rine, Jasper D.
APPLICANT: Hampton, Randolph
APPLICANT: Hampton, Randolph
TITLE OF INVENTION: CHOLESTEROL SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/002,581
FILING DATE: 17-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 16-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 ATGCTCGTTGGCTTCCTCTTGGACTGGGTCTCAACCACCTGGGGA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                            3 MetLeuValValPheLeuLeuTrp...GlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 MetLeuValValPheLeuLeuTrp...GlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                         42.50
3.542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                       80.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31, 259
                                                                                                                                                                                                                                                                                    Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09272/005001
                                                                                                                                                                          from: 1 to: 2556
                                                                                                                                                                                                                                                                                                         Length:
Gaps:
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alignment_block:  0S-09-471-276-831\_COPY\_1\_16 \times 0S-08-699-103B-11 
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                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-972-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-699-103B-11 from: 1 to: 2731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/08699103B Patent No. 6107462
                                                                                                                                                                                                                        Sequence 1, Application US/08972927 Patent No. 6166290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650/854-0875
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                   1694 ATGCTCGTTGGCTTCCTCTTGGACTGGGTCTCAACCACCTGGGGA 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: GENES AND PROTEINS CONTROLLING TITLE OF INVENTION: CHOLESTEROI. CVANDEROY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rine, Jasper D. APPLICANT: Hampton, Randol
                                                           CORRESPONDENCE ADDRESS
                                                                                                   APPLICANT: LL, YU-PING
APPLICANT: LL, Ze-Sheng
TITLE OF INVENTION: GLITPATHIONE-S-CONJUGATE TRANSPORT IN
TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                        3 MetLeuValValPheLeuLeuTrp...GlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Green, Grant D. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/002,581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/699,103B FILING DATE: 16-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 2200 Sand
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C.
  STREET:
                 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: One Commerce Square, 2005 Market Street, 22nd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H: 2731 base pairs nucleic acid
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Floor
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3.542
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                                                                                                                                                                                   Philip A
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alignment_block:
us-09-471-276-831_COPY_1_16 x us-08-972-927-1
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                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-972-927-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: cDNA
US-08-972-927-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-08-972-927-1 from; 1 to: 5232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                             APPLICANT: I
APPLICANT: I
                   COMPUTER READABLE FORM:
                                                                                                                                                                                NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                       TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN TITLE OF INVENTION: PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 564 ATGTCAGGTTTGCTGTCATATATGCTCTTGTGGGGGATA...TGG 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
TELEPHONE: 215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Doyle Leary Ph.D., Kathryn
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/031,040 FILING DATE: 18-NOV-1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                              ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C. STREET: One Commerce Square, 2005 Market Street, 22nd STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp 15
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FILING DATE: 08-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                         COUNTRY: US
ZIP: 19103-7086
                                                                                  STATE:
                                                                                                   CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 18-NO
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 5232 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                             , Application US/08972927 6166290
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                                                                             Pennsylvania
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                                                                                                                                                                                                                                                           Rea, Philip A
Lu, Yu-Ping
Li, Ze-Sheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S
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3.542
80.000
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Percent Identity: 53.333
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-972-927-2
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US-08-972-927-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-:
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Ratio: 3.542
Percent Similarity: 80.000
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Patent No. 6183968
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandma
APPLICANT: Lal, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                               APPLICANT: Guegier, Karl J.
APPLICANT: Busghe, Mariah R.
TITLE DF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
TITLE DF INVENTION: RECEPTONS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION
NUMBER OF SEQUENCES: 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               951 ATGTCAGGTTTGCTGTCATATATGCTCTTGTGGGGGATA...TGG 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60 FILING DATE: 08-0CT-1997 ATTORNEY/AGENT INFORMATION: NAME: Doyle Leary Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/031,040 FILING DATE: 18-NOV-1996 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                        ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                             COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetSerMetLeuValValPheLeuLeuTrpGlyValThrTrp 15
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Doyle Leary Ph.D., Kathryn REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            831-494
                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                            Reddy, Roopa
                                                                                                                                                                                                                                                                                                                                                                                                        Yue, Henry
                                                                                                                                                                                                                                                                                                                                                                                                                          Lal, Preeti
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bandman, Olga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 60/061,328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 53.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9596-1202
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-276-531-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-632-470-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-276-531-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Lynn E. Multy, Ph. D.
REGISTRATON NUMBER: 42,918
REFERENCE/DOCKET NUMBER: PA-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-41
INFORMATION FOR SEQ ID NO:
                                                                                                                         COMPUTER RENDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                ATTORNEY/AGENT INFORMATION:
NAME: BERRIDGE, WILLIAM P
REGISTRATION NUMBER: 30,00
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE
STREET: P.O. BOX 19928
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MABILAT, CLAUDE
APPLICANT: RAGULT, DIDER
APPLICANT: RAGULT, DIDER
TITLE OF INVENTION: NUCLEOTIDE FRAGMENTS CAPABLE OF
TITLE OF INVENTION: HER DIZING SPECIFICALLY TO RICKETTSIA RDNA OR RRNA AND
TITLE OF INVENTION: THEIR USE AS PROBES OR PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: PANCTU
CLONE: 1514169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                726 TTGCTGATGTGGACTCTAACATGGGGG 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                      APPLICATION NUMBER: US/08/632,470 FILING DATE: 08-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                           STREET: P.O. BOX
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/079,677 FILING DATE: March 27, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3, Application US/08632470
5976791
                                                                                                                                                                                                                                                     22320
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5.250
88.889
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Percent Identity: 66.667
WPB 38238
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seq_documentation_block:
; Sequence 27, Application US/08299810A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-299-810A-27
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US-08-299-810A-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-632-470-53 from: 1 to: 1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: KOSSAU, Rudi
APPLICANT: Van Heuverswyn, Hugo
TITLE OF INVENTION: HYBRIOILATION PROBES FOR THE
TITLE OF INVENTION: DEFECTION OF BRANHAMELLA CATY
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (703)-836-2787
INFORMATION FOR SEQ ID NO: 53:
                                                                                                                                                                                               TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,838
REFERENCE/DOCKET NUMBER: 80/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEPAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TGGGGGATAACCTGGGGA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (703)-836-6400
                IMMEDIATE SOURCE:
CLONE: 16S rRNA Gene
                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hillson, Randall A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 TrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                          ORGANISM:
                                                                                                                       TOPOLOGY:
                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Merchant & Gould STREET: 3100 No. 5721097west Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1484 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5721097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minneapolis
                                                                                                                                                                                                                                                                                                                                    Hillson, Randall A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X
Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                          Branhamella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-1994
                                                                                              DNA (genomic)
                                                                                                                                    single
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                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/299,810A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 6
Gaps: 0
Percent Identity: 83.333
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-864-224-1
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US-09-471-276-831_COPY_1_16 x US-08-299-810A-27
                                                                                                                                                                                                      alignment_scores:
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Ratio: 7.000
Percent Similarity: 100.000
                                                      Align seg 1/1 to: US-08-864-224-1 from: 1 to: 2220
                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-299-810A-27 from: 1 to: 1485
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5851808
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                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: BC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2220 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Elledge, Stephen J.
APPLICANT: Liu, Qinghua
TITLE OF INVENTION: Repoid Subcioning Using Site-Specific
TITLE OF INVENTION: Recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 TGGGGGATAACTTGGGGA 112
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                  Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
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                                                                                                                                                                                                                                                                               /desc " "DNA"
                                                                                                                                                42.00
5.250
88.889
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Percent Identity: 83,333
                                                                                                               9
Gaps: 0
Percent Identity: 66.667
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Antelman, Douglas APPLICANT: Gregory, Richard J. APPLICANT: Wils, Kenneth N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            673 ATTCTATTCTGGGGGGTGGGGTGGGGG 699
                              FEATURE
                                                                                                                                                             LOCATION:
FEATURE:
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TITLE OF INVENTION: Retinoblastoma Protein
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                                                                                                                    PEATURE
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TOPOLOGY: lir
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CITY: San Francisco
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alignment_block:
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                            INFORMATION FOR SEQ ID NO: 19:
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FEATURE:
 SEQUENCE CHARACTERISTICS:
LENGTH: 4026 base pair
                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
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                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                NAME: Fitts, Renee A. REGISTRATION NUMBER:
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4026 base pairs
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Gaps: 0
Percent Identity: 66.667
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Quality:
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US-08-801-092-19
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                                                                                                               Patent No.
                                                                                                                           Sequence 33, Application US/08801092
                                                                                                GENERAL INFORMATION:
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                          APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
APPLICANT: Wils, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression
TITLE OF INVENTION: Retinoblastoma Protein
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 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
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Gaps: 0
Percent Identity: 66.667
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to: 4026

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US-08-801-092-33
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TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4249 base pairs
TYPE: nucleic acid
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NAME: FILLS, Renee A.
REGISTRATION NUMBER: 35.136
REFERENCE/DOCKET NUMBER: 016930-001020
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APPLICATION NUMBER: US 08 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
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MEDIUM TYPE: Floppy
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FEATURE:
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LOCATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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FILING DATE: 14-FEB-1997
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US-08-343-401A-3
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Ratio: 5.250
Percent Similarity: 88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1703 ATTCTATTCTGGGGGGGTGGGGTGGGGC 1729
                                                                                                                                                                                                        CLONE:
FEATURE:
                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 4283 base pairs
                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                               FEATURE:
                                                                                                                                                                                                                                        MOLECULE TYPE: D
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Andree, Christophe TITLE OF INVENTION: Improved 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Eriksson,
APPLICANT: Andree, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Swain, William F
APPLICANT: Macklin, Michael D
                                                                                   FEATURE:
NAME/KEY:
                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LeuLeuLrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/343,401A FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 53701-2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: PO BOX
                LOCATION:
                                 NAME/KEY:
                                                                LOCATION:
                                                                                                                     LOCATION:
                                                                                                                                        NAME/KEY:
                                                                                                                                                                       LOCATION:
                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                           TOPOLOGY: circular
                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                           nucleic acid
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PO Box 2113
                                                                                                                                                                       exon
713..721
              sig_peptide
713..1049
                                                                                 CDS
                                                                                                                     981..1253
                                                                                                                                   exon
                                                                join(713..721, 981..1253)
                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                            double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Improved Wound Healing
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Percent Identity: 66.667
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-343-401A-3
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                                                                                  alignment_block:
                                                                                                                                                               alignment_scores
                                 Align seg 1/1
                                                                                                                  Percent Similarity:
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                                                                US-09-471-276-831_COPY_1_16 x US-08-445-265A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08445265A Patent No. 5697901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 608-251-5000
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APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 Sout
CITY: Madison
  8 LeuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Quartes a minuter street
                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
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Ratio:
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                               to: US-08-445-265A-1 from: 1 to: 4283
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                                                                                                                                                                                                                                                                            other nucleic acid
/desc = "Plasmid DNA"
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5.250
88.889
                                                                                                               42.00
5.250
88.889
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                                                                                Gaps: 0
Percent Identity: 66.667
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Percent Identity: 66.667
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US-08-990-442-1
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                                                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                        US-09-471-276-831_COPY_1_16 x US-08-990-442-1
                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 608-251-500
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Berson, Bennett J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 53703
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Eriksson,
    APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Berson, Bennett
REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WH
                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4283 base pairs
Haynes, Joel R
Schmaljohn, Connie S
Fuller, Deborah L
Schmaljohn, Alan
                                                                                                                                                                                                                                                                                                                           88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         double
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1480 ATTCTAFTCTGGGGGGTGGGGTGGGGC 1506
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-990-442-1
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GENE DELIVERY BY MICRONEEDLE INJECTION

ADDRESSEE: Quaries & ____,
street; 1 South Pinckney Street

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 US/08/990,442

310558.90028

DESCRIPTION: /desc = "Plasmid DNA"

join(713..721, 981..1250)

Gaps: 9
Gencent Identity: 66.667

Align seg 1/1 to: US-08-990-442-1 from: 1 to: 4283

seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-760-615-7

Sequence 7, Application US/08760615
Patent No. 6200959
GENERAL INFORMATION:

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seq_documentation_block:
                                                                                                                                                                                      alignment_block:
us-09-471-276-831_COPY_1_16 x us-08-760-615-7
                                                                                                                                                                                                                                                                                                                                                        US-08-760-615-7
                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-132-808-1
                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                           Align seg 1/1 to: US-08-760-615-7 from: 1 to: 4326
                                                                                                                                                                                                                                                Percent Similarity:
Sequence 1, Application US/09132808
                                                                                       TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "Expression vector DESCRIPTION: construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: GENETIC
TITLE OF INVENTION: RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: pwrg7077
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                                                                                                                       8 LeuLeuleuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /function- "Human Cytomegalovirus OTHER INFORMATION: Intron A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 4326 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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1250..2062
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2912..3314
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5.250
88.889
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                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 66.667
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-09-132-808-1
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                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/1na/6B_COMB.seq:US-08-910-647-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-132-808-1 from: 1 to: 4328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08910647 Patent No. 6251433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6197332
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                           1862 ATTCTATTCTGGGGGGTGGGGTGGGGC 1888
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                    APPLICANT: Zuckermann et al.
TITHE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94608-2916
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ponald Zuckermann et al.
TITLE OF INVENTION: Clarid-Conjugated Polyamide Compounds and Related
TITLE OF INVENTION: Compositions and Methods Thereof
                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                           STREET: 4560 Horto
CITY: Emeryville
STATE: California
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ZIP: 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LeuLeuTrpGlyValThrTrpGly 16
                                                                 ZIP: 94608-2916
                                                                              COUNTRY:
                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
DEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         California
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                                                                                                                                     4560 Horton Street
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                                                                                                                                                          Chiron Corporation
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5.250
88.889
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Percent Identity: 66.667
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alignment_block:
us-09-471-276-831_COPY_1_16 x Us-08-910-647-2
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; MOLECULE TYPE: DNA (genomic)
US-08-910-647-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-910-647-4
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                ATTORNEY/AGISHT INFORMATION:
NAME: TUJILE SHAFON M.
REGISTRATION NUMBER: 38.459
REFERENCY/ACCKTF NUMBER: 12.18
REFERENCATION INFORMATION:
TELEPONN: (310) 523-2706
TELEPONN: (310) 553-3342
INFORMATION FOR SEO ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6251433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08910647
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TELEFAX: (510) 655-3342
INFORMATION FOR EGO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC POSYMS-DOS
SOFTMARE: PALEDILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/06/910,647
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                 CLASSIFICATION: 514
                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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94608-2916
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5.250
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                                                                                                                      1218.002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-910-647-4
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Ratio: 5.250
Percent Similarity: 88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5641665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                       MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KhāLIDI, SDITIN
TITLE OF INVENTION: PLASHIDS SUITABLE FOR IL-2 EXPRESSION
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISED Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Parker, Suzanne APPLICANT: Margalith, Michal
                   ORIGINAL SOURCE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                            FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                   NAME: Ways Vensko, Nancy
REGISTRATION NUMBER: 36,298
REFERENCE/DOCKET NUMBER: VICAL.043A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
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                                                                                                                                          TOPOLOGY:
                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
NAME/KEY: Coding Sequence
                                                                                                                                                          STRANDEDNESS:
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Gaps: 0
Percent Identity: 66.667
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alignment_block:
us-09-471-276-831_COPY_1_16 x us-08-345-913-1
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; OTHER INFORMATION:
US-08-345-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1689)..(2159)
US-08-818-562-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
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                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-564-313-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-818-562-1
                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-818-562-1 from: 1 to: 4928
                                                                                                                                                                                                                                                                                                                                                                                               US-09-471-276-831_COPY_1_16 x US-08-818-562-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-345-913-1 from: 1 to: 4928
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                                                                                                                                          Sequence 1, Application US/08564313
Patent No. 5910488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 1
LENGTH: 4928
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hobart, Peter M.
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Patent No. 6147055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Margalith, Michal
APPLICANT: Parker, Suczanne E.
APPLICANT: Matthi, Shirin
TITLE OF INVENTION: Plasmids Suitable for IL-2 Expression
FILE REFERENCE: 1530.008001
CURRENT APPLICATION NUMBER: US/08/818,562
CURRENT FILING DATE: 1997-03-14
ENRILER APPLICATION NUMBER: US 08/345,913
EARLIER FILING DATE: 1994-11-28
UNBER OF SOD ID NOS: 3
UNBER OF SOD ID NOS: 3
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                                                                                                                                                                                                                                                                      2388 ATTCTATTCTGGGGGGGTGGGGTGGGGC 2414
                       APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASM
                                        APPLICANT:
NUMBER OF SEQUENCES:
                                                                                   APPLICANT:
                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuLeuTrpGlyValThrTrpGly 16
                                                                                                                           INFORMATION:
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Ratio:
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                                                                                Nabel, Gary
                                                         Lew, Denise
                                                                                                  Nabel, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.00
5.250
88.889
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5.250
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PLASMIDS SUITABLE FOR GENE THERAPY: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 66.667
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alignment_block:
US-09-471-276-831_COPY_1_16 x US-08-564-313-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; CLONE: HLA-B7 and Beta-2 US-08-564-313-1
                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-06069-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-564-313-1 from: 1 to: 4965
                                                                                                                                                                                                                               Sequence 1, Application PC/TUS9406069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                              3021 ATTCTATTCTGGGGGGTGGGGTGGGGC 3047
CORRESPONDENCE ADDRESS:
ADDRESSE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 07-JUN-1993
ATTORNEY/ACENT INFORMATION:
NAME: Israelsen, Ned
                                                                                  NUMBER OF SEQUENCES:
                                                                                                 APPLICANT: Marquet, Magda TITLE OF INVENTION: PLASMIDS SUITABLE
                                                                                                                                     APPLICANT: Lew, Denise
                                                                                                                                                  APPLICANT: Vical incorporated
APPLICANT: Regents of the University of Michigan
APPLICANT: Nabel, Elizabeth
APPLICANT: Nabel, Glary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 619-235-8550
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COMPONENTING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0
FILING DATE: 01-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U:
ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 620 Newport
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Israelsen, Ned REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                LeuLeuTrpGlyValThrTrpGly 16
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5.250
88.889
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Percent Identity: 66.667
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                                                                                                    FOR GENE THERAPY
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: PCT-US94-06069-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                  Sequence 3, Application US/08910647 Patent No. 6251433 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
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                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: Polynucleotide Delivery NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/0
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Israelsen, Ned
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                    COUNTRY:
                                                                                                                       STREET: 4560 Hor
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TOPOLOGY: cir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US94/06069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            ADDRESSEE:
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                                                                        94608-2916
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                                                                                                                                        4560 Horton Street
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                                                                                                                                                                                                                                                   Zuckermann et al
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                                                                                                                                                            Chiron Corporation
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5.250
88.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 9
Gaps: 0
Percent Identity: 66.667
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; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-910-647-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-073-836-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08073836 Patent No. 5650306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2643 ATTCTATTCTGGGGGGGGGGGGGGGGC 2669
                                                                                                              CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
NAME: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION
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                                                         TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yeng, Zhi-yong
APPLICANT: Liu, Jinsong
TITLE OF INVENTION: RECOMBINANT NUCLEIC
TITLE OF INVENTION: HIV GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                         TELEFAX:
                                                                                                                                                                                                 FILING DATE: 07-JU
                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 92122
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                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La
CITY: San Diego
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/910,647
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                     California
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                                                                                                                                                                                                                                                                                                                                                                                                                                         4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5107 base pairs
                                         (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nabel,
                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (510) 923-2706
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88.889
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N: 514
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                                                                                                                                                                                                                       US/08/073,836
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; TOPOLOGY: linear US-08-073-836-3

LENGTH: 5653 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

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alignment_scores:
Quality:
Ratio:
Percent Similarity:
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US-09-471-276-831_COPY_1_16 x US-08-073-836-3
                                                                                                                                                        : STRANDEDNESS: single
TOPOLOGY: unknown
; MOLECULE TYPE: Other nucleic acid
US-08-235-277-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block;
; Sequence 1, Applicatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-235-277-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 42.00
Ratio: 5.250
Percent Similarity: 88.889
                                                                                                                                                                                                                                                                                                   ATTORNEY/ACENT INFORMATION:

NAME: ODION, NO. 5733543man F.

RECISTRATION NUMBER: 24,618 2.008-68

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEPA: (703) 413-3000

TELEPA: (703) 413-3200

TELEPX: (703) 413-3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-073-836-3 from: 1 to: 5653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dequence 1, Application US/08235277 Patent No. 5733543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: NABEL, GARY J
APPLICANT: WOFFENDIN, CLIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1286 ATTCTATTCTGCGGGGTGGGGTGGGGC 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERNTING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTING HELBASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/OB/235,277
FILLING DATE: 29-RR-1994
CLASSIFICATION: 436
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: YANG, NIN-SIN
APPLICANT: SHEEHY, MICHAEL J
TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES
TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1755 S. CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C. STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 LcuLeuTrpGlyValThrTrpGly 16
                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
42.00
5.250
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Gaps: 0
Percent Identity: 66.667
Length: 9
Gaps: 0
Percent Identity: 66.667
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// Spn2_6/pcodata/2/ina/Sp_Com8. seq: US-09-20-90-61: 7, 40, 0142.66 2.69 (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2007.26) (2
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Database sequences: 351203
Database length: 113238999
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Query length:
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"O-YGGT2_JUSPO_Spool_W089471276_frunak_07012002_142445_19901/app_query.fasta_1.274

"Delissed_Batents_NA. -OPMT-fastap -SUFFIX=rni -GAPOP=12.000

-GAPEXT=4.000 -HINMATCH=0.100 -LODGCL=0.000 -LODGEXT=0.000

-GAPOP=4.500 -GAPEXT=7.000 -KGAPOP=10.000 -KGAPEXT=0.500

-GAPOP=6.000 -FGAPEXT=7.000 -KGAPOP=10.000 -KGAPEXT=0.500

-EGAPOP=6.000 -EGAPEXT=7.000 -KGAPOP=10.000 -KGAPEXT=0.500

-EGAPOP=6.000 -EGEXPEXT=7.000 -STAFT1 - HAVREX-DIOSUMGP=FCT

-TRANS-100 -THE_NIM=0 -ALIGN=45 -MODE—LOCAL-OUTFMT=FCS

-NORM-CXT -THE_NIM=0 -ALIGN=45 -MODE—LOCAL-OUTFMT=FCS

-NORM-CXT -THE_NIM=0 -ALIGN=45 -MODE—LOCAL-OUTFMT=FCS

-OUTFMENTS-175 -MODE—LOCAL-OUTFMT=FCS

-OUTFMENTS-175 -MODE—LOCAL-OUTFMT=FCS

-OUTFMENTS-175 -MODE—LOCAL-OUTFMT=FCS

-DOBLOCAL-OUTFMT=FCS

-DOBLOCAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7, 2002 4:54
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1624
1624
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
ADDRESSEE: DNAA neuer-
correct: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21, Application US/08985950
o. 6140076
                                                                                                                                                                                                                                                                                                                                                           Adema, Gosse
                                                                                                                   DNAX Research Institute
                                                                                                                                                                                                                                                                                         Isolated Mammalian Monocyte Cell Genes;
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alignment_block:
US-09-471-276-831 x US-08-985-950-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : LOCATION: 1722
; OTHER INFORMATION: /note: "nucleotide 1722 designated
US-08-985-950-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: NJAC

PRIOR APPLICATION NUMBER: US 60/041,279

PRIOR APPLICATION NUMBER: US 60/03,3181

PRIOR APPLICATION NUMBER: US 60/03,3181

PRIOR APPLICATION NUMBER: US 60/03,3181

PRIOR APPLICATION NUMBER: US 60/03,252

ATTORREST/AGENT INFORMATION:

REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0670K

TELEPONE: (650)496-1204

INFORMATION FOR SED ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 2790 base pairs

STRANDEDNESS: SINGLE

STRANDEDNESS: SINGLE

STRANDEDNESS: SINGLE

TOPOLOGY: Linear

TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allgnment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-985-950-21 from: 1 to: 2790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPAILINE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA ReLEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMERE: US/08/985,950
FILING DATE: 05-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                  324 CAGGGGGGCCAGGAGCCCAGGAGTACCGTCTATATAGAGAAAAGAAAAC 373
                                                                                                                                                          277 AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT 323
                                                                                                                                                                                                                                                               227 CCGGACCCACGTGCAGGCAGGCACCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                    177 ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                    50 roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu..... 63
                                                                                                                                                                                                  34 luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
                                                                                                                                                                                                                                                                                                17 OValThrGluAlaAlaIlePheTyrGluThrGln***SerIcuTrpAlaG 34
64 .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                    1 MetSerMetLeuValValPheLeuLeuUrpGlyValThrTrpGlyPr
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LOCATION: 1722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
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California
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1,449
56.198
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Gaps: 7
Percent Identity: 33.884
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-345-468-11
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US-09-471-276-831 x US-09-345-468-11
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LENGTH: 2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Busfield, S.
APPLICANT: VILIEVAL, J.
APPLICANT: Vandrot-Perrus, M.
APPLICANT: Vainchenker, M.
APPLICANT: Vainchenker, M.
TTULE DE INVENTION: GUTCOPROTEIN VI AND USES THEREOF
EILE REFERENCE: 7853-147
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CURRENT FILING DATE: 1999-06-30
CURRENT FILING DATE: 1999-06-30
NUMBER OF EGO ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                       281 AAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGGG 330
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yArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerL 106
                                                                                                       .....CCAGGC......TCTGTGATCAGCTGGGGGAGCCC 180
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seq_documentation_block:
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                                                                               alignment_block: us-08-985-950-11
                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                              US-08-985-950-11
                                               Align seg 1/1 to: US-08-985-950-11 from: 1 to: 1620
                                                                                                                               Percent Similarity:
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Patent No. 6140076
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650)496-120 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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; LOCATION: (1)..(732)
US-09-135-782-3
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                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-135-782-3 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Method for Cloning And Producing The NspI Restriction TITLE OF INVENTION: Endonuclease In E. coli And Purification Of The TITLE OF INVENTION: Recombinant NspI Restriction Endonuclease FILE REFERENCE: NEB-143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/135,782 CURRENT FILING DATE: 1998-08-18
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ORGANISM: No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                               441 CTTAACATCTATGAATGATAATGAAATCAAGCGAAAGTTTCAATTGTTGA 490
                                                                                                                                             394 GATCATAGATTTCCG.
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                                                           71 sLeuAspSer......ProAlaIleLysHlsGlnPhe...LeuLeuT 84
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US-09-471-276-831 x US-09-172-108-48
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                                                                                                                                                                                                                                                        Sequence 45, Application US/09172711 Patent No. 6160105
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SEQ ID NO 48
LENGTH: 285
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                                                   APPLICANT: Cunnisham, Mary Jane
APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott R.
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: MOUNTORING TOXICOLOGICAL RESPONSES
FILE REFERENCE: PA-0011 US
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CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 56
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APPLICANT: Zweiger, Gary B.
APPLICANT: Panzer, Scott R.
APPLICANT: Sellhamer, Jeffrey J.
TITLE OF INVENTION: ARRERS FOR PEROXISOMAL
FILE REFERENCE: PA-0012 US
CURRENT APPLICATION NUMBER: US/09/172,711
CURRENT FILING DATE: 1998-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                              151 GATCACACCTGGCCTGAGGACATTCCTGCTGTGCCAGGGGACAGT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 AGTCC.....CTTGCCCAGGCCCTGGCTTTCTGCCAATCCAGTGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 .....AspValProGlyProProGlyAspSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 ATGTCTCTGCTGACTACTGTACTACTTCTCTGGGGTTTCATTCTGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCAACTGACACCCTGTATATT.....CAAGGAAGCCTCGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerGlyLeuSerThrGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.50
1.863
61.538
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alignment_block:
US-09-471-276-831 x US-09-172-711-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: 700607235H1 US-09-172-711-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 61
SOPTMARE PERL PROGRAM
SEQ ID NO 45
LENGTH 285
LENGTH 285
TYPE: DNA
ORGANISM: Homo sapiens
FEMTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
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Ratio: 1.863
Percent Similarity: 61.538
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APPLICANT: SODA, KENJI

APPLICANT: TANAKA, HIDCHIKO

APPLICANT: INGOE, HIROYUKI

APPLICANT: INGOEL, KENJI

APPLICANT: ESAKI, NOBUYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-172-711-45 from: 1 to: 285
                    COUNTRY. USA.

ZIT: 2204-074
ZIT: 2204-074
ZOMENTER ERANALE FORM.

COMPUTER ERANALE FORM.

COMPUTER: ELAN PC COMPALIS.

COMPUTER: LEW PC COMPALIS.

COMPUTER: LEW PC COMPALIS.

COMPUTER: LEW PC COMPALIS.

COMPALIS.

SOFTMARE: PCLOTION BATA:

SOFTMARE: PCLOTION BATA:

PELLOW LOW BATE:

PELLOW LOW BATE:

ATTORNEY ADELICATION BATA:

PELLOW LOW BATE:

PELLOW BATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08641038A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: RECOMBINANT L-METHIONINE GAMMA-LYASE NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 GATCACACCTGGCCTGAGGACATTCCTGCTGCCAGGGGACAGT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 AGTCC.....CTTGCCCAGGCCCTGGCTTTCTGCCAATCCAGTGCCCTG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 ATGTCTCTGCTGACTACTGTACTTCTCTGGGGTTTCATTCTGGGCCC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: FALLS CHURCH
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....AspValProGlyProProGlyAspSer 56
(703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 36.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 65
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STATE: VA COUNTRY: USA ZIP: 22040-0747 COMPUTER READARLE FO
GENERAL INFORMATION: APPLICANT: SODA, KEN APPLICANT: TANAKA, H APPLICANT: INOUE, HI APPLICANT: INACAKI, INOUE, APPLICANT: INACAKI, NO TITLE OF INVENTION: NUMBER OF SEQUENCES:
ည်လမှ
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-059-178-1
81 eLeukeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyKeu 97
70ValHisLeuAppSerproblilalieLysHisclnph 81
61 alGlnGluTrpGlyAlaGlnGluFro
49 ProGlyProPro
33 AlaGluSerGluHis ***LeuLysThrLeuGlyGlnCysAspAlaAspVa 49 110
16 lyProValThrGluAlaAlaTlePheTyrGluThrGln***SerLeuTrp 32 ::: ::: 754 GACCCTATACGTCTGCAGGGCCTCAAGGACATGACCGGTGCGGTGCTCTC 803
2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrp.G 16 1:111 1:11
Align seg 1/1 to: US-08-641-038A-1 from: 1 to: 1320
alignment_block: US-09-471-276-831 x US-08-641-038A-1
alignment_scores: 74.50 Length: 117 Quality: 74.50 Length: 117 Ratio: 1.242 Gaps: 6 Percent Similarity: 51.282 Percent Identity: 29.060
IS-01
TYPE: nucleic acid STRANDEDNESS double TOPOLOCY: linear thought the state of the st
INF

MEDIUM TYPE: Floppy disk

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seq_documentation_block:
; Sequence 1, Application US/08642541
; Patent No. 5891704
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US-09-471-276-831 x US-09-059-178-1
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; LOCATION: 61..1254
US-09-059-178-1
                                                                                               seq_name: /cgn2_6/ptodata/2/ina/58_COMB.scq:US-08-642-541-1
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WIRELY JR. GERALD H
REGISTRATION HUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0020-39(
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
TELEPHONE: (703) 205-8000
INFORMATION FOR SED ID NO: 1:
SEQUENCE GINARCTERISTICS;
LENGTH: 1320 base pairs
TYPE: Nucleic acid
TYPE: Nucleic acid
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
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                                                                                                                                                  1004 CCTT.....CGAACTCAAGGGCGGCATCGGTGCCGGGGGGGGGTT 1043
                                                                                                                                                                                                                                                                                                                                                 904 CGGCAGCCGCAGGTGGAGCTGATCCATTACCCGGGCCTGGCGAGCTTCCC
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 954 GCAGTACACCCTGGCCGGCCAGCAGATGAGCCAGCCGGGCGGCATGATCG 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                854 GCATGGACCGCCACTGCGCCAACGCTCAGGTGCTGGCCGAGTTCCTCGCC 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 GCCCCATGACGCCGCACTGTTGATGCGCGGCATCAAGACCCTCAACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754 GACCGTATACGTCTGCAGGGCCTCAAGGACATGACCGGTGCGGTGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           704 GCCATGGCGACATCACTGCTGGCATTGTGGTGGGCAGCCAGGCACTGGTG 753
                                                                                                                                                                                                                                                                                                                                                                                          81 cLcuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeu 97
                                                                                                                                                                                                                                                                             70 ...ValHis......LeuAspSerProAlaIleLysHisGlnPh 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 AlaGluSerGluH1s****LeuLysThrLeuGlyGlnCysAspAlaAspVa 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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1.242
51.282
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Percent Identity: 29.060
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	69	61 alGlnGluTrpGlyAlaGlnGluPro
	61 890	49 lProGlyProProGlyASpSerArgLeuProAlaV 6
	49 840	33 AlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspVa (
	32 790	1
	16 740	2 SerMetLeuValValPheLeuLeuLeuTrGSLyvalThrTpr.G I 2 SerMetLeuValValPheLeuLeuLeuTrGSLyvalThrTpr.G I 591 GCCATGGCGACATCACTGCTGGCATTGTGGTGGGCAGGCA
		Align seg 1/1 to: US-08-642-541-1 from: 1 to: 1369
		alignment_block: US-09-471-276-831 x US-08-642-541-1
		alignment_scores: Outlity: 74.50 Length: 117 Ratio: 1.242 Gaps: 6 Percent Similarity: 51.282 Percent Identity: 29.060
		; MOLECULE TYPE: DNA (genomic) ; FEATURE; ; NAME/KEY: CDS ; LOCATION: 481241 US-08-642-541-1
		STRANDEDNESS: double TOPOLOGY: linear
		TELEFAX: (202) 822-0168 TELEX: 90-4030
		RECISTRATION NUMBER: 36,217 REFERENCE/DOCKET NUMBER: 31276-20002.21
		NAME: MILITAD ROBERT A
		FILING DATE: 03-MAY-1996 CLASSIFICATION: 424
		40 541
		OPERATING SYSTEM: PC.DOS/MS-DOS SOFTWARE: Patentin Release #1.0. Version #1.30
		; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible
		; ZIP: 20006-1888 ; COMPUTER READABLE FORM:
		COUNTRY: USA
		hington
		EE: MORRISON & FOERSTER
		EKEFKOM AND
PRODUCED	METHIONINASE	TITLE OF INVENTION: METHIONINASE, PURIFIED RECOMBINANT
		YUYING, TAN NEWTON: GEORGESSION NORTHER

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alignment_block:
US-09-471-276-831 x US-08-642-541-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
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US-08-642-541-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/642,541
FILING DATE: 03-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MILIDAIN, ROBERT A:
REFERENCE/POCKET INUBER: 31276-20002
TELEFONNE: (202) 887-1500
TELEFONNE: (202) 887-1500
TELEFON (202) 887-1500
TELEFON (202) 887-1500
TELEFON (202) 887-1500
TELEFONE: (202) 887-1500
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                                                                                                                                                                                                                                Align seg 1/1 to reverse of: US-08-642-541-3 from: 1 to: 1369
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Percent Similarity:
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Patent NO. 5891704
GENERAL INFORMATION:
APPLICANT: YUYING, TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YUYING, TAN
TITLE OF INVENTION: HIGH
TITLE OF INVENTION: METH
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           991 CCTT.....CGAACTCAAGGGCGGCATCGGTGCCGGGCGGCGGTT 1030
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629 GACCGTATACGTCTGCAGGGCCTCAAGGACATGACCGGTGCGGTGCTCTC 580
                                                                                                                679 GCCATGGCGACATCACTGCTGGCATTGTGGTGGGCAGCCAGGCACTGGTG 630
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                                                    16 lyProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrp 32
                                                                                                                                                                2 SerMetLeuValValPheLeuLeuLeuTrpGlyValThr.....Trp.G 16
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ZIP: 20006-1888
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CITY: Washington
STATE: DC
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1.242
51.282
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METHIONINASE, PURIFIED RECOMBINANT METHIONINASE PRODUCE
THEREFROM AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                            Gaps: 6
Percent Identity: 29.060
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33 AlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspVa 49

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DEBANTING SYSTEM: Windows SOFTMARE: FastSDE for Windows Version 2.0b CURRENT APPLICATION NUMBER: US/09/260,889 FILING DATE: APPLICATION NUMBER: US/09/260,889 FILING DATE: CLASSIFICATION: 424 PRIOR APPLICATION NUMBER: 08/914,377 FILING DATE: 19-MG-1997 APPLICATION WINBER: 08/942,541 FILING DATE: 03-MAY-1996 APPLICATION NUMBER: 08/942,541 FILING DATE: 03-MAY-1996 APPLICATION NUMBER: 03/95 APPLICATION NUMBER	entation_block. 1. Application US/09260889 10. 6221854 10. 121854 10. 121854 10. 121854 10. 121854 10. 121854 10. 121855 10. 121854 10. 121855 10. 121855 10. 121855 10. 121855 10. 121855 10. 121855 10. 121855 10. 121855 10. 12185 10.	

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alignment_block:
US-09-471-276-831 x US-09-260-889-1
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-260-889-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09260889 Patent No. 6231854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                FILING DATE: 03-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/9
FILING DATE: 19-AUG-1997
APPLICATION NUMBER: 08/6
                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: TAN, YUYLIG
TITLE OF INVENTION: METHIONINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             991 CCTT......CGAACTCAAGGGCGGCATCGGTGCCGGGCGGCGGTT 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           941 GCAGTACACCCTGGCCCGCCAGCAGATGAGCCAGCCGGCGGCGCATGATCG 990
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                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COL
                      NAME: Murashige, Kate H REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 2000 Pennsylvania Avenue, NW, suite 5500 CITY: Washington STATE: DC
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                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                          20006-1888
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                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                            Diskette
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1.242
51.282
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                                                                                                                                                              08/914,377
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                   29,959
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31276-20002.11
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-384-106A-8
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US-09-471-276-831 x US-09-260-889-3/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8,
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MOLECULE TYPE:
ANTI-SENSE: YI
                                                                                                                                                                                  APPLICANT: Sherr Ph.D., Charles J.

APPLICANT: Downing M.D., James
APPLICANT: Hiral Ph.D., Hiroshi
APPLICANT: Hiral Ph.D., Hiroshi
APPLICANT: Ohuda, Tsukasa
TITLE OF INVENTION: InK4C-P19 and InK4d-P19, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6,
NUMBER OF SEQUENCES: 25
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LENGTH: 1369 base pairs
TYPE: nucleic acid
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TELEPHONE: 202-887-1500
                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                379 CCTT.....CGAACTCAAGGGCGGCATCGGTGCCGGGCGGCGGTT 340
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                                                                        CITY: Washington
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                      COUNTRY:
                                                     STATE:
                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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20005
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                                                 D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08384106A
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1.242
51.282
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                                                                                                                                                                                                                    and Uses Thereof
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COMPUTER READABLE FORM:

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seq_documentation_block:
Sequence B Application PC/TUS9601643
SERERAL INFORMATION:
APPLICANT: St. Jude Children's Research Hospital
TITLE OF INVENTION: InKic-pl8 and InKid-pl9, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDK4 and CDK6, and Uses Thereof
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96.01643-8
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Ratio: 1.542
Percent Similarity: 48.485
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TELEPHONE: 202-771-2400
INFORMATION FOR SED.ID NO: 8:
SEQUENCE IGHAPOTERISTICS:
LENGTH: 501 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                            431
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NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                        346 CAAGAGGGTCACACTGCTGTGGTCAGCTTTCTGGCAGCTGAATCTGATCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 .....CTGAAGGTCCTAGTGGAGCACGGGGCTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 ATGTCAACGTGCCTGATGGCACCGGGGGCACTTCCAATCCATCTGGCAGTT 345
                                                                                                                                                                                                                                                                     87 ThrGInGIYAT9TYAT9CYSAT9SerGIYLENSETTHGIYTFD 101
87 ThrGINGIYAT9TYAT9CYSAT9SECGIYLENSETTHGIYTFD 101
431 .....AGCTGGCACTGCAGAGAGAGGGCCTCAGGACCTCCGTGG 466
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                                                                                                                                                                                                                                                                                                                                                                                                                      70 lHis.LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAsp 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 GlnGlu.....TrpGlyAlaGlnGluProVa 70
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FILING DATE: 06-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1..501
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His.LeuaspSerProAla11eLysH1sG1nPheLeuLeuThrGlyAsp	70 1 396 C
TrpGlyAlaGlnGluProVa 70III::::: ACTGCTGTGGTCAGCTTTCTGGCAGCTGAATCTGATCT 395	62 G 346 C
OPTOGLYASpSerArgLeuProAlaVal 61	48 spVa 296 ATGTC
1uHis***LeuLysThrLeuGlyGlnCysAspAlaA 48 :::	31 uT 268
hrGluAlaAlaIlePheTyrGluThrGln***SerLe ?	17 ProValThrGluAI ::: 229 CCAGTCCATGACGC
PCT-US96-01643-8 from: 1 to: 501	Align seg
PCT-US96-01643-8	alignment_ US-09-471
74.00 Length: 99 .542 Gaps: 6 8.485 Percent Identity: 30.303	alignment_ Percent S
THE PROPERTY OF THE PROPERTY O	MEDITIA TYPE: CDA MEDITIA TYPE: Flop MEDITIA TYPE: MEDITIA TIPE MEDITIA TON INMERSE MEDITIA MEDITIAN INMERSE MEDITIAN INFORMATION INMERSE MEDITIAN INFORMATION I
	STATE:
EE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 New York Ave., N.W. Washington	; ADDRESSEE: STREET: Was

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alignment_block:
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TELEPOMMUNICATION INCOMMATION:
TELEPIANE: 202-371-2640
TELEPIAN: 202-371-2540
TELEPIAN: 202-371-2540
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L.
NAME: OX, Samuel L.
                                                                                                                                             322
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Downing M.D., James APPLICANT: Hirai Ph.D., Hiroshi APPLICANT: Okuda, Tsukasa
                                             350 ATGTCAACGTGCCTGATGGCACCGGGGGCACTTCCAATCCATCTGGCAGTT
                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                        48 spValProGlyProProGlyAspSerArgLeuPro.....AlaVal 61
                                                                                                                                                                                 31 uTrpAlaGluSerCluHis***LeuLysThrLeuGlyClnCysAspAlaA 48
                                                                                                                                                                                                                                                                                17 ProvalThrGluAlaAlaIle.....PheTyrGluThrGln***SerLe 31
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62 GlnGlu.....TrpGlyAlaGlnGlnProVa 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-FEE CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30
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alignment_block:
US-09-471-276-831 x US-08-384-106A-19
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                                                               Align seg 1/1 to: US-08-384-106A-19 from: 1 to:
                                                                                                                                                  Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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APPLICANT: bowning M.D., James
APPLICANT: Hirai Ph.D., Hiroshi
APPLICANT: Okuda, Tsukasa
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                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 555 base pairs
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FOX SAMUEL L.
FOX SAMUEL SO, 353
                                                                                                                                                                   Ratio:
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1100 New York Ave., N.W.
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                                                                                                                                                                                                                                                                      CDS
55..552
                                                                                                                                                                                                                                                                                                                                          linear
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1.542
48.485
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                                                                                                                                                Percent Identity: 30.303
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                                                                  555
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31 uTrpAlaGluSerGluHis++*LeuLySThrLeuGlyGlnCysAspAlaA :: :: 322	48 349
48 spvalproglyproproglyAspSerArgLeuproAlaval	399
62 ClnGlu	70 449
70 lHis.LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAsp:: ::: :::: ::: ::: ::: ::: :::	86 484
89	
seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-240-906-1	
Sequence 1, Application US/09240906 Fatent No. 6243965 GENERAL INFORMATION: APPLICANT: ROUSSEL, MARTINE F. APPLICANT: SMEYNE, RICHARD APPLICANT: SMEYNE, RICHARD APPLICANT: STRUENCE, TACK P191NK4D AND P27K1P1 TITLE OF INVESTION: CELLS THAT LACK P191NK4D AND P27K1P1 FILE REFERENCE: 1340-1-025 CURRENT RAPLICATION NUMBER: US/09/240,906 CURRENT FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 8 SOFTWAREE PATENTIN VET. 2.0 SED ID NO 1 LENGTH: 555 TYPE: DNA CORANISH: Homo sapiens	ACTIVITY AND
alignment_scores: 99 Quality: 74.00 Length: 99 Retio: 1.542 Gaps: 6 Percent Similarity: 48.485 Percent Identity: 30.303	
alignment_block: US-09-471-276-831 x US-09-240-906-1	
Align seg 1/1 to: US-09-240-906-1 from: 1 to: 555 17 ProValThrGluAlaAlallephgTyrGluThrGln***SerLe	3 L
CysAspAla CACGGGGCT	48
48 spValproGlyProDroGlyAspSerArgLeuDroAlaVal	399
62 GINGIUTrpGIyAlaGINGINPTOVA	70 449
70 lHis.LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAsp	86

alio US

322CTGAAGGTCCTAGTGGAGCACGGGGCTG 349

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alignment_block:
US-09-471-276-831 x PCT-US96-01643-7
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Quality:
Ratio:
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PCT-US96-01643-7
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Sequence 7, Application PC/TUS9601643
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
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TOPOLOGY: line
MOLECULE TYPE: c
ORIGINAL SOURCE:
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ZIP: 2000.
ZIP: 2000
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POSITION IN GENOME:
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LENGTH: 555 base pairs
TYPE: nucleic acid
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: St. Jude Children's Research Hospital
TITLE OF INVENTION: INX4c-pl8 and InX4d-pl9, Inhibitors of
TITLE OF INVENTION: Cyclin Dependent Kinases CDX4 and CDX6, and Uses Thereof
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600 TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
                                                                                                   450 CCATCGCAGGGACGCCAGGGGTCTCACACCCTTGG.........
31 uTrpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaA 48
                                                                                                                                                                              17 ProvalThrGluAlaAlaIle.....PheTyrGluThrGln***SerLe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 ThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fox, Samuel L. REGISTRATION NUMBER: 30,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....AGCTGGCACTGCAGAGAGGGGCTCAGGACCTCGTGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.00
1.542
48.485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 99
Gaps: 6
Percent Identity: 30.303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0656.050PC01
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alignment_block:
US-09-471-276-831 x PCT-US96-05252-1
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                                                                                                                                      alignment_scores:
                                                                                                                                                                                                      PCT-US96-05252-1
                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9605252 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-AR-1955
FILING DATE: 17-AR-1950
FILING DATE: 17-AR-1950
FILING DATE: 17-AR-1950
REGISTRATION UNBER: 32,762
REGISTRATION UNBER: 32,762
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPAILDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALCHILI Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: p19: A Cell Cycle Inhibitor NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400 CAAGAGGGTCACACTGCTGTGGTCAGCTTTCTGGCAGCTGAATCTGATCT 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350 ATGTCAACGTGCCTGATGGCACCGGGGCACTTCCAATCCATCTGGCAGTT 399
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 ThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 lHis.LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAsp 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 GinGlu.....TrpGlyAlaGlnGluProVa 70
                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco
                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 023078-059910PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             spValProClyProProGlyAspSerArgLeuPro.....AlaVal 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ....AGCTGGCACTGCAGAGAGGGGGCTCAGGACCTCGTGG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US96-05252-1
                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                        H: 706 base pairs
nucleic acid
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                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           California
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                                                               74.00
1.542
48.485
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                                                               Percent Identity: 30.303
                                                                                                               Length:
                                                                                         Gaps:
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alignment_scores:
                                                                                                             ; TOPOLOGY: 1;

MOLECULE TYPE:

US-08-667-939A-13
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GENERAL INFORMATION:
APPLICANT: LUO, S
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                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Datentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 CCAGTCCATGACGCAGCCCGCACTGGATTCCTGGACACC....... 267
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 CAAGAGGGTCACACTGCTGTGGTCAGCTTTCTGGCAGCTGAATCTGATCT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ATGTCAACGTGCCTGATGGCACCGGGGCACTTCCAATCCATCTGGCAGTT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 .....CTGAAGGTCCTAGTGGAGCACGGGGCTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 ThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 ProValThrGluAlaAlaIle.....PheTyrGluThrGln***SerLe 31
                                                                                                                                                                                                                                                                     TELEPHONE: ZUZ -
TELEPHONE: ZUZ-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 24-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                  NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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Quality:
Ratio:
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                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/667,939A
                                                                                                                                                                                                                                                                                                                                                                                  25,618
                                                                                                                                                                                                                                                                                                                                                               LUO-2A
Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Suite 300
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-667-939A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-667-939A-14
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US-09-471-276-831 x US-08-667-939A-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application Patent No. 5998166
GENERAL INFORMATION:
                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT IMPORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25.618
REFERENCE/DOCKET NUMBER: LUO-2A
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC compatible

OPERATING SYSTEM: PC -DOS/MS-DOS

SOFTWARE: PATCHIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/667,939A

PAILING DATE: 44-UN-1396

PRIOR APPLICATION DATA: 1996

PRIOR APPLICATION DATA: 1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LUO, Shun
TITLE OF INVENTION: CD16-II VARIANTS
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337
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LENGTH: 765 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 uAlaLeuAspGlyAlaSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 euSerLysLeuLeuGluLeu. ThrGlyProLysValLeuAlaCysSerLe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 ATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACAGTCGACGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 GGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 rGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnL 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AspSerProAlaIleLysHisGInPheLeu....LeuThrGlyAspTh 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 erArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHisLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCCTCGGTGGGTGTTCA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4, Application US/08667939A
5998166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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STREET: 533 STREET: 531 STREET: 501 COUNTRY: 601 COUNTRY: 602 STATE: 6010 STAT	seq_documentalion_block	287 TCAGTGACCCGGTGCAGC 120 uall_elahsiG[;Alase 120 uall_elahsiG]	73 99 87 04	1 to	alignment_scores:
anhattan Circle, Sulte 2 proximation Circle, Sulte 2 proximation of the comparible processes allo, version proximation of the circle proximation o	lock: Cation US/08483376 0 10N: ION: Sil, Vimila ancy, Maureen A. 11, Robert J. Sil, Indra K. Sil, Indra K. TION: Expression BMCES: 4 ADDRESS:	TAGAAGTCC r 126 l 355 A 355 /ina/5B_C	Leu ##############################	US-08-667-939A-14 from: spalaaspvalProGly ACTCTGAAGTGCAAGGAGGCCTACTC AAAAAAGAGGTTTTAAAAAA AAAAAGTTTAAAAAA	: 74.00 Lengt : 1423 Gap : 57.143 Percent Identit
01 F. C.	or.	GTTGC	rGlyAspTh 87 AGTCGACA 24 rp***GlnL 10C 28 aCysSerLe 12	to: oproG CTGAG	h: 91 s: 7 y: 35.165

PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/830.356
FILING DATE: 05-FEB-1992
PRICE APPLICATION DATA:
APPLICATION UNMERE: US 07/353.854
FILING DATE: 18-MAY-1989
ATTORNEY/ACENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION UNUMER: 33.878
REFERENCE/DOCKET NUMBER: 10-948
TELEPHONE: (303) 49-8080
INFORMATION: FOR SEQ ID NO: 15-ELEPHONE: (303) 49-8080
INFORMATION FOR SEQ ID NO: 15-ELEPHONE: (303) 49-8080
INFORMATION FOR SEQ ID NO: 15-ELEPHONE: (304) 49-8080
INFORMATION: 131.182
INMEXICEY: exon
LOCATION: 131.182
INMEXICEY: exon
INMEXICEY: exon
INMEXICEY: exon
INMEXICEY: exon
INMEXICEY: exon
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LOCATION

FEATURE

LOCATION

FAUTURE

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NAME/KEY:
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FEATURE:
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LOCATION:
FEATURE:
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NAME/KEY:
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NAME/KEY:
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FEATURE:
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                                  exon
5636..5917
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4768
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3256..3351
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2822..3038
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2605..2728
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2269..2460
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2041..2187
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5372.
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4158.
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3912.
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3447.
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4517
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3702.
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1828..1948
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100 200	Seq_documentation_block: Sequence 3. Application US/09193191 PRICENT No. 6.330078 PRICENT NO. 6.330078 PRICENT NO. 6.30078 PRICENT NO. 6.30078 PRICENT NO. 6.30078 PRICENT NO. SUHANG-YONG TITLE OF INVENTION: METHOD FOR CLONING THE METHIT RECOMBINANT METHIT OF INVENTION RESTRICTION ENDONUCLEASE FILE REFERENCE: MSpHI CURRENT FILING DATE: 1998-11-17 UNDRES OF SEQ ID NOS: 12 SOFTWARE: PRECITY OF SEC 10 NOS: 12 SOFTWARE: PRICENT NOS: 12 SOFTWARE: 135 SOFTWARE: 135 SOFTWARE: 135 SOFTWARE: 131-31-31-31-31-31-31-31-31-31-31-31-31-	ame: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-09-193-19	109 GluieuthrolyProlysvalleuAlaCysSorLeuAlaLeuAsp 123	92 rgCysArgSerGlyLouSerThrGlyTrp***GlnLouSerLysLouLou 108 5296 CGAGTGTCCCTGGGGAGTAACAGATGCGCCTTGAGTCAGCAAAATTT 5247	81	70 ValHisLeuAspSerProAlalleLysHisGIn	54 yAspScrArg LeurroAlaValdingluTrpGlyAligInglurn 69	40ysThrLeuclyclinysAspAlaAspValProclyProprocl 54 5496 TCAGGCGTGAAAAANCTCCAANGTACCGCCGGTCTCGCCCGTCTCCAGG 5447	6 AGAGGCAGAGGCAGGCAGCATCAAACGGCTTACCAGGCTACGGTACT 5	39	27 rGln***SerLeuTrpAlaGluSerGluHis***Leu	1 ProGLYWAITH-TEPGLYPOVALTH-GLANALALEPHETYFGLUTH 27 11 1	Align seg 1/1 to reverse of: US-08-483-376-1 from: 1 to: 6386	alignment_block: us-09-471-276-831 x us-08-483-376-1/rev	alignment_scores: Ouality: 73.00 Length: 149 Ratio: 1.106 Gaps: 5 Percent Similarity: 44.295 Percent Identity: 20.805
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alignment_block:
US-09-471-276-831 x US-09-193-191-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: BETHELINS: NOVEL CYSTEINE-RICH GROWTH
TITLE OF INVENTION: MODULATING PROTEINS
                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 NAMAGACGCATCAGGTAATCACAATCTTTTAAAATCGAGAAGTTGTGAG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 GATCATCGATTCCCG...ATGGAACGTTGGGGAGCTAGTGAGCCTCCACA 440
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 hrGlyAspThrGlnGlyArgTyrArg......CysArg 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 sLeuAspSerProAla......IleLysHisGlnPhe...LeuLeuT 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 19910819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
                                          TISSUE TYPE: Kidney
                                                               ORGANISM:
                                                                                                                               TOPOLOGY:
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                      TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerGlyLeuSerThrGly 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1155 Avenue of the Americas
                                                                                                                                                                                                                                                           :: (212)790-9090
(212) 869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                               Homo sapiens
                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennie &
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1.959
66.071
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Percent Identity: 37.500
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6
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alignment_block:
US-09-471-276-831 x US-07-668-648-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-429-998-3
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08429998
Patent No. 5885961
GENERAL INFORMATION:
APPLICANT: Shoyab, Mohammed
APPLICANT: Plowman, Gregory D.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PLOWMAN, GREGORY D.
TITLE OF INVENTION: MODULAFING PROTEINS
TITLE OF INVENTION: MODULAFING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 ATCCTGCTTCCAAAGATCAG......349
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                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 TGGCTCCTGGGGGTGCTGCC 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 euAlaLeuAspGlyAlaSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 GATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGTGTTATGGTCGA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 uLeu.........GluLeuThrGlyProLysValLeuAlaCysSerL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280 GATGGCCATCACTGCCGCCACGGGGCTTCCACTGCAGTGCAGACGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 TCTCAGGGACTTCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 CTGCCAGGTTGATGCCCACTGCTGTGCGGGCCACTCCTGCATCTTTACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 erGluHis***LeuLysThr...LeuGlyGlnCysAspAlaAspValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 CTGTGGCCTGCCTGGACCCCGGAGGAGCCAGCTACAGCTGCTGCCGT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LeuTrpGlyValThrTrp......GlyProValThrGluAlaAlaI1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 erProAlaIleLysHisGlnPheLeuLeuThrGlyAspThrGlnGlyArg 90
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                                                                                                                                                                                                 CITY: New York
STATE: New York
                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GTAACAACTCCGTGGGTGCCATCCAGTGCCCT 381
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                                                                                                                                                                                                                                                   1155 Avenue of the Americas
                                                                                                                                                                      USA
   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                     Pennie &
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1.172
43.571
                                                                                                                                                                                                                                                                                     Edmonds
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alignment_block:
US-09-471-276-831 x US-08-429-998-3
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US-08-429-998-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-429-998-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (212) 869-9741 INFORMATION FOR SEQ ID NO: 3:
                                            382 GATAGTCAGTTCGAATGCCCGGACTTCTCCACGTGCTGTGTTATGGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
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REFERENCE/DOCKET NUMBER: 56
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 13-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                     107 uLeu......GluLeuThrGlyProLysValLeuAlaCysSerL 120
                                                                                                                                                                                                                             330 ATCCTGCTTCCAAAGATCAG......349
                                                                                                                                                                                                                                                                                                                         280 GATGGCCATCACTGCTGCCCACGGGGCTTCCACTGCAGTGCAGACGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                 230 TCTCAGGGACTTCCAGTTGCTGCCCCTTCCCAGAGGCCGTGGCATGCGGG 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 CCCCTTCTGGACAAATGGCCCACAACACTGAGCAGGCATCTGGGTGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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120 euAlaLeuAspGlyAlaSer 126
                                                                                                                                                                              91 TyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                                                                                         74 erProAlaIleLysHisGinPheLeuLeuThrGlyAspThrGlnGlyArg 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GlyProProGlyAspSerArgLeuProAlaValGlnGluTrp.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 CTGTGGCCTGCCTGGACCCCGGAGGAGCCAGCTACAGCTGCTGCCGT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LeuTrpGlyValThrTrp......GlyProValThrGluAlaAlaIl 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/668,648 FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 27-APR-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                  Quality:
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212) 869-9741
                                                                                                                                        .....GTAACAACTCCGTGGGTGCCATCCAGTGCCCT
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1.172
43.571
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alignment_block:
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LOCATION:
US-08-431-333-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-431-333-3
                                                                                                                                               Align seg 1/1 to: US-08-431-333-3 from: 1
                                                                                                                                                                                     US-09-471-276-831 x US-08-431-333-3
                                                                                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212)790-9
TELEFAX: (212) 869-97
INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US 0
FILING DATE: 13-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,333
FILING DATE: 27-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (212)790-9090
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NAME: Misrock, S. Leslie
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130 CCCCTTCTGGACAAATGGCCCACACACTGAGCAGGCATCTGGGTGGCCC 179
                                                                         80 CTGTGGCCTGCTGCACCCCGGAGGAGCCAGCTACAGCTGCTGCCGT 129
                                   23 ePheTyrGluThrGln......***SerLeuTrpAlaGluS 35
                                                                                                         10 LeuTrpGlyValThrTrp......GlyProValThrGluAlaAlaIl 23
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                                                                                                                                                                           Quality:
Ratio:
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SYSTEM: PC-DOS/MS-DOS
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1.172
43.571
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seq_documentation_block:
    Sequence 3, Application PC/TUS9102321
    GENERAL INFORMATION:
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                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: ONOO
TELEPHONE: (206)484-480
TELEPHONE: (206)484-4775
TELEPHONE: (206)484-4775
TELEPHONE: (206)484-4775
SINFORMATION FOR SEQ 1D NO: 3:
SUBJUNCE CHARACTERISTICS:
LENGTH: 1779, base, pairs
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TREE: Floppy disk
COMPUTER: 1EM PC COMPABLIBLE
OPERATINE SISTEM: PC-DOS/MS-DOS
SOFTMARE: Detentin Release *1.0, Version #1.25
SOFTMARE: Detentin Release *1.0, Version #1.25
CURRENT APPLICATION NUMBER: PCT/US91/02321
APPLICATION NUMBER: PCT/US91/02321
FILING DATE: 19910403
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                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shoyab, Mohammed APPLICANT: Shoyab, Mohammed APPLICANT: Plomman, Gregory D. TITHELINS: NOVEL CYSTEINE-RICH GROWTH TITLE OF INVENTION: MODULATING PROTEINS
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CORRESPONDENCE ADDRESS:
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STATE: Washington
                                                                                                                                                                     TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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E: Kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bristol-Myers Squibb Company
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seq_documentation_block: seq_ence 35, Application US/08464517 Patent No. 386540x GENERAL INFORMATION: APPLICANT: BEACH, DAVId H. TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS: ADDRESSEE: LAHIVE & COCKFIELD STRET: 60 State Street CITY: Boston STATE: MA CONNTY: USA ZIP: 02109 CONNTYER READABLE FORM: COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible SOPTMARE: ASCII(text) COMPUTER: ASCII(text) COMPUTER: ASCII(text) COMPUTER: ASCII(text) COMPUTER: ASCII(text)	120 ewhaleuwspGlyAlaSer 126	91 TyrargCýsArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLySLe 107 :::::	65	35 erGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPro 50 11::::::: 180 CTGCCAGGTTGATGCCCACTGCTGTCTTACCG 229 51 GlyProProGlyAspSerArgLeuProAlaValGlnGluTTp 64 ::: 11	10 LeuTrpGlyValThrTrpGlyProValThrGluAlaAla11 23	alignment_block: US-09-471-276-831 x PCT-US91-02321-3 Align seg 1/1 to: PCT-US91-02321-3 from: 1 to: 1779	alignment_scores: Quality: 71.50 Length: 140 Ratio: 1.172 Gaps: 6 Percent Similarity: 43.571 Percent Identity: 23.571	; NAME/KEY: CDS ; LOCATION: 11779 PCT-US91-02321-3

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seq_documentation_block:
sequence 35, Application US/08246361A; Pattent No. 598582; GENERAL INFORMATION:
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; MOLECULE TYPE:
US-08-464-517-35
                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-246-361A-35
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US-09-471-276-831 x US-08-464-517-35/rev
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: US-08-464-517-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1624 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILING DATE: 16-OCT-1992

APPLICATION NUMBERS US 07/888,178
PILING DATE: 26-MAY-1992
PRIOR APPLICATION DATE: 18-MAY-1991
PILING DATE: 18-MAY-1991
APPLICATION NUMBER: US 07/701,514
APPLICATION NUMBER: 18-ORNATION:
NUMBER, AGENT 18-ORNATION:
NUMBER, AGENT 18-ORNATION:
                                                                                                                                                                                                          383
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APPLICANT: BEACH, David H.
                                                                                                                                                                                                                                                             100 y 100
                                                                                                                                                                                                                                                                                                                433 CTAGGAAATGGCCCGGGAGGGAAGGGGGCGAGTGAAGGGATTAGGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                 483 CAAGCCGCCGAGGTGTCTGCGCTGAGCGTGGCCACACCGATGCAGCTTT 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 ThrLeuGlyGlnCysAspAlaAspValProGlyProProGlyAspSerAr 57
                                                                                                                                                                                                                                                                                                                                                               84 ThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGl 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 ...AspScrPro.................AlaIleLysHisGlnPheLeuLeu 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 heTyrGluThrGln***SerLeuTrpAlaGluSerGluHis***LeuLys 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Matthew P. Vincent
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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FILING DATE:
                                                                                                                                                                                                          C 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHisLeu.... 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuTerTrp.GlyValThrTrpGlyProValThrGluAlaAlaIleP 24
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-471-276-831 x US-08-246-361A-35/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 227-594
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             533 GCCAGCGCCACGCAGAAAAACCCGCTTCCTCGCCCCTGCATCTGCTGA 484
                                                                                                                                                                                                                                    624 TTCTGGGGGCTCTTCGGGCGCGCGTGGGGCGACGCG......GTGCAG 584
                                                                                                                                                                                                                                                                                                                    674 GTGCTTCTCTGGAGGGATAGAATGTGATCCTCGAGCAGAAACCATCGTGT 625
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NAME: Matthew P. Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0: FILING DATE: 26-MAY-1992 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                          583 CGTCTAGGGCCGCCGCAGGCCGGGGGCAGGGCTCCCAGCGGTTCCCCCGC 534
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483 CAAGCCGCCCGAGGTGTCTGCGCTGAGCGTGGCCACACCGATGCAGCTTT 434
                                   73 ..AspSerPro..........AlaIleLysHisGlnPheLeuLeu 83
                                                                                                                                                                                              41 ThrLeuGlyGlnCysAspAlaAspValProGlyProProGlyAspSerAr 57
                                                                                                                                                                                                                                                                              24 heTyrGluThrGln***SerLeuTrpAlaGluSerGluHis***LeuLys 40
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
FILING DATE: 19-MAN
CLASSIFICATION: 439
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CITY: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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                                                                                                           gLeuProAlaValGlnGluTrpGlyALaGlnGluProValHisLeu.... 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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Gaps:
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seq_documentation_block:
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                                                                                                                US-09-471-276-831 x US-08-463-772-35/rev .
                                                                         Align seg 1/1
                                                                                                                                                                       Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: MITELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Matthew P. Vincent
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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674 GTGCTTCTCTGGAGGGATAGAATGTGATCCTCGAGCAGAAACCATCGTGT 625
                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII(text)
                  APPLICATION NUMBER: US 07/963,308 FILING DATE: 16-OCT-1992 APPLICATION NUMBER: US 07/888,178
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                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/463,772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,709
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                                                                                                                                                                                       Quality:
Ratio:
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                                                                         to reverse of: US-08-463-772-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                     71.00
1.315
53.465
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                                                                         to: 1624
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seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-05000-35
                                                                    alignment_scores:
                                                                                                                                     ; TOPOLOGY: 1:
; MOLECULE TYPE:
PCT-US93-05000-35
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   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 35, Application PC/TUS9305000 GENERAL INFORMATION: APPLICANT: MITOTIX
                                                                                                                                                                                                                                                                                            TELEFAX: 616-861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 517-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1624 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: US/07/888,178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 CTAGGAAATGGCCCGGGAGGGAAGGGGCGAGTGAAGGGATTAGGTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 TTCTGGGGGCTCTTCGGGCGCCGTGGGGCGACGCG.....GTGCAG 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 y 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGl 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ThrLeuGlyGlnCysAspAlaAspValProGlyProProGlyAspSerAr 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 heTyrGluThrGln***SerLeuTrpAlaGluSerGluHis***LeuLys 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Lexington
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                                                                                                                                                                                               1: 1624 base pairs
NUCLEIC ACID
DEDNESS: double
                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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71.00
1.315
53.465
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Percent Identity: 26.733
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                        Length:
Gaps:
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alignment_block:
us-09-471-276-831 x PCT-US93-05000-35/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-786-527A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08786527A Patent No. 5969210
                                                                                                                                                     TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: D5848
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                  ATTOHNEY/AGENT INFORMATION:
NAME: Adler, Benjamin A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft WO
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sharma and Montminy TITLE OF INVENTION: No. 596921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             583 COTTCTAGGGCCGCCGCAGGCCGGGGGCAGGGCTCCCAGCGGTTCCCCCGC
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                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/786,527A FILING DATE: January 21, 1997 CLASSIFICATION: 800
                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word for Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 LeuLeuLeuTrp.GlyValThrTrpGlyProValThrGluAlaAlafleP
                                           STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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                                                                                       nucleic acid
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                                                                                                                403 bp
                                     linear
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   other nucleic acid
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                                                                                                                                                                                                                                                                     35,423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-786-527A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-667-939A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08667939A Patent No. 5998166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LUO, Shun
TITLE OF INVENTION:
                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                           ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
ADDRESSEE: BROWDY AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 CCAGCGCCTTAAGGCCTGGCTTGTAGC 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: USA
                  NAME: BROWDY, Roger L. REGISTRATION NUMBER: 25,618
                                                                                          FILING DATE: 03-MAY-1995
                                                                                                                                                                              APPLICATION NUMBER: US/08/667,939A
                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
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TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                         20004
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                                                                                                                                                                                                                                                                                                                                                                                                                              419 Seventh Street, N.W., Suite 300
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59.740
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                                                                                                         US 08/433,123
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   LUO-2A
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141 CCTGGGCCTCCTTCTTAAGGCAGGGCCAGGCCAATGGTGGCCCCAGGCTG 190 50 ProGlyProProGlyAspSerArg.....LeuProAlaVa

94 rgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLeuGluLeu 110 AGAGTCCGTGAGCTG 290

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-667-939A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-667-939A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 70.50
Ratio: 1.808
Percent Similarity: 49.367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-471-276-831 x US-08-667-939A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/08667939A
Patent No. 5998166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LUO, Shun
TITLE OF INVENTION: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/433,123
FILING DATE: 03-MAY-1995
                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 TGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTC 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 erArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHisLeu 72
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LOCATION: 7..615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                         FILING DATE:
                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 630 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rGlnGlyArgTyrArgCysArgSerGlyLeuSerThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....ACACAGTGGTTTCACAATGAG.....AGCCTC
                                                                                                                                                                                                                                                20004
                                                                                                                                                                                                                                                                                                                Washington
                                                                                                                                                                                                                                                                                           D.C
                                                                                                                                                                                                                                                                                                                                  E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                        USA
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                                                                      24-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                              CD16-II VARIANTS
                                                                                           US/08/667, 939A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 79
Gaps: 6
Percent Identity: 34.177
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-471-276-831 x US-08-667-939A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08667939A
Patent No. 5998166
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 STREET: 41. CITY: Washington craTE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                    CURRENT APPLICATION DATA:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTC 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 CAGTGGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 CC.....ACACAGTGGTTTCACAATGAG.....AGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 GlyGlnCysAspAlaAspValProGly.....ProProGly.AspS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
                                        SOFTWARE:
                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             COUNTRY: USA
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
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TOPOLOGY: lir
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                                                                                           419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                   LUO, Shun
                                     PatentIn Release #1.0, Version #1.30
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49.367
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US/08/667, 939A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25,618
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Caps: 6
Percent Identity: 34.177
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seq_documentation_block:

; Sequence 15, Application:

; Patent No. 5998166
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US-09-471-276-831 x US-08-667-939A-12
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-667-939A-12 from: 1 to: 765
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 765 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,518
REFERENCE/DOCKET NUMBER: LUG-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFEAX: 202-737-3528
               COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk
COMPUTER: JEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAICHILD READASS # 1.0, Version #1.30
                                                                                                                                                                                                                                                                                                            APPLICANT: LUO, Shun
TITLE OF INVENTION: (
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 TGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTC 333
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                                                                                                                                                      COUNTRY:
                                                                                                                                                                           STATE:
                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rGlnGlyArgTyrArgCysArgSerGlyLeuSerThr........................99
                                                                                                                                   20004
                                                                                                                                                                                                                                                                                                                                                                            5, Application US/08667939A 5998166
                                                                                                                                                                           D.C.
                                                                                                                                                                                                                   419 Seventh Street, N.W.,
                                                                                                                                                      USA
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1.808
49.367
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Gaps: 6
Percent Identity: 34.177
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                                                                                                                                                                                                                   Suite 300
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seq_documentation_block:
; Sequence 16, Applicati
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MOLECULE TYPE:
US-08-667-939A-15
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-667-939A-16
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                                                                                                                                                                                                                                                                                                                                      sequence 16, Application US/08667939A
Patent No. 5998166
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08,
FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 03-MAY-1956
ATTORNEY/ACENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: JEM PC compatible
OPERNTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                         APPLICANT: LUO, Shun TITLE OF INVENTION: CONUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 CC.....ACACAGTGGTTTCACAATGAG.....AGCCTC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 GGACAGTGTGACTCTGAAGTGCCAGGGAGCCTACTCCCCTGAGGACAATT 169
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LENGTH: 765 base pairs
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TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 TGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTC 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AspSerProAlaIleLysHisGlnPheLeu....LeuThrGlyAspTh 87
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                                                                                                               ZIP:
                                                                                                                                 COUNTRY:
                                                                                                                                                  STATE: D.C
                                                                                                                                                                    STREET: 419 Seven
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                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                            20004
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                                                                                                                                                                                            419 Seventh Street, N.W., Suite 300
                                                                                                                                 ASU
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1.808
49.367
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6
34.177
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seq_documentation_block:
    Sequence 9, Applicatio
    Patent No. 6140076
                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-985-950-9
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                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: LUO-
REFERENCE/DOCKET NUMBER: LUO-
TELEPHONE: 202-628-6197
TELEPHONE: 202-628-6197
TELEPHON: 202-6737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                            TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes, NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          299 TGCAGCTAGAAGTCCATATCGGCTGGCTGTTGCTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           249 CAGTGGAGAGTACAGGTGCCAGACAAACCTCTCCACCCTCAGTGACCCGG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 ATCTCAAGCCAGGCCTCGAGCTACTTCATTGACGCTGCCACAGTCGACGA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 CC.....ACACAGTGGTTTCACAATGAG.....AGCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 rGlnGlyArgTyrArgCysArgSerGlyLeuSerThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AspSerProAlaIleLysHisGlnPheLeu....LeuThrGlyAspTh 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 erArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHisLeu 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 GlyGlnCysAspAlaAspValProGly...........ProProGly.AspS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                         CITY: Palo Alto
STATE: Californ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
  OPERATING SYSTEM:
                                                                                                  COUNTRY:
                                                                                                                                                                  STREET:
                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .....GlyTrp***GlnLeu 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                 94304-1104
                                                                                                                                                                                                                                                                                                             , Application US/08985950 6140076
                                                                                                                      California
                                                                                                                                                            901 California Avenue
                                                                                                                                                                                                                                                                    Adema, Gosse Jan
                                                                                                  USA
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                    IBM PC
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                                  Floppy disk
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1.808
49.367
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PC-DOS/MS-DOS
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Percent Identity: 34.177
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alignment_scores:
                                                       seq_documentation_block
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                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-345-468-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-985-950-9 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-471-276-831 x US-08-985-950-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
GENERAL INFORMATION:
                   Sequence 2, Application US/09345468 Patent No. 6245527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (650)496-1204 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DX TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,1
                                                                                                                                                                                                                         294
                                                                                                                                                                                                                                                                                                       255
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                                                                                                                                        331 ATTATAAGCCCCCTGGATGGTCTGAGCACAGTGACTTCCTGGAGCTG 377
                                                                                                                                                                                                                                                                                                                                                                                  205 AGAGGGAGGATAGAGCCAAGTACAAAGATAGTTATAATGTGTTTCGACTT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 TGTGACTTTCATGTGCCGGGGCCCGGTTGGGGGTTCAAACATTCCGCCTGG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                        64 rpGly.AlaGlnGluProVal.....HisLeuAspSerProAlaIleLy 78
                                                                                                                                                                            95 erGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLeuGluLeu 110
                                                                                                                                                                                                                                                          78 sHisGlnPheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgS 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/033,181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 568 base pairs
                                                                                                                                                                                                                   .....GTAAGTGAAGGAAATGCCGGGCTTTATCGCTGCCTCT 330
                                                                                                                                                                                                                                                                                                    .....AlaValGlnGluT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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24..428
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87..428
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1.769
46.988
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APPLICANT BUSÍCICI. S.
APPLICANT VILLENJ. J.
APPLICANT JANDOUC PETTUS. M.
APPLICANT LANDOUC PETTUS. M.
APPLICANT VAINCHNER, W.
TITLE OF INVENTION CHYOPROTEIN VI AND USES THEREOF
FILLE REPERENCE. 725.314
CURRENT APPLICATION NUMBER. US/09/345.468
CURRENT FILINC DATE: 199-06-30
NUMBER OF SEQ ID NOS: 24
SOFTMARE: PASISED FOR WINDOWS Version 3.0
SEQ ID NO 2.
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; TYPE: DNA
; ORGANISM: Homo sepiens
US-09-345-468-2
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US-09-471-276-831 x US-09-345-468-2
                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-424-406-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: US-09-345-468-2 from: 1 to: 1017
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                                                                                                                                                                                                      Sequence 8, Application US/08424406 Patent No. 5667997
                                                                                                                                                                                   GENERAL INFORMATION:
                               APPLICANT: Voelker, Toni Alois
APPLICANT: Davies, New Maelor
APPLICANT: RULZON, Deborah S.
TITLE OF INVENTION: Medium Chain Thioesterases in Plants
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                             314 TCGTTGCCACGGGAGTTTTTGCC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                      264 CTCCTACCAGAACGGAAGCCTCTCGTCCCTGCCCAGCGACCAGCTGGAGC 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 GACCCTCCGGTGCCAGGGACCTCCGGGCGTGGACCTGTACCGCCTGGAGA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 IleLysHisGinPheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCy 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 LeuProAlaValGlnGluTrpGlyAlaGlnGluProVal.HisLeuAspS 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 CTTCTGTCTTGGGCTGTCT...GGGGCGTGTGCCCAGCGCAGAG..... 65
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                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                      euThrGlyProLysValLeuAla 117
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E: Calgene, Inc.
1920 Fifth Street
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1.131
48.800
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seq_documentation_block:
   Sequence 6, Application US/08464523B
   Patent No. 5723761
                                                                              alignment_block:
US-09-471-276-831 x US-08-464-523B-6
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                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-464-523B-6
Align seg 1/1 to: US-08-464-523B-6 from: 1 to: 1474
                                                                                                                                                                                                              Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEO ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 1474 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1027 TTTGGAGACCCAGGAGCTATGCTCTCTCGCCCTTGAA 1063
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
COMPUTER: Apple Macintosh
OPRAPTING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/261, FILING DATE: 16-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: DONNA E. SCHEFET
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/464,523B
FILING DATE: 02-UNI-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA.
APPLICATION NUMBER: PCT/US94/13131
PILING DATE: 10-NOV-1994
PRIOR APPLICATION NOTA: 0.
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APPLICANT: Ling Yuan
APPLICANT: Jean Kridl
APPLICANT: Deborch Hawkins
APPLICANT: Deborch Hawkins
APPLICANT: Abbrey Jones
AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 977 AGCAACGTGAAGTACATTGGGTGGATTCTCGAGAGTATGCCAACAGAAGT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/1:
FILING DATE: 10-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CGNE 100-1WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UP
ZIP: 95616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1920
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA to mRNA
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1.302
46.903
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                                                                                                                                                                                                  Length: 113
Gaps: 8
Percent Identity: 30.088
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117 CCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCAGT 166

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US-07-880-913-1
                                      alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-880-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 1, Application US/07880913
Patent No. 5292651
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 4160
TELECOMMUTICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-3400
TELEPHONE: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEO 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GUTHRIE, ELLEN P.
APPLICANT: TAKON COTT, ELIZABETH M.
APPLICANT: TAKON CHRISTOPHER H.
TITLE OF INVENTION: METHOD FOR PRODUCING THE NAEI
TITLE OF INVENTION: METHOD FOR PRODUCING THE NAEI
TITLE OF INVENTION: RESTRICTION ENCONICLEASE AND METHYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 GACCCTCCGGTGCCAGGGACCTCCGGGCGTGGACCTGTACCGCCTGGAGA 216
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 ATGAAGAGAGTCTG......
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CITY: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                        ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IleLysHisGlnPheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCy 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLeuGlut 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              er.....ProAla 76
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Quality:
Ratio:
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                                                                                                                                                                                                                                                        3664 base pairs
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Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRONSTEIN, ROBERTS
  106
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APPLICANT: Chaux, Pascal
APPLICANT: Stroobant, Vincent
APPLICANT: Boon, Thierry
APPLICANT: wan der Bruggen, P
TITLE OF INVENTION: MAGE-3PE
TITLE OF INVENTION: BY HLA CL

Stroobant, Vincent

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C

600 Atlantic Avenue

NUMBER OF SEQUENCES:

MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

Pierre

GENERAL INFORMATION:

INFORMATION FOR SEQ ID NO:

TELEPHONE:

: 617-720-3500 617-720-2441

TELECOMMUNICATION INFORMATION:

NAME: Van Amsterdam, John R. REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L04

L0461/7017

SEQUENCE CHARACTERISTICS:

OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/928,615

ATTORNEY/AGENT INFORMATION:

FILING DATE: CLASSIFICATION:

COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

COUNTRY: U.S.A. ZIP: 02210-2211 CITY: Boston STATE: MA STREET:

COMPUTER:

IBM Compatible Diskette

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alignment_block:
US-09-471-276-831 x US-07-880-913-1
                                                         seq_documentation_block:
                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-928-615-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-07-880-913-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Sequence 1, Application US/08928615 Patent No. 5965535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2191 TGGGGTTCCTCAACTCCGGCCGCG.....TTTCGTACTTGTCGCTCT.. 2232
                                                                                                                                                                                             2473 AGTCGCTGACGCGC 2486
                                                                                                                                                                                                                                                                                                                        2423 CCGACTCGCGCGAAGCGGGCGTGGGCAGAGCTCGGTGTCGACGCAATGGG 2472
                                                                                                                                                                                                                                                                                                                                                                                                                                              2373 CACCAACCATCGTGGGTGGCTCCAAGAACATGGCGGAGCTGACCTCGGC 2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2279 GCGGCACCCACGGTGGGGGAGACGTTGAAGGACCTCATGGCCGGGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2233 ....GCAGAACAAGTTCGCCCCCTATTTCACCTGGCCTGAGCCGACCGGT 2278
                                                                                                                                                                                                                                                      102 **GlnLeuSerLys 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 uTrpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAsp.... 46
                                                                                                                                                                                                                                                                                                                                                                            86 AspThrGlnGlyArgTyr.ArgCysArgSerGlyLeuSerThrGlyTrp* 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 erProAlalle..........LysHisGlnPheLeuLeuThrGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 Leu.ProAlaValGinGluTrpGlyAlaGinGluProValHisLeuAspS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 TrpGlyProValThrGluAlaAlaIlePheTyrGluThrGln***SerLe 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......AlaAspValProGlyProProGlyAspSerArg 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 3664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2328
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	1234 GGCCAAATGTGCTCTGTGCTCATTGCGCCTTCAGGGT 1270
	112 yProLysValLeuAlaCysSerLeuAlaLeuAspGly 124
RGT 1233	96 GlyLeuSerhrelyrp***GloLeuSerLysLeuLeuGluLeuThAG1 112 96 GlyLeuSerhrelyrp***GloLeuSerLysLeuLeuGluLeuThAG1 112 1199 GTGGCAACCTTGGGCTGGGGATGCTGGGCACAGT 1233
Ser 95 TCA 1198	79 isGlnpheLeuleuthrGlyasgthrGnGlyargTyrargCysarger 79 isGlnpheLeuleuthrGlyasgthrGnGlyargTyrargCysarger 79 isGlnpheLeuleuthrGlyargthrafic 79 isGlnpheLeuleuthrafich 79 isGlnph
узн 79 1165	62 nGluTrpClyAlaGlnGluProValHisLeuAspSerProAlaileLysH :::: :::::: 1147 GTCATGGGGAGAAGAAGA
1G1 62 :: 	46 AspAlaAspValProGlyProProGlyAspSerArgLeuProAlaValG1
	Align seg 1/1 to: US-08-928-615-1 from: 1 to: 4204
	us-09-471-276-831 x us-08-928-615-1
	ilignment_scores: 79 Ouality: 69.00 Length: 79 Percent Similarity: 45.570 Percent Identity: 29.114
	ANTI-SENSE: NO FEATURE: NAME/KEY: Coding Sequence LOCATION: 24653406 IS-08-928-615-1
	TYPE: nucleic acid STRANDEDESS: single TOPOLOGY: Linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
	LENGTH: 4204 base pairs



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/SIDS2/gcgdata/geneseq-geneseqn/NAL2001. Db
/SIDS2/gcgdata/geneseqn/NAL2001. Db
/SIDS2/gcgdata/geneseqn/NAL2001. Db
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/SIDS2/gcgdata/geneseqn/geneseqn/NAL2001. Db
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Query leng
Database:
                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn/NA2001
/SIDS2/gcgdata/geneseq/geneseqn/NA2001
/SIDS2/gcgdata/geneseq/geneseqn/NA1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 930621
Database length: 428662619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query: US-09-471-276-831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Command line parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: Jan 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -0=/-G9n2_1/USPFO_SPOO1/US09471276/runat_07012002_142445_19912/app_query.fasta_1.274
-0=/-K_Geneseq_1101 -0pfW1-fastap -SUPF1X-rung -GAPDP-12.000
-GAPEXT-4.000 -MINANGTH-0.100 -LODEXT-0.000
-GAPEXT-0.000 -GAPEXT-0.0050 -XGAPEXT-0.000
-GAPEXT-0.000 -GAPEXT-0.0050 -XGAPEXT-0.000
-GAPEXT-0.000 -GAPEXT-0.000 -XGAPEXT-0.500
-EGAPEXT-7.000 -XGAPEXT-0.000 -XGAPEXT-0.500
-EBLOP-6.000 -EGAPEXT-7.000 -XGAPEXT-0.500
-EBLOP-6.000 -EGAPEXT-1.000 -XGAPEXT-1.000
-VGAPEXT-1.000
-VGAPEXT-1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of: US-09-471-276-831 to: N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (sec):
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                                                          1. DAT: AAF29475
1. DAT: AAF29475
8. DAT: AAV69335
3. DAT: AAV69339
3. DAT: AAV6939
3. DAT: AAA54602
3. DAT: AAA54602
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1. DAT: AAC7633274
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DAT: AAA54591

D. DAT: AAA54611

D. DAT: AAA54609

B. DAT: AAA54609

B. DAT: AAV69338

DAT: AAV69338
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3. DAT: AAV23273

3. DAT: AAA54600

3. DAT: AAV69329

3. DAT: AAA54592

3. DAT: AAA54592
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.DAT: AAA54597
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DAT: AAS02103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EScore
                  T:AAA54595
T:AAV38992
T:AAI51413
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      mentation
.00 1274.1
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    XXXXXXXXX
                                                                                                                                                               seq_name:
  Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
                                Human 5' EST isolated from a
                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ42284
                                                            (first entry)
                                cDNA library SEQ ID NO:43
                                                                                                                                                                                           77.5.50

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151.14
126.18
                                                                                                                                                                                         2.0e+03
1.3e+04
1.59.58
1.95.52
1.98.89
2.07.53
2.13.06
2.35.33
3.24.52
1.16.00
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us-09-471-276-831 x AAZ42284
                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX42265 to AAX43075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAX4651 to AAX4538 represent the EST-related proteins corresponding to AAX42265 to AAX43052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated regions (UTRs) and upstream regulatory regions which control the location, development stage, rate, and quantity of protein synthesis, as well as stability of mRNA. The ESTs are also useful as probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping, and to obtain full length cDNA clones. The ESTs can also be used in foremste procedures to identify individuals, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. The products may also be used in gene therapy protocols. The nucleic acids encoding signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell. The protects encoded by the EST sequences may be useful in treating a polyperide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating a variety of human conditions. Secreted proteins have
therapeutic value, and the identification of new secreted proteins is
valuable. AAZ42240 to AAX42264 and AAX64644 to AAX64650 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 195; 837pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel secreted protein 5' expressed diagnostic, forensic, gene therapy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-1998;
28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09953051-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome mapping; upstream regulatory sequence;
forensic; location; development; protein synthesis; stability;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forensic; location; development;
regulation; identification; ss.
                  34 luSerGtuHis****LeuLysThrLeuGlyGlnCysAspAlaAspValPro
                                                                                                                                                      35
                                                                                                                                                                                        1 MetSerMetLeuValValPheLeuLeuTrpGlyValThrTrpGlyPr 17
AGTCCGAACACTGACTGAAAAACCCTTGGCCAATGTGACGCTGACGTGCCA 184
                                                                                                             oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                   ATGTCCATGCTCGTGGTCTTTCTTCTTGCTGTGGGGTGTCACCTGGGGCCC
                                                                        AGTGACAGAAGCAGCCATATTTTATGAGACGCAGSCCAGCCTGTGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-038446/03
                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                    Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
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98US-0069047
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                                                                                                                                                                                                                                                                                                                            655.00
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Percent Identity: 97.619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tag sequences used in and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glordano
                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                               80 T; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT;AAV88297
                                                                                                              Expressed sequence tog: secreted protein; heematopolesis regulator; tissue growth, octivin, inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385
W09845437-A2
                                           Homo sapiens
                                                                                                                                                                                                                   EST clone GD177
                                                                                                                                                                                                                                                                                                                                                            AAV88297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185
                                                                                          receptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                              12-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGCTCCCTGGCTCTCGATGGCGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGlyAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aCysSerLeuAlaLeuAspGlyAlaSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGCCTGTGCACCTTGACTCACCTGCCATCAAGCACCAGTTCCTGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nGluProValHisLeuAspSerProAlaIlcLysHisGlnPhcLeuLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCCGCCTGGAGACTCCAGACTTCCAGCTGTTCAAGAATGGGGGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGMCCCAGCTGAGCAAGCTCCTGGAGCTGACAGGGCCAAAAGTCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGGTGACACCCAGGGCCGCTACCGCTGCCGCTTCGGGCTTGTCCACAGGA
                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                            cDNA; 276 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                         human;
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Agostino P Racie LA, New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, testes, brain, WPT; 1999-070078/06 (GEMY) GENETICS INST INC 10-APR-1997; 10-APR-1998; 15-OCT-1998 A, Spaulding 97US-0837312 98WO-US06956 < 7 Lavallie | Treacy M; ER, мссоу JM, Merberg

The present sequence represents an expressed sequence tog (EST), and is a polynucleotide of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or machiorating medical conditions in humans and animals, although no supporting data is given. Suggested activities and include nutritional activity, humans stimulating or suppressing activity, haemstopolasis regulating activity, tissue growth activity, hemostatic activity, inhibit activity, receptor/ligand activity, anti-inflammetory activity, codherin/tumour invasion suppressor activity, theoret inflammetory activity, codherin/tumour invasion suppressor activity, to activity, activity, activity. BST sequences are also stated to be useful for gene

Claim 1; Page 348-349; 641pp; English

ovary, pituitary, retina and colon cDNA libraries

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seq_documentation_block:
ID AAC87257 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC87257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
      Oblagnosting abnormal levels of growth hormone activity in livelei-
comprising aspying growth to discreptional activity of protein-
expression level of hormone-regulatable liver genes, as diagno-
markers of liver pathology
                                                                                                                                                                                                                                                                                                                                                                                        Mouse; growth hormone; GH regulatable gene; liver pathology; hypertrophy; hepatocellular lesion; hyperplasia; altered expression level; clone 5; diagnostic marker; gigantism; acromegaly; diabetes, hepatotropic; transgenic animal; drug screening; drug discovery; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 276 BP;
    expression
markers of
                                                                                P-PSDB: ADB48724, AAB48725, AAB48726, AAB48727, AAB48728, AAB48730, AAB48730, AAB48731, AAB48732, AAB48733, AAB48734, AAB48735, AAB48739, AAB48737, AAB48737, AAB48738, AAB48739,
                                                                                                                                                                                                                              05-MAY-1999;
                                                                                                                                                                                                                                                             05-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse liver growth hormone-induced cDNA clone 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC87257 standard; cDNA; 1908 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 AGTCCGAATCACTGCTGAA.ACCCTTGGCCAATGTGACGCTGACGTGCCA
                                                                                                                                                                                                                                                                                                                            WO200066787-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                Kopchick JJ, Tiong
                                                                                                                                                                                               (UYOH-) UNIV OHIO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGly.AlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTCCATGCTCGTGGTCTTTCTCTTGCTGTGGGGTGTCACCTGGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGAGCCTGTGCACCTTGACTCACCTGCCATCAAGCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnGluProValHisLeuAspSerProAlaIleLysHisGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCCGCCTGGAGACTCCAGACTTCCAGCTGTTCAAGAATGGGGTGGCCC
                                                                                                                              2001-007239/01
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g assaying growth
n level of hormone
f liver pathology
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                 and protein
as diagnostic
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Claim 1; Page 51-52; 65pp; English
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transgenic nonhuman mammals comprising a GH-induced transgene which exhibit or have a propensity to develop a liver pathology; an assay for drugs which inhibit the development of, or which treat all liver pathology, comprising administering the drug to the transgenic animal; and preventing or treating a liver pathology in a patient comprising administering a drug which inhibits the expression of a 6H-induced gene. The method of the invention is used for dispossing abnormal levels of GH S-2 hydroxyacid oxidase, interferon alpha/beta receptor, growth hormone receptor, proteasome z-subunit, and coogulation factor V. Two novel quest, clone 5 (AACGPT25) and clone 45 (AACGPT28) are also upregulated in response to abnormally high GH levels. Conversely, expression of the gene encoding 3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4 isomerase appears to be downregulated. The invention also relates to growth hormone identified a number of genes whose expression in the liver is altered by high GH levels. The genes which are upregulated are those encoding alpha-fetoprotein, corticosteroid binding globulin, fetuin, rab8-interacting protein, paraoxonase-3, cytochrome P450IIIA, activity in the liver is thought to be deleterious to health, causing an increase in liver size as a consequence of both hyperplasia and hepatocyte hypertrophy, and hepatocellular lesions which progress with age. Studies in transgenic mice which express high levels of bovine activity in the liver or predicting a change in the condition of the liver in response to abnormal levels of GH activity. The GH-regulatable liver genes and proteins are useful as diagnostic markers of liver pathology. Assays for the expression of these genes is useful for the The invention relates to a method of diagnosing abnormal levels of growth hormone (GH) activity in the liver, or predicting a change in the condition of the liver in response to abnormal GH activity. The method with the level of GH activity in the liver, or with an expected change in the condition of the liver as the result of GH activity. Excessive involves correlating the level of expression of certain specific genes with diabetes, as other causative agents may act directly or indirectly upon the same genes. The present sequence represents the novel mouse liver cDNA clone 5, expression of which is upregulated by abnormal GH diagnosis of liver pathologies associated with gigantism or acromegaly or

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Sequence 1908 BP; 525 A; 475
C; 477 G; 431 T; 0 other;
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alignment_scores: Percent Similarity:

Quality: Ratio:

139.50 1.744 57.971

Percent

Identity: 29.710 Gaps:

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seq_name:

999

349 100 299 249

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94

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seq_documentation_block:
ID AAS02105 gtandard
                                                                            The sequence represents the coding sequence of human MAMCO 511 variant #46 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome). Inflammatory disorders (e.g. psoriasis and asthma), renal disorders, embryonic disorders, brain-related disorders
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-211461/21
P-PSDB; AAU01394.
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                  Cushing's disease)
                                    (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-related disorders, pituitary-related disorders (
                                                                                                                                                                                                                                        Disclosure: Page 300-301; 362pp; English.
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                                                                                                                                                                                                                                                                                                         nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 51, TANGO , TANGO 499 or TANGO 509 secreted or transmembrane protein, useful the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGGCCCTTGGCT
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108..1007
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                  and neurodegenerative diseases
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ID AAA54610 standard;
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                  12-MAY-2000; 2000WO-US13228
                                                             16-NOV-2000.
                                                                                                        WO200068383-A2
                                                                                                                                                                                                                                                              Office
                                                                                                                                                                                                                                                                                                         autoimmunity;
                                                                                                                                                                                                                                                                                                                              Leukocyte immunoglobulin like receptor; LIR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                         Leukocyte immunoglobulin like receptor coding sequence (LIR-9s1).
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                                                                                                                                                                                                                                                                                                            ds.
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Homo

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seq_documentation_block:
ID         AAA54608 standard;
XX
                                                                                 seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-471-276-831 x AAA54610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAA54610 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 109-110; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                  457
                                                                                                                                                                                                                                                                                                    407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1999;
                                                                                                                                                                      108
                                                                                                                                                                                                                                                                                                                                                                                  366 AGAACCCTGGGACACACAGAACCCACTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    316 CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGGAAGCCC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
                                                                                                                                                                                                                                                     92 ArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLe 108
                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu..... 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                                                                      uGluLeu 110
                                                                                                                                                                                                                  CGCTGTTACTACTACAGCCCTGCAGGGTCAGAGCCCAGCGACCCCCT
                                                                                                                                                                                                                                                                                                 AGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCAGGGAGATAC 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAGCCCTGCCCTCATGGTTCTGCCTCTGCCTCGGGCTGAGTCTGGGCCC 218
                                                                                                                                GGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP 50
                                                                                                                                                                                                                                                                                                                                       ysHisGlnPheLeuLeuThrGlyAspThrGln......GlyArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-687645/67
                                                                                                                                                                                                                                                                                                                                                                                                                           .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                 /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54608
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1.612
55.833
                    cDNA; 1016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent
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                                                                                                                                                                                                                                                                                                                                                                                  .GAGCCCAAGAACA 406
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US-09-471-276-831 x AAA54608
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                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAA54608 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmunity;
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                                                                                    223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 104-105; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200068383-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukocyte immunoglobulin like receptor coding sequence (LIR-9ml).
  270 CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGGAAGCCC
                                                                                                                                                                   173 CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1016 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Host cells transformed with a vector which are capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-687645/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukocyte immunoglobulin like receptor; LIR; gene therapy;
                                     50 roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.....
                                                                                                                                                                                                            17 ovalThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                           1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                                                                                                                                                        GTGAGCCCTGCCCTCATGGTTCTGCTCTGCCTCGGGCTGAGTCTGGGCCC
                                                                                    AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT
                                                                                                                       luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disorders; immune system; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0310463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 69..968
                                                                                                                                                                                                                                                                                                                                                                                                                                                108.00
1.612
55.833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= Leukocyte immunoglobulin like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 A; 310 C; 282 G; 193 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ę
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity:
                                                                                                                                                                                                                                                                                                                                          to: 1016
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Gaps:
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34.167

63 269 50 ω **4** 172

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seq_documentation_block:
ID AAS02065 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human: MANCO 511; transmembrane protein; diagnostic; asthus in tumuno logical disorder; arthititis; graft rejectio; renal disorder; acquired lumunodeficiency syndrome; inflammatory disorder; psoriasis; AIDS; embryonic disorder; brain; ocrobral oodema; ischaemia; tumour; prostate; cerebrovascular disease; piculiary; Cushing's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          461
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                                                           Claim 1; Fig 7; 362pp; English
                                                                                                                                                                          P-PSDB;
                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                      20-SEP-1999;
                                                                                                                                                                                                                                                                                                                  20-SEP-2000; 2000WO-US25982
                                                                                                                                                                                                                                                                                                                                                                                  WO200121631-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neurodegenerative disease; Parkinson's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MANGO 511 cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                      nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 347, TANGO 149 or TANGO 509 secreted or transmentrane protein, useful the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCTGTTACTACTACAGCCCTGCAGGCCTGGTCAGAGCCCAGCGACCCCCT 460
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                                                                                                                                                                        2001-211461/21.
DB; AAU01330.
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                                                                                                                                                                                                                        SJ,
                                                                                                                                                                                                                      Sharp JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                      9905-0399723
                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag" b
231..1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product* "MANGO 511"
/note* "The coding se-
claimed in Cl
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108..1007
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                                                                                                                                                                                                                        Fraser
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                                                                                                                                                                                                                      Barnes
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Claim 1"
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                                                                                                                                                                                                                      Kingsbury
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EH XXX
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1D AAS02102 standard;
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                                                                                                                                                                                                                                                                                                                                                 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400
                                                                                                                                                                      Human MANGO 511, variant #1 cDNA sequence.
                                                                                                                                                                                                       18-JUL-2001
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                                                           neurodegenerative disease; Parkinson's disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                             92
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                                                                                                                                                                                                                                                                                                                                                   506
                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                    CDNA; 1477
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disorders (e.g. arthritis, graft rejection and acquired imamnoaeficiency syndrome), infiammatory disorders (e.g. psorlasis and asthma), renal disorders, entryonic disorders, brain-related disorders (e.g. cerebral oedema), cerebrovascular diseases (e.g. ischaemia), tumours, prostate-related disorders, pitultary-related disorders (e.g. Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's disease).
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322 T; 0 other;

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34.167
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GTGAGCCCTGCCTCATGGTTCTGCTCTGCCTCGGGCTGAGTCTGGGCCC
                                                                 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
     211
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CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG 261 34

luSerGluHis***LeuLysThrLenGlyGln..CysAspAlaAspValP AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT 308 50

roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu..... 63

CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGAAGCCC 78 358

ysHisGlnPheLeuLeuThrGlyAspThrGln......GlyArgTyr . GAGCCCAAGAACA 91 399

CGCTGTTACTACTACAGCCCTGCAGGCTGGTCAGAGCCCAGCGACCCCCT ArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLe 108 499

449

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS02102

immunological disorder; arthritis; graft rejection; renal disorder; acquired immunoder[cloney syndrome; inflammatory disorders; psoriasis; acquired immunoder[cloney syndrome; corebral oddema; ischaemla; tumour; prostate; cerebrovascular disease; pituitary; Cushing's disease; Human; MANGO 511; transmembrane protein; diagnostic; asthma

Homo sapiens

The sequence represents the coding sequence transmembrane protein. The nucleic acid and are useful for the diagnosis, prognosis and

polypeptide sequences treatment of immunological of human MANGO 511

Key Location/Qualifiers

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wariant #1 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunological disorders (e.g. arthritis, graft rejection and acquired immunological disorders, biflammatory disorders, pscriasis and asthma), renal disorders, embryonic disorders, brain related disorders (e.g. technaema), cerebrovascular diseases (e.g. ischmaema), cumours, prostate-related disorders, plunitary-related disorders (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 295-296; 362pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kirst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200121631-A2
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                                                                 359
                                                                                                                               309
                                                                                                                                                                                                                                                                  212 CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cushing's disease) and neurodegenerative diseases (e.g. Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents the coding sequence of human MANGO 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-MAR-2001
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4
                                                                                                                                                                                                                                                                                                                                                                   1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                                                                                                                                 luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP 50
                                                                                                                                                                                                                                                                                                                                     GTGAGCCCTGCCCTCATGGTTCTGCTCTGCCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid encoding INTERCEPT 307, MARGO 511, TARGO 51, TARGO, TARGO 499 or TARGO 509 secreted or transmembrane protein, useful the diagnosis and treatment of arthritis, psoriasis and Parkinson's
                                                                                                                                  CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGAAGCCC
                                                                                                                                                              roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.....
                                                                                                                                                                                                AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT
                                                                                                                                                                                                                                                                                                oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
AGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCAGGGAGATAC
                           ysHisGlnPheLeuLeuThrGlyAspThrGln......GlyArgTyr 91
                                                                 AGAACCCTGGGACACACAGAACCCACTG....
                                                                                            .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-211461/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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1.612
55.833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         374 G; 322 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                    to: 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identity:
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440
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Disclosure; Page 296-297; 362pp; English

New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 351, TANGO 351, TANGO 351, TANGO 495 or TANGO 509 secreted or transmembrane protein, useful for the diagnosis and treatment of arthritis, psoriasis and Parkinson's disease -

WPI; 2001-211461/21 P-PSDB; AAU01392.

Kirst SJ,

Sharp JD,

Fraser CC,

Barnes

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Kingsbury

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(MILL-) MILLENNIUM PHARM INC

20-SEP-1999;

9908-0399723

The sequence represents the coding sequence of human MANGO 511 variant #2 transmembrane protein. The nucleic acid and polypeptide sequences are useful for the diagnosis, prognosis and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunodeficiency syndrome). Inflammatory disorders (e.g. psortiasis and asthme), renal disorders, embryonic disorders, brain-related disorders (e.g. sections), ocrebrowascular diseases (e.g. schemila) tumours, prostate-related disorders, pituitery-related disorders (e.g. useful and performer protections).

alignment_scores:

Quality: Ratio:

108.00 1.612

Length: Gaps:

120 6

Sequence 1477

BP;

393 A;

390

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322 T;

0 other;

Cushing's disease)

and neurodegenerative diseases (e.g. Parkinson's

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seq_documentation_block:
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                                                                                                                                                                                                                                   immunological disorder; arthritis; graft rojection; renal disorder; acquired immunodeficiency syndrome; inflammatory disorders; psorlasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pitultary; Cushing's disease; neurodegenerative disease; parkinson's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500
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                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                               Human; MANGO 511; transmembrane protein; diagnostic; asthma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 uGluLeu 110
                                                                                           WO200121631-A2
                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2001 (first entry)
                              20-SEP-2000;
                                                               29-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCTGTTACTACTACAGCCCTGCAGGCTGGTCAGAGCCCAGCGACCCCCT 499
                                                                                                                                                                                                                                                                                                                                                  MANGO 511,
                              2000WO-US25982
                                                                                                                        /product=
                                                                                                                                         /*tag-
                                                                                                                                                      Location/Qualifiers
108..1007
                                                                                                                                                                                                                                                                                                                                                  variant #2 cDNA sequence
                                                                                                                          "MANGO 511,
                                                                                                                          variant #2"
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alignment_block:
US-09-471-276-831 x AAS02103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS02104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                             Human: MANCO 511; transmembrane protein; diagnostic; asthma; immunological disorder; arthritis; graft rejection; renal disorder; acquired immunodeficiency syndrome; infiammatory disorders, psociasis; AIDS; embryonic disorder; brain; cerebral oedema; ischaemia; tumour; prostate; cerebrovascular disease; pitultary; Cushing's disease; neurodegenerative disease; Parkinson's disease; ss.
20-SEP-1999;
                                                  20-SEP-2000; 2000WO-US25982
                                                                                                     29-MAR-2001
                                                                                                                                                       WO200121631-A2
                                                                                                                                                                                                                                                                                                                                                                     OMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human MANGO 511, variant #3 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 GTGAGCCCTGCCCTCATGGTTCTGCTCTGCCTCGGGCCTGAGTCTGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 uGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 AGAACCCTGGGACACACAGAACCCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGGAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 ArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLe 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 ysHisGinPheLeuLeuThrGlyAspThrGln.......GlyArgTyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.....
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99US-0399723
                                                                                                                                                                                                                                                                                      Location/Qualifiers 108..1007
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/product- "MANGO 511, variant #3"
/transl_except- (pos:201..203, aa
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seq_documentation_block:

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV44827

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alignment_block:
US-09-471-276-831 x AAS02104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence represents the coding sequence of human MANGO 511 variant #3 trainmembrane protein "The nucleic acid and polypeptide sequences are useful for the diagnosts, prognosts and treatment of immunological disorders (e.g. arthritis, graft rejection and acquired immunological disorders (e.g. arthritis, graft rejection and acquired immunological disorders (e.g. arthritis, graft rejection and acquired setum y, renal disorders, embryonic disorders (e.g. psoriasis and sathme), renal disorders, occeptionascular disorders (e.g. Ischmennia) cumonirs, prostate-related disorders, pitultary-related disorders (e.g. prostate-related disorders, pitultary-related disorders (e.g. parkinson substitution).
500
                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361, TANGO 499 or TANGO 309 secreted to the diagnosis and Parkinson's for the diagnosis and treatment of arthritis, psoriasis and Parkinson's disease
                                                                                        450 CGCTGTTACTACTACAGCCCTGCAGGCTGGTCAGAGCCCAGCGACCCCCT
                                                                                                                                                                                                                                                                              359 AGAACCCTGGGACACACAGAACCCACTG.....GAGCCCAAGAACA
                                                                                                                                                                                                                                                                                                                                                                             309 CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGAAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212 CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 GTGAGCCCTGCCCTCATGGTTCTGCTCTGCCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1477 BP; 392 A; 390 C; 373 G; 322 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 298-299; 362pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding INTERCEPT 307, MANGO 511, TANGO 351, TANGO 361, TANGO 499 or TANGO 509 secreted or transmembrane protein, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU01393
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                                                                                                                                                                                                                                                                                                                                                                                                                       50 roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
GGAGCTG 506
                                          uGluLeu 110
                                                                                                                                     ArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLe
                                                                                                                                                                                   AGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCAGGGAGATAC
                                                                                                                                                                                                                                 ysHisGlnPheLeuLeuThrGlyAspThrGln.......GlyArgTyr 91
                                                                                                                                                                                                                                                                                                                            .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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1.612
55.833
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Gaps: 6
Percent Identity: 34.167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kingsbury
                                                                                                                                         108
                                                                                                                                                                                      449
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alignment_scores:
Quality:
Ratio:
                                                                            erythematosus haemolytic andemia thrombocytopaenia insphylaxis allergy, colorectal or breast cancer, lymphoma, leukaemia infection by allergy, colorectal or breast cancer, lymphoma, leukaemia infection by intracellular pathogens etc). The antagonists are also useful as munomodulators and inhibitors of viral (e.g. human immune deficiency or dengue viruses) entry into cells. The proteins may also be used to screen for specific binding agents, i.e. (ant)agonists, for raising antibodies (Ab), and for identification of particular cells or tissues. The Ab can be used therapeutically as antagonists; as assay reagents for diagnostic determination of the levels of expression of the proteins and for affinity purification of the proteins. The DNA and its fragments are useful as hybridisation (chromosome mapping) and diagnostically to measure ever the protein and diagnostically to measure
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding Fc receptor-like polypeptides or their fragments - and related vectors, transformed cells and antibodies, useful for treating and diagnosing diseases of the haematopoletic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gentz RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FC receptor-like protein; phagocytosis inducer; rheumatoid arthritis; immune complex related disease; systemic lupus erythematosus; allergy; haemolytic anaemia; thrombocytopaenia; anaphylaxis; cancer; luphoma; leukaemia; infection; immunomodulator; viral entry inhibitor; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAV44827
                                                                                                                                                                                                                                                                                                              invention. Cells containing the DNA are used to express the recombinant protein, and to screen for specific (ant)agonists. The proteins are used to induce phagorytosis, and their (ant)agonists are used to treat immune complex related diseases (e.g. rheumatoid arthritis, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes the Fc receptor-like IV protein (FcR-IV) of the
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-JUN-1997;
21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9831806-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FcR-IV; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FcR-IV coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-0CT-1998
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                                                                          Sequence 1550 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                immune systems
                                                                                                         expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW69234
                                                                                                                                                                                                                                                                                                                                                                                                            Fig 4A; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0049872
97US-0034205
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70..1437
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22..69
  1.633
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                                                                            363
                                                                          A,
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Length:
Gaps:
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                                                                            0 other;
  121
7
  × 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-471-276-831 x AAV44827
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Cosman DJ;
                                                                                                                                                                                                                                                                                                                                                                                                               09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 euLeuGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 CTGAGCCAGGCTCTGTGATCAG....CTGGGGGAACTCTGTGACCATCTG
                                                                                                                                                                                                                                                                                                                                LIR-pbm2; immunoregulator; leukocyte immunoglobulin-like receptor;
therapeutic; treatment; disorder; ITIM; MHC class I receptor; inhi
                                                                                                                                                                                                                                                                                                                                                                                Human LTR-pbm2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV69337 standard; DNA; 1625 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
                            (IMMV ) IMMUNEX CORP...
                                                             24-APR-1997;
                                                                                         23-APR-1998;
                                                                                                                          29-OCT-1998
                                                                                                                                                       WO9848017-A1
                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                 negative signalling; autoimmune disease; suppressor; LIR; ss
                                                                                                                                                                                                                                                                                                                cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV69337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 laGluSerGluHis***LeuLysThrLeuGlyGln...CysAspAlaAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACCCCTGTTACTATCGCAGCCCTGTAGGCTGGTCACAGCCCAGTGACC 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTGAGTCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCAGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerMetLeuValValPhe....LeuLeuLeuTrpGlyValThrTrpGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCCAGCACCCTGGGACAGACAGAACCCACTG......GAGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TrpGlyAlaGlnGluProValHisLeuAspSerProAla
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                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV69337
                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                             97US-0842248
                                                                                            98WO-US08244.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                  Location/Qualifiers
30..1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.893
                                                                                                                                                                                      /product= "LIR-pbm2
                                                                                                                                                                                                       /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
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63 164 48 118

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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV23273
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US-09-471-276-831 x AAV69337
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ITMS), whilst other LIR family members lack ITMS. By analogy with the structure and function of known MHIC Class I receptor molecules, LIRs having ITMS are inhibitory receptors mediating negative signalling, whilst those lacking ITMS are activatory receptors. Failure of a receptor that mediates negative signalling could result in autoimmune diaesases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIR) polypeptide LIR-pbm2. This sequence can be administered therapoutically to treat disorders associated with insufficient/defective amounts of LIR polypeptide. LIR-P302 and certain other LIR family members contain cytoplasmic immunoreceptor tyrosine based inhibitory motifs
                                                                     364 CCCTGGAGCTG 374
                                                                                                                                     107
                                                                                                                                                                                                                                                                                                                                       264 AACAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 GCCCAGCACCCTGGGACAGACAGAACCCACTG......GAGCCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1625 BP; 399 A; 523 C; 425 G; 278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other species
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; Page 83-85; 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with suppressed immune function
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAW82551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
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                                                                                                                                 euleuGluleu 110
                                                                                                                                                                                                      ATACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTCACAGCCCAGTGACC 363
                                                                                                                                                                                                                                                                                                                                                                                                   IleLysHisGlnPhe....LeuLeuThrGlyAspThrGlnGlyAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTCAGGGGACCCTGGAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ValProGlyProProGlyAspSerArgLeuProAla. ValGlnGlu....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerMetLeuValValPhe....LeuLeuLeuTrpGlyValThrTrpGl 16
                                                                                                                                                                                                                                                             gTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....TrpGlyAlaGlnGluProValHisLeuAspSerProAla 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: AAV69337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encodes a novel leukocyte immunoglobulin-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103.50
1.617
52.893
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                                                                                                                                                                                                                                                                                                                                                                                                       90
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seq_documentation_block

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alignment_block:
US-09-471-276-831 x AAV23273
                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                        Align seg 1/1 to: AAV23273
                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            gp49 component and RoeRi or a detectable marker; (2) a recombinant nucleic solid encoding human gp49 or a human gp49-RoeRi fusion as above; (3) a cell or vector comprising the recombinant nucleic acid as in (2), and (4) an antibody which selectively binds to gp49. Mammallan gp49 or its related bMA can be used to treat an undesired immune response, especially a mast cell-related disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell-surface member of immunoglobulin super-family, human gp49 useful to treat undesired immune responses, especially mast cell-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes human 9p49 polypeptide HM18. The present remains also describes (1) a fusion polypeptide comprising a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arm
                                                                                                                                                                                                                                                                                                                                  Sequence 1625 BP; 400 A; 519 C; 429 G; 277 T; 0 other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Fig 1A-B; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-193318/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9809638-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; gp49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gp49 HM18 encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV23273 standard; cDNA; 1625 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bone marrow;
                          33 laGluSerGluHis***LeuLysThrLeuGlyGln...CysAspAlaAsp 48
                                                                                                                3
                                                                                                                                            2 SerMetLeuValValPhe.....LeuLeuLeuTrpGlyValThrTrpGl 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP,
CTGAGCCAGGCTCTGTGATCAG....CTGGGGGGAACTCTGTGACCATCTG
                                                                                  yProValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpA
                                                                                                                GCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTGAGTCTGGG
                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Austen KF,
                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell-surface member; FceRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HM18; HM43; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96US-0025846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US15586
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1.617
52.893
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                                                                                                                                                                        from: 1
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                                                                                                                                                                                                                                              Percent Identity: 36.364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katz
                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                        1625
                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response; mast cell;
ss.
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7
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54600
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                                               Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat outcommune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cosman DJ, Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leukocyte immunoglobulin like receptor coding sequence (pbm2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA54600 standard; cDNA; 1625 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              280 AACAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCAGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 GCCCAGCACCCTGGGACAGACAGAACCCACTG......GAGCCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90
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Sequence 1625 BP; 399 A; 523 C; 425 G;
                                                                                                                                                                                                                                                                                 Example 9; Page 88-90; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 IleLysHisGlnPhe.....LeuLeuThrGlyAspThrGlnGlyAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValProGlyProProGlyAspSerArgLeuProAla.ValGlnGlu....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....TrpGlyAlaGlnGluProValHisLeuAspSerProAla 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-687645/67
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/product= Leukocyte immunoglobulin like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Borges L;
278 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
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24-APR-1997;

97US-0842248 98WO-US08244

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alignment_block:
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ID AAV69329 standard:
                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV69329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127
                                                                                                                                                          CDS
                                                                                                                                                                                                                             IR-18A3; immunoregulator; leukocyte immunoglobulin-like receptor; LTR: therapeutlo; treatment; disorder; ITTM; MHC class I receptor; inhibitor cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      364 CCCTGGAGCTG 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 euLeuGluLeu 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 GTGTCAGGGGACCCTGGAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAA
                                                                                                                                                                                                                                                                                                      Human LIR-18A3 cDNA
                                                                                                                                                                                                                                                                                                                                  09-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                   AAV69329;
                                                                                                                                                                                                                                                                                                                                                                                             AAV69329 standard; DNA;
                                          23-APR-1998;
                                                                                                 WO9848017-A1
                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysL 107
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52.893
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1.617
                                                                                                                                                        Location/Qualifiers
168..2126
                                                                                                                             /product- "LIR-18A3"
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alignment_scores
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US-09-471-276-831 x AAV69329
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                                                                                                                                                                                        406
                                                                                                                                                                                                                                                                                                                                                                                 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIR) polypeptide LIR-18A3. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-609990/51
                                    107 uLeuGluLeuThr.....
                                                                                                                                                                                                                                                                                        365 AGCACTCTGGATTACACGGATCCCACAGGAGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 CAGGACCCACGTGCAGGCAGGCACCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2777 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     produce probes for detecting LTR nucleic acids or isolating LTR DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 56-59; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetSerMetLeuValValPheLeuLeuTrpGlyValThrTrpGlyPr
CCTGGAGCTGGTGACAGGAGCCTACATCAAACCCACCCTCTCAGCCC
                                                                                                                                   ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe
                                                                                                                                                                                        AGGGCCAGTTCCCCATCCCATCCATCACCTGGGAACATGCAGGGCGGTAT
                                                                                                                                                                                                                                                                                                                                                                                    CAGGGGGGCCAGGAGCCCAGGAGTACCGTCTATATAGAGAAAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                            roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ovalThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                      ysHisGlnPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
                                                                                                                                                                                                                                                                                                                                   .....TrpGlyAlaGlnGluProValHisLcuAspSerProAlafleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence encodes a novel leukocyte immunoglobulin-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103.00
1.288
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                657 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                840 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                754 G; 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identity: 30.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                               63
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alignment_scores:
                                                                                               alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54592
                                               Align seg 1/1 to: AAA54592
                                                                              US-09-471-276-831 x AAA54592
                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                   Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of discorders mediated directly or indirectly by defectively not discorders mediated directly or polypeptides. The LIR polypeptides can be used longer autoLimnune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 606 TCACAGGTGGCATTTGATGGCTTCAGT 632
                                                                                                                                                                                                                       Sequence 2777 BP; 657 A; 840 C; 754 G; 526 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 63-66; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-687645/67
P-PSDB; AAB04170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cosman DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmunity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukocyte immunoglobulin like receptor; LIR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukocyte immunoglobulin like receptor (LIR) coding sequence (18A3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA54592 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAY-2000; 2000WO-US13228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200068383-A2
...SerLeuAlaLeuAspGlyAlaSer 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GlyProLysValLeuAlaCys... 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCCAGCCCGTGGTGAACTCAGGAGGGAATGTAATCCTCCAGTGTGAC
                                                                                                                                                        Quality:
                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorders; immune system; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0310463
                                                                                                                            103.00
1.288
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product∴ Leukocyte immunoglobulin like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
168..2126
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                                               from: 1
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                                                                                                                            Percent Identity: 30.000
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
21-MAR-1997;
06-DEC-1996;
09-DEC-1996;
16-DEC-1996;
                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                              Human: type I transmembrane protein; immunoglobulin-like domain; 

PDP03: activated monocyte; Y801; KYE03; control; development; 

differentiation; mammalian immune system; transplantation rejection; 

degenerative condition; autoimmune response; transplantation rejection; 

graft versus host disease; inflammatory condition; desection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          556
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                                                                                                                                 11-JUN-1998
                                                                                                                                                                  W09824906-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human monocyte gene designated KLM67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV38608 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 uteuGluteuThr.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 CAGGGGGGCCAGGAGCCCAGGAGTACCGTCTATATAGAGAAAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 CAGGACCCACGTGCAGGCAGGGCACCTCCCCAAGCCCACCCTCTGGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 ATGACCCCCATCCTCACGGTCCTGATCTCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACAGGTGGCATTTGATGGCTTCAGT 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...SerLeuAlaLeuAspGlÿAlaSer 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTGTTACTATGGTAGCGACACTGCAGGCCGCTCAGAGAGCAGTGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGGCCAGTTCCCCATCCCATCACCTGGGAACATGCAGGGGGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysHisGinPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....GlyProLysValLeuAlaCys...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
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                                                                                                                                                                                                                                                                                                                                 screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
96US-0032252.
96US-0762187.
96US-0033181.
                                                          97US-0041279
                                                                                           97wo-us21101
                                                                                                                                                                                                                                                                                                                                    SS
                                                                                                                                                                                                                                      Location/Qualifiers
177..2135
                                                                                                                                                                                                     /product= KLM67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us-09-471-276-831 x AAV38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAV38608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-333325/29.
P-PSDB; AAW62782.
                                                                                                                                                                                                                                         374
                                                                                                                                                                                                                                                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2790 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Pages 95-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Phillips
                                                                                                                                                                                                                                                                                                                  324 CAGGGGGGCCAGGAGCCCAGGAGTACCGTCTATATAGAGAAAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHE ) SCHERING CORP
                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                                                                                                                                                                                                                                                                          34
                 CCTGGAGCTG
                                                       uLeuGluLeu 110
                                                                                                                                                                  AGGGCCAGTTCCCCATCCCATCCATCACCTGGGAACATGCAGGGCGGTAT
                                                                                                                                                                                                                                      AGCACCCTGGATTACACGGATCCCACAGGAGCTT......GTGAAGA 414
                                                                                                                                                                                                                                                                                                                                                 roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGACCCACGTGCAGGCAGGCCACCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                        CGCTGTTACTATGGTAGCGACACTGCAGGCCGCTCAGAGAGCAGTGACCC
                                                                                                                            ArgCysArgSerGlyLeuSerThr . . . GlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                   ysHisGlnPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
                                                                                                                                                                                                                                                                          ......TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                                                                                                                                                                                                                                                                                                                       AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT 323
                                                                                                                                                                                                                                                                                                                                                                                                                        luSerGluHis***LeuLysThrLeuGly ..GlnCysAspAlaAspValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zurawski
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1.449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 33.884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               752 G; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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78 373 63

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designated KTEQ3. The genes are found in activated monocytes. The specification also describes other proteins encoded by activated monocytes, which are designated PDF03 and YEQ1 The genes function in controlling development, differentiation, and/or physiology of the mammal in minume system. The products can be used for treating encountries, degeneration or arrophy. They can be used for treating e.g. cancerstion, degeneration, degenerative conditions, factly versus bost autoimment responses, transplantation rejection, graft versus bost disease, or inflammatory conditions. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated activated monocyte cell gene(s) - used to develop
products for treating e.g. cancer, degenerative conditions,
autoimmune responses, transplant rejection or inflammatory
                                                                                detection, diagnosis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAV38992-96 and AAV38608 represent human monocyte genes, collectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G, Zurawski SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McClanahan TK,
T; 1 other;
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ID AAV69328 standard; cDNA; 2922 BP
                                                                                                                                                                                                                             alignment_scores:
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                           Align seg 1/1
                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-PSG2 This sequence can be administered wherepeatically to treat disorders associated with insufficient/defective mounts of LIR polypeptide. LIR-PSG2 and certain other LIR family members contain cytoplasmic immunoreceptor tytosine-based inhibitory motifs (ITIMS), whilst other LIR family members lack ITIMS. By analogy with the structure and function of known MRC Class I receptor molecules, LIRs having ITIMS are althibitory receptors mediating negative signalling whilst those lacking ITIMS are activatory receptors. Failure of a receptor that mediates negative signalling could result in suppressed immune timesters. The structure of a receptor mediating activatory signalling could result in suppressed immune function, They are also useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW82544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIR-9362; immunoregulator; leukocyte immunoglobulin-like receptor; LIR; therapeutic; treatment; disorder; ITIN; MHC class I receptor; inhibitor cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human LIR-P3G2 cDNA
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                                                                                                                                                                                                                                                                                                     Sequence 2922 BP;
                                                                                                                                                                                                                                                                                                                                                                         produce probes for detecting LIR nucleic acids or isolating LIR DNA from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 50-53; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosman DJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-1997;
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                              AAV69328
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                                                                                                                                                                                                                                                                                                     683 A;
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                              from: 1
                                                                                                                                                                                                                                                                                                     882 C; 789 G; 568 T; 0 other;
                                                                                                                                                  Gaps: 7
Percent Identity: 33.884
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   seq_documentation_block:
                                                                                                                                                                                                                          Cosman DJ,
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Example 3; Page 57-60; 117pp; English
                                                   tunction
                                                                    Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
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310..2262
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54591
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                                                                                                                                                                                                                                                                                                                                                                      Leukocyte immunoglobulin like receptor (LIR) coding sequence (P3G2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGGCCAGTTCCCCATCCATCACCTGGGAACATGCAGGGCGGTAT
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/product^ Leukocyte immunoglobulin like receptor
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                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54611
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                                                                                                                                                                                                                                        documentation_block:
AAA54611 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Host cells transformed with a vector which are capable of expressing a leukoyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or the LIR polypeptides can be used to treat autoimmune of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune diseases and disease stakes with suppressed immune function.
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               CDS
                                                              Homo sapiens
                                                                                           Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human; ds
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                                                                                                                                             Leukocyte immunoglobulin like receptor coding sequence (LIR-9s2).
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Ratio:
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                                                                                                                                                                                                                                                                                                                         657
               Location/Qualifiers 73..834
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1.449
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Gaps:
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                                                                                              seq_documentation_block:
                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54609
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               11-APR-2001
                                                                                                                                                            413
                                                                                                                                                                            316
                                                 AAA54609;
                                                                              AAA54609 standard; cDNA; 1007 BP
                                                                                                                                                                                                                           363 CCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCAG
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                                                                                                                                                            AGCCCAGCGACCCCCTGGAGCTG
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                                                                                                                                                                                                                                                                                          ...GAGCCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCA 362
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               (first entry)
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alignment_block:
US-09-471-276-831 x AAA54611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides. The LIR polypeptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can used to produce the LIR polypeptide. LIR coding sequences may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 112-113; 117pp; English
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                                                  61 alGlnGlu.....TrpGlyAlaGlnGluProValHisLeu 72
                                                                                                                                                                 45 CysAspAlaAspValProGlyProProGlyAspSerArgLeuProAla.V
TTAAAGAGGGAAGCCCAGAACCCTGGGACACACAGAACCCACTG.....
                                                                                                               TGTGACCATCCGGTGTCAGGGGACCCTGGAGGCCCCAGGAATACCGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson
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2.207
54.667
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                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 37.333
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                                                                                                                                                                                                                           to:
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                                                                                                               271
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Leukocyte

immunoglobulin like receptor coding sequence (LIR-9m2).

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alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune polypeptides. The LIR polypeptides can be used to treat autoimmune
                                              103 InLeuSerLysLeuLeuGluLeu
                                                                                                                                                                                                         338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1007 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 107-108; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukocyte Lmmunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cosman DJ, Anderson DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-NOV-2000
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                                                                                                                                                                                                                                                                                                                  294 TTAAAGAGGGAAGCCCAGAACCCTGGGACACACAGAACCCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                   244 TGTGACCATCCGGTGTCAGGGGACCCTGGAGGCCCAGGAATACCGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases and disease states with suppressed immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAY-2000; 2000WO-US13228
                                                                                                                                                           89
                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 CysAspAlaAspValProGlyProProGlyAspScrArgLeuProAla.V
                                                                                                    CCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCAG 434
                                                                                                                                                                                                                                                                                                                                                                 alGlnGlu.....TrpGlyAlaGlnGluProValHisLeu
AGCCCAGCGACCCCCTGGAGCTG
                                                                                                                                                                                                                                                        AspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAspThrGln..
                                                                                                                                                                                                         ...GAGCCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCA 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-687645/67
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                                                                                                                                                .....GlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***G 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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2.207
54.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 A;
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Gaps:
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV44826
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AAV44826 standard; DNA; 1991 BP (first entry)

FcR-III coding sequence

FC receptor-like protein; phagocytosis inducer; rhewmatoid arthritis; Immune complex related diseasa; systemic lupus erythematosus; allergy haemolytic anaemia; thrombocytopaenia; anaphylaxis; cancer; lymphoma; leukaemia; infection; immunomodulator; viral entry inhibitor; therapy allergy;

Location/Qualifiers 73..1944

/*tag b 121..1941 /product~ FcR-III 73..120 /*tagu /*tag~

(HUMA-) HUMAN GENOME SCI INC Murphy M, 97US-0034205 97US-0049872 98WO-US01184 Ni J, Olsen HS,

Ruben SM;

useful for treating and diagnosing diseases of the haematopoietic Nucleic acid encoding Fc receptor-like polypeptides or their fragments - and related vectors, transformed cells and antibodies.

Claim 2; Fig 3A; 141pp; English.

seq-documentation_block.

DAVA4826 standard; DAVA
AC AAVA4826;

XX ACAAVA4826;

XX ACAAVA4826;

XX FC RECEPTOT-like proton in the proton in th dengue viruses) entry into cells. The proteins may also be used to screen for specific binding agents, i.e. (ant)agonists, for raising antibodies (Ab), and for identification of particular cells or tissues. The Ab can be used therapeutically as antagonists; as assay reagents for diagnostic determination of the levels of expression of the proteins and for affinity purification of the proteins. The DAA and its fragments are useful as hybridisation probes or primers for isolating related genes, in situ hybridisation (chromosome mapping) and diagnostically to measure This sequence encodes the Fc receptor-like III protein (FcR-III) of the invention. Cells containing the DNA are used to express the recombinant protein, and to screen for specific (ant)agonists the proteins are used to induce phagocytosis, and their (ant)agonists are used to treat immune complex related diseases (e.g., rheumatoid arthritis, systemic lupus allergy, colorectal or breast cancer, lymphona, leukemia, infection by intracellular pathogens etc). The antagonists are also useful as immunomodulators and inhibitors of viral (e.g. human immune deficiency or erythematosus, haemolytic anaemia, thrombocytopaenia, anaphylaxis,

BP; 430 A 660 Ç 548 ç, 353 T; 0 other

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seq_documentation_block:

ID ANV6338 standard; DNA; 2194 BP.

AC AAV6338;

AC AV63338;

AC AV69338;

XC O9-FEB-1999 (first entry)

XX Human LIR-pbm17 cDNA.

XX LIR-pbm17; immunoregulator; leukoo

XW LIR-pbm17; immunoreceptor tyrosin

XW therapeutic; treatment; disorder;

XW therapeutic; treatment; resorder;

XW therapeutic; treatment; resorder;

XW therapeutic; treatment; disorder;

XW therapeutic; treatment;
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                                                                                                                                                                                                                                                                                                                   LR-pbm17; immunoregulator; leukocyte immunoglobulin-like receptor; therapeutic; treatment; disorder; ITHM; MHC class I receptor; inhibitor; cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; LIR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 GAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AAGAACAAGGCCAGATTCTCCATCCCATCCATGACACAGCACCATGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 ATAAAGAGGGAAGCCCAGAGCCCTTGGACAGAAATAACCCACTGGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 CGTGACCATCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPro 50
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Ratio:
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1.560
42.029
                                                                                                                                                                             Location/Qualifiers 67..1962
                                                                                                                         /product- "LIR-pbm17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAV69338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-471-276-831 x AAV69338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIR) polypeptide LIR-phm17. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective amounts of LIR polypeptide. LIR-F302 and certain other LIR family members contain cytoplasmic immunoreceptor typosine-based inhibitory mobilis (ITIMS), whilst other LIR family members lack ITIMS. By analogy with the structure and function of known MHC Class I receptor modecules, LIRs having ITIMS are inhibitory receptors mediating negative signalling, whilst those lacking ITIMS are activatory receptors. Failure of a receptor that mediates negative signalling could result in suppressed immune function. They are also useful to produce probes for detecting LIR nucleic acids or isolating LIR DNA from the reservice.
                                                                                                                                                                                                                                          198
                                                                                                                                                                                                                                                                                                                                                           169
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P-PSDB; AAW82552.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2194 BP; 479 A; 729 C; 597 G; 389 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence encodes a novel leukocyte immunoglobulin-like receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with suppressed immune function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-APR-1998;
        298 AAGAACAAGGCCAGATTCTCCATCCCATCCATGACACAGCACCATGCAGG 347
                                                                                                                     248 ATAAAGAGGGAAGCCCAGAGCCCTTGGACAGAAATAACCCACTGGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPro 50
                                                                                                                                                                                                                                                                                                                                                                                                            GlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGly.....
                                                        oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGACGCCCGCCCTCACAGCCCTGCCTCTGCCTTGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                                                                                                                                                                             .....CCAGGC......TCTGTGATCAGCTGGGGGAGCCC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0842248
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1.560
42.029
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Gaps: 6
Percent Identity: 28.986
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247 8 65 168 166 ω 116

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alignment_block:
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                          Align seg 1/1
                                                       US-09-471-276-831 x AAA54601
                                                                                               Percent Similarity:
                                                                                                                                                                                                      Host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LTR), can be used to produce the LTR polypeptide. LTR coding sequences may be used in the gene therapy of discorders mediated directly or indirectly by defective or insufficient amounts of any of the LTR polypeptides can be used to treat autolimnune disease and disease states with suppressed immune function.
                                                                                                                                                                                                                                                                                                                                                             Loukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 GAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCG 397
                                                                                                                                                                                                                                                                                                                     Example 9; Page 92-95; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cosman DJ, Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Leukocyte immunoglobulin like receptor coding sequence (pbm17).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA54601 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 ysLeuLeuGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerL
MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGLyPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCCCTGGAGCTG 411
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                                                                                                           Quality:
Ratio:
                            60:
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                            AAA54601
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                                                                                             90.50
1.560
42.029
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                                                                                                                                                                               479 A;
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                          from:
                                                                                                                                                                             729 C;
                                                                                         Length: 138
Gaps: 6
Percent Identity: 28.986
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                                                                                                                                                                             597 G; 389 T; 0 other;
                          to:
                            2194
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seq_documentation_block:
ID AAV69334 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV69334
                                                                                                                                                                                                                                                                                               LIR-pbm36-2; immunoregulator; leukocyte immunoglobulin-like receptor; therapeutic; treatment; disorder; ITN, MHC class I receptor; inhibitor; cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; LIR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
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Cosman DJ;
                            (IMMV ) IMMUNEX CORP
                                                            24-APR-1997;
                                                                                           23-APR-1998;
                                                                                                                         29-0CT-1998.
                                                                                                                                                        W09848017-A1
                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             Human LIR-pbm36-2 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV69334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398 ACCCCCTGGAGCTG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348 GAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298 AAGAACAAGGCCAGATTCTCCATCCCATCCATGACACAGCACCATGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 ATAAAGAGGGAAGCCCAGAGCCCTTGGACAGAAATAACCCACTGGAACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 GlyProProGlyAspSerArgLeuProAlaValGlnGluTrpGly.... 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAspValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysLeuLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuScrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AlaIleLysHisGlnPheLeuLeuThrGlyAspThrGln......Gl 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGTGACCATCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCAACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....CCAGGC.......
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                            97US-0842248
                                                                                           98WO-US08244.
                                                                                                                                                                                    /product· "L1R-pbm36-2"
                                                                                                                                                                                                   /*tag..
                                                                                                                                                                                                                     Location/Qualitiers
171..1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 2446 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .TCTGTGATCAGCTGGGGGAGCCC 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
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WPI; 1998-609990/51. P-PSDB; AAW82548.

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alignment_block:
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                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA54597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-471-276-831 x AAV69334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having TTMs are inhibitory receptors mediating negative signalling, whilst those lacking ITMs are activatory receptors. Failure of a receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to produce probes for detecting LIR nucleic acids or isolating LIR DNA from the country of the country
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amounts of LIR polypeptide. LIR-P3G2 and certain other LIR family members contain cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (ITIMS), whilst other LIR family members lack ITIMS. By analogy with the structure and function of known MHC Class I receptor molecules, LIRs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-pma6-2. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective
                                                                                                                                                                                                                                                                                                                                                                                         459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2446 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                      107 uLeuGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AGCACCCTGGATTACACGGATCCCACAGGAGATT.....GTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 CAGGGGATCCTGGAGACCCAGGAGTACCGTCTGTATAGAGAAAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 ysHisGinPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP
                                                                                                                                                                                                                                                                                                                                                                                                                        ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCAGGCTCTGTGATC...ACCCAGGGGAGTCCCGTGACCCTCTGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
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                                                                                                                                                                                                                                                        CCTGGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                         CGCTGTTTCTACGGTAGCCACACTGCAGGCTGGTCAGAGCCCAGTGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGGCCAGTTCCCCATCCCGTCCATCACCTGGGAACACACCGGGCGGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                                            518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.50
1.377
53.719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function
                                                                                                 2446 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 7
Percent Identity: 33.884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
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US-09-471-276-831 x AAA54597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAA54597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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Sequence 2446 BP;

611 A:

692 C;

557 G;

586 T;

0 other;

and disease states with suppressed immune function.

Quality:

Ratio:

53.719 89.50 1.377

Percent Identity: 33.884

Length:

121

318 CAGGGGATCCTGGAGACCCAGGAGTACCGTCTGTATAGAGAAAAGAAAAC

.....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL 78

roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....

63 317 50 270 34

AGCCAGGCTCTGTGATC...ACCCAGGGGAGTCCCGTGACCCTCTGGTGT luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP

54

221 CCGGACCCACGTGCAGGCAGGGACCCTCCCCAAGCCCACACTCTGGGCTG

17 oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG

171 ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCC

1 MetSerMetLeuValValPheLeuLeuTrpGlyValThrTrpGlyPr 17

from: 1

6

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host cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-APR-2001 (first entry)
                                                                                                                                                                                                                                      Example 9; Page 77–79; 117pp; English.
                                                                                                                                                                                                                                                                                                                                      Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAB04173.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687645/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cosman DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borges L;
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF29475
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riboxymas and antibodies, are useful for preventing, treating and diagnosting disorders associated with abstrant expression or activity of GPVI. These disorders include bleeding disorders for the disorders include bleeding disorders thrombotic disorders (e.g. thrombotic orbits) blood vessel injury. thrombotic disorders (e.g. thrombotic orbits) income actuation of the coronary articlies) histories and stroke and isorders, coronary actuary and cerebral arteridises see of stroke and isorders. Coronary actuary and cerebral arteridisorders and stroke and incoretion), immunological diseases (e.g. atthromotionic liver disorders, preferably they are used to prevent acture embryonic liver disorders. Preferably they are used to prevent acture
                                                                                                                                                                                                                  nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein y (1GPVI). Also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein VI,
and diagnosing h
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06-DEC-1999;
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blood vessel injury; thrombotic disorder; haemornhagic disorder;
ischaemia; cardiovascular disease; immunological disoase; liver c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; monocyte inhibitory receptor precursor; TANGO 268; c
cerebroprotective; cytvostalic; anticoaquiant; thrombolytic;
antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
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                                                                                                                                                                                                                                                                                          The present sequence is given in a specification relating to an
                                                                                                                                                                                                                                                                                                                                                                                        immunological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Busfield SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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                                                                                                                                                                                                                                                                                                                                                                                                               diagnosing hemorrhagic disorders,
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                                                                                                                                                                                                                                                                                                                                           English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  thrombotic
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                                                                                                                        platelet membrane glycoprotein receptor; bleeding disorder;
blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
                                                                                                                                                                        antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI
                                                                                                                                                                                            cerebroprotective; cytostatic; anticoagulant; thrombolytic;
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                                Homo sapiens
                                                                             cancer; ds
                                                                                                                                                                                                                      Human; monocyte inhibitory receptor precursor; TANGO 268; cardiant;
                                                                                                                                                                                                                                                                   Human monocyte inhibitory receptor precursor DNA
                                                                                                                                                                                                                                                                                                                                                                                                               AAF29472 standard; DNA;
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                                                                                                    ischaemia; cardiovascular disease; immunological disease; liver disorder;
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DR WPF; 2001-080877/99. DR WPF; 2001-080877/99. PP PSDB, ABA61263. XX New genes encoding human platelet-expressed collagen receptor, PT ABA61263. PT ABA61263. XX New genes encoding human platelet expressed collagen receptor, PT and diagnosing hemorrhagic disorders, thrombotic diseases and rimmonlogical disorders in the present sequence is given in a specification relating to an isolated conclusion actid molecule encoding a platelet membrane glycoprotein receptor city of the present sequence is given in a specification relating to an isolated collagonsing disorders associated TANGO 268. The GPV polymucleotides city of the colles are useful for preventing, treating and collagonsing disorders associated with aberrant expression or activity of city. These disorders associated with aberrant expression or activity of city. These disorders activity of the collagonsing disorders activity of the collagonsing and combatal rice yields and anyocardial disorders occupant activity and cerebral artery diseases (e.g. attrombotic disorders and antipulating angioplasty after associate disorders and anyocardial diseases (e.g. attrombotic disorders and carbotic disorders. Squantial, cardiovaccular diseases (e.g. attrombotic disorders and anyocardial diseases (e.g. attrombotic disorders and anyocardial diseases (e.g. attrombotic disorders and anyocardial dispasses (e.g. attrombotic disorders and anyocardial disorders and anyocardial disorders and anyocardial disorders and anyocardial disorders. Squantial disorders and anyocardial disorders are used to prevent acture especially of the colon and liver. Squantial disorders and disorders and anyocardial dispasses and anyocardial d	14-FEB-2000; (MILL-) MILI Busfield SJ, Qian MD, Ki	PN W0200100810-A1. XX PD 04-JAN-2001. XP 30-JUN-2000; 2000W0-US18152. PR 30-JUN-1999; 99US-0345468. PR 30-JUN-1999; 99US-034546. PR 06-DEC-1999; 99US-0454824. PR 14-FEB-2000; 2000US-0503387.
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seq_documentation_block:
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                              with suppressed immune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIR-pbm36-4; Immunoregulator; leukocyte immunoglobulin-like receptor; therapeutic; treatment; disorder; ITMM, MMC class I receptor; inhibitor; cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; LIR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-FEB-1999
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P-PSDB; AAW82549.
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Example 9; Page 74-77; 112pp; English.
                                                               Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                  Cosman DJ;
                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                         24-APR-1997;
                                                                                                                                                                                                                                                                                                                                 23-APR-1998;
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(LIR) polypoptide LIR phm36-4. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective amounts of LIR polypoptide. LIR PBG2 and cortain other LIR family members contain cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (TTMS), whilst other LIR family members lack (TTMS, By nanlogy with the structure and function of known MRC class: receptor molecules LIRS having TTMS and function of known MRC class: receptors molecules LIRS whilst those acking LTMS are activatory receptors. Failure of signalling, whilst those acking LTMS are activatory receptors. Failure of activatory signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to

This sequence encodes a novel leukocyte immunoglobulin-like receptor

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alignment_block:
US-09-471-276-831 x AAV69335
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16-NOV-2000.
                                       WO200068383-A2
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                    Leukocyte immunoglobulin like receptor; LIR; gene autoimmunity; autoimmune disorders; immune system;
                                                                                                                                                                                                                                                                                                   Leukocyte immunoglobulin like receptor coding sequence (pbm36-4).
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Ratio:
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1.320
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/producto Leukocyte immunoglobulin like receptor
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV69339

seq_documentation_block:

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alignment_block:
US-09-471-276-831 x AAA54598
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                                                                                                              471 CGCTGTTTCTACGGTAGCCACACTGCAGGCTGGTCAGAGCCCAGTGACCC
521 CCTGGAGCTG 530
                                                       107 uLeuGluLeu 110
                                                                                                                                                                                                                                421 AGGGCCAGTTICCCCATCCCATCCATCACCTGGGAACACACAGGGCGGIIAT
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                                                                                                                                             92 ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe 107
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alignment_scores:
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                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence encodes a novel leukocyte immunoglobulin-like receptor (LIR) polypeptide LIR-phanev, This sequence can be administered therapeutically to treat disorders associated with insufficiently defective amounts of LIR polypeptide. LIR-PSG2 and certain other LIR family members contain cytoplasmic lumnunoreceptor tyrosine-based shibitory motifs (ITIMS), whilst other LiR family members leck LITMS: By analogy with the structure and function, of known MRC Class; L receptor molecules, LIRs transfer and contains of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIR-phanew: immunoregulator: leukocyte immunoglobulin-like receptor; therapeutic; treatment; disorder; ITHK, MHC class; receptor; inhibitor; cytoplasmic immunoreceptor tyrosine-based inhibitory motif; activator; negative signalling; autoimmune disease; suppressor; LIR; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                having ITIMs are inhibitory receptors mediating negative signalling, whilst those lacking ITIMs are activatory receptors. Failure of a receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human LIR-pbmnew cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-FEB-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV69339 standard; DNA; 2061 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW82553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-0CT-1998
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                                                                                                                                                                                                                                                                                                                                                              Sequence 2061 BP; 431 A; 684 C;
                                                                                                                                                                                                                                                                                                                                                                                                          produce probes
other species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 9; Page 92-94; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-609990/51.
                      67
                                                           MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
                      ATGACCCTCACCCTCTCAGTCCTGATTTGCCTCGGGCTGAGTGTGGGCCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     suppressed immune function
                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                               Ratio:
                                                                                                           :01
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                                                                                                                                                                                                                                                                                                                                                                                                                                for detecting LIR nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0842248.
                                                                                                              AAV69339
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                                                                                                                                                                                                                         84.50
1.207
50.360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "LIR-pbmnew"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  '*tag-
                                                                                                           from:
                                                                                                                                                                                                                            Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                              558 G; 388 T; 0 other;
                                                                                                              to:
                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                               Gaps:
                                                                                                                                                                                                                         9
: 30.935
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                                                                                                                                                                                                                                                                                                                                                                                                                                isolating LIR DNA from
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seq_documentation_block
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Leukocyte immunoglobulin·like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
                                                                P-PSDB; AAB04178
                                                                                             WPI; 2000-687645/67
                                                                                                                                       Cosman DJ,
                                                                                                                                                                                    (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                  12-MAY-1999;
                                                                                                                                                                                                                                                                               12-MAY-2000; 2000WO-US13228
                                                                                                                                                                                                                                                                                                                               16-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                         WO200068383-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  autoimmunity; autoimmune disorders; immune system; human; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leukocyte immunoglobulin like receptor; LIR; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leukocyte immunoglobulin like receptor coding sequence (pbmnew).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA54602 standard; cDNA; 2061 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGATAAGGAGGGACTCCCATGGGCCCGGAAGAGACACAGAACCCACTG...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCGTGACCCTCTGGTCAGGGGCCCCTGGAGACTGAGGAGTACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAsp..... 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCACTCTTTTAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProLysValLeuAla 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACAGTGCAGGGCGATACCGCTGCTACTATGAGACCCCTGCAGGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....ValProGlyProProGlyAspSerArgLeuProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .AspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT; AAA54602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .GAGCCTGGAGCCAAGGCCAAGTTCCACATTCCATCCACGGTGTA 335
                                                                                                                                       Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                  9908-0310463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 67..1839
                                                                                                                                                                                                                                                                                                                                                                                                                      /product= Leukocyte immunoglobulin like receptor
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                                                                                                                                       Ŋ,
                                                                                                                                       Borges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .AGCCTCTGTGATAGCTCGGGGGAA 194
                                                                                                                                       Į.
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Disclosure; Page 97-100; 117pp; English

tunction

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seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-471-276-831 x AAA54602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; tomato; monkey; dog; sea urchin; oxpressed asquence tag; ESI diagnostics; forensic test; gone, mapping; genetic disorder;
                                                                                                                                                                                                                                                                                                                436
                                                                                                                                                                                                                                                                                                                                                                                          386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              insat cells transformed with a vector which are capable of expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypoptide. LIR coding sequences may be used in the gene therapy of discordurs mediated directly or the LIR polypoptides can be used to treat autoimmune of the LIR polypoptides. The LIR polypoptides can be used to treat autoimmune diseases and disease states with suppressed immune function.
                                                                                                 Human EST-derived coding sequence SEQ ID NO:
                                                                                                                                                                                                                  AAH98291 standard; cDNA; 11520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2061 BP; 431 A; 684 C; 558 G; 388 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a.ValGlnGlu.....TrpGly.....AlaGlnGluProValHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGACCCTCACCCTCTCAGTCCTGATTTGCCTCGGGCTGAGTGTGGGCCC 116
                                                                                                                                                                                                                                                                                                                                                                                       CAGAGCCCAGTGACCCCCTGGAGCTGGCGACAGGATTCTATGCAGAA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCGTGACCCTCTGGTGTCAGGGGCCCCTGGAGACTGAGGAGTACCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          luSerGluHis***LeuLysThrLeuGlyGlnCysAspAlaAsp.....
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                                                                                                                                                                                                                                                                                                                CCCACTCTTTTAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                            **GlnLeuSerLysLeuLeuGluLeu....ThrGly.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGACAGTGCAGGGCGATACCGCTGCTACTATGAGACCCCTGCAGGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGATAAGGAGGGACTCCCATGGGCCCGGAAGAGACAGAACCCACTG...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .AspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp* 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ....GAGCCTGGAGCCAAGGCCAAGTTCCACATTCCATCCACGGTGTA
                                                                                                                                                                                                                                                                         /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH98291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2061
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blodiversity; gene therapy;

nutrition; ss

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alignment_block:
US-09-471-276-831 x AAH98291/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AAH98291
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                              4133
                                                                                                                                                                                            4182
                                                                                                                                                                                                                                                         4232
4033 GTTTCATTCCTTATAGGTGCCCTTACTGAGTCCAATGCAGGTCTTTACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of movel proteins from a variety of organisms, including human, dog, ont, horse, cow, pig, hamster, monkey, macaque, yeast, bacteris, fruit fly sea urchin and tomato. These were derived from expressed sequence tags (EST8) from the organism of interest. They can be used in dispositics, forensics, gene mapping, identification of mutations, to assess prodiversity and for nutritional purposes. The present sequence is a CDNA prodiversity and for nutritional purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11520 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 274-277; 1275pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, antibodies and research use -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang
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03-AUG-2000;
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                            76 laIleLysHisGln.PheLeuLeuThrGlyAspThrGlnGlyArgTyrAr 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                 the invention.
                                                                                                                                                                                                                        erLeuTrpAlaGluSerGluHis***LeuLysThrLeuGlyGlnCysAsp
                                                                                                                            GCTTTGGTGCCGAAGCCCCTCTCGGATATCAAGCAAGTTCCTGCTGCTGA
                                                                                                                                                         AlaAspValProGlyProProGlyAsp...SerArgLeuProAlaValG1 62
                                                                                                                                                                                          AGTTGTGGATAGAGTCCAACTACCCCCA.GGCCCCTTGGGAGAACATCAC
                                                                                                                                                                                                                                                       GAAGACATTCACTGTTTTGCTCTTTTGCATTCTGATGGACCCTCAACCGG
                                                                                                                                                                                                                                                                                                                      ACCAGAGGCCCCATGACCCTGGACAGACCAGGGGGAGGGGGGCCACCATGCT 4233
                                                                                           nGluTrpGlyAlaGlnGlu.....ProValHisLeuAspSerProA
                                                                                                                                                                                                                                                                                   .....IlePheTyrGluThrGln***S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0617746.
2000US-0631451.
2000US-0663870.
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1.269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3683 A; 2698 C; 2617 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Du P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 122
Gaps: 5
Percent Identity: 32,787
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398
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC76536
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antidiabetic, hypotensive; dermatological; inmunosuppressive; antidiabetic, hypotensive; dermatological; antifungal; antidrematic; antithyroid; and antibacerial; antiviral; antifungal; antidrematic; antithyroid; and antianaemic. The sequences can be used for determinif the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder, nucleic acids can be used to express ORFX proteins in gene therapy wereness. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                  AC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 316. The ORFX sequences have activities such as cytostatic; hepacotropic; vulnerary; antipacriatic; antiparkinsoniam; noctropic; neuroprotective; osteopathic; antipacriatis; articorvulsant; antiarthritic; immunospressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-1999;
02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; bone damage; cartilage damage; antitifiammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antianaemic: gene therapy; cancer; proliferative disorder; hypertension; neurodegemerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunostimulant, thrombolytic coagulant vasotropic antidabetic hypotensive dermatological; immunosuppressive antihiflammatry; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF2091 polynucleotide sequence SEQ ID NO:4181.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB42327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 3374; 5507pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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99US-0127636.
99US-0127728.
                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                            al; antiviral; antifungal; antirheumatic;
The sequences can be used for determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3934
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                                                                    disorder. The
            XEXEX
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                                                                                                  17-JUL-1998 (first entry)
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                                  Human gp49 HM43 encoding cDNA
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seq_documentation_block
ID AAV23274 standard:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-471-276-831 x AAC76536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308 GTGGCATCATAGGCGGCATCGTGGCAGGGCTCGTCTCTGACTACACCAAT 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   505 ACCACTGCTGTCTGCTGACCTGGGGGACTCACAAGAGCCTGAAGGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 sGlnPheLeuLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerG
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                                                                                                                                                        CTACATGCTCATCTCTGCCGACGTCCTAGCCTGCTTGCTC
                                                                                                                                                                                                                       LeuGlu.LeuThrGlyProLysValLeuAlaCysSerLeu 120
                                                                                                                                                                                                                                                                                          GGCCTCTGCTGGCTGGGCTCATCTCCCCCACGGGCTGGAACAATGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGCTC
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                                                                                                                                                                                                                                                                                                                                                     lyLeuSerThrGlyTrp***GlnLeuSerLys.....Leu
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                                                                                              /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV23274
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alignment_block:
US-09-471-276-831 x AAV23274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes human gp49 polypeptide HM43. The present invention also describes: (1) a fusion polypeptide comprising a human gp49 component and FceR1 or a detectable marker; (2) a recombinant nucleic acid encoding human gp49 or a human gp49-FccR1 fusion as above; (3) a cell or vector comprising the recombinant nucleic acid as in (2), and (4) an antibody which selectively binds to gp49. Mammalian gp49 or its related object and selectively binds to gp49. Mammalian gp49 or capacially a mast cell-related disease.
                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 2A-B; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell-surface member of immunoglobulin super-family, human gp49 useful to treat undesired immune responses, especially mast cell-related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9809638-A1.
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bone marrow;
                                                                                              210
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260
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AGCACTCTGGATTACACGGATCCCACAGGAGCTT
                                                                                              CAGGGGAGCCTGGAGACGCAGGAGTACCATCTATATAGAGAAAAGAAAAC
                                                                                                                                             roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                                                                                                                                                                                                                                              CAGGACCCACGTGCAGGCCAGGGCCCCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                          oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                                                                                                                                                                                                                                                                                                                                                                                            ATGACCTCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGCCTGGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                        MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr 17
                                                                                                                                                                                            AGCCAGGCTCTGTGATC...ACCCAAGGGAGTCCTGTGACCCTCAGGTGT
                                                                                                                                                                                                                                           luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP
                                               .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
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cell-surface member; FceRI; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV23274
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53.719
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Identity: 32.231
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seq_documentation_block;
ID_ANVESS32 standard; b)
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AC AANESS32;
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DT 09-FEB-1999 (first of the control of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV69332 standard; DNA;
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P-PSDB; AAW82546.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        negative signalling; autoimmune disease; suppressor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human LIR-pbm25 cDNA
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93..1412
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e.g. for treating autoimmune diseases with suppressed immune function Leukocyte immunoglobulin-like receptor, LIR, polypeptides - useful, e.g. for treating autoimmune diseases or disease states associated

Example 9; Page 62-64; 112pp; English.

receptor that mediates negative signalling could result in autoimmune diseases, whilst failure of a receptor mediating activatory signalling could result in suppressed immune function. They are also useful to (LIR) polypeptide LIR-pbm25. This sequence can be administered therapeutically to treat disorders associated with insufficient/defective amounts of LIR polypeptide. LIR-P3C2 and cortain other LIR family members contain cytoplasmic immunoreceptor tyrosine-based inhibitory motifs (TTMS), whilst other LIR family members lack TTMS. By analogy with the structure and function of known MHC Class I receptor molecules, LIRs having TTMs are inhibitory receptors mediating negative signalling, whilst those lacking TTMs are activatory receptors. Failure of a produce probes for detecting LIR nucleic acids This sequence encodes a novel leukocyte immunoglobulin-like receptor or isolating LIR DNA from

347 A; 495 C; 430 G; 333 T; 0 other

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alignment_block:
US-09-471-276-831 x AAV69332
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Ratio:
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                                                                                                                                                                                                                                                                                                                                    Leukocyte immunoglobulin like receptor; LIR; gene therapy; autoimmunity; autoimmune disorders; immune system; human;
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  (IMMV ) IMMUNEX CORP
                                        12-MAY-1999;
                                                                              12-MAY-2000; 2000WO-US13228
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                                        9905-0310463
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93..1412
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Percent Identity: 32.231
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US-09-471-276-831 x AAA54595
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                                                                                                  seq_documentation_block:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expressing a leukocyte immunoglobulin like receptor (LIR), can be used to produce the LIR polypeptide. LIR coding sequences may be used in the gene therapy of disorders mediated directly or indirectly by defective or insufficient amounts of any of the LIR polypeptides can be used to treat autoimmune polypeptides. The LIR polypeptides can be used to treat autoimmune
                                                                                                                                                                              431
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P-PSDB; AAB04171.
  23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leukocyte immunoglobulin-like receptor (LIR) nucleic acids, useful for treating autoimmune diseases and disease states with suppressed immune
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                                        AAV38992;
                                                                            AAV38992 standard;
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blignment_block:
US-09-471-276-831 x AAV38992
                                                                                                                                                                                    alignment_scores:
Quality:
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06-DEC-1996;
09-DEC-1996;
                                                                                                                                                                                                                                                                      controlling development, differentiation, and/or physiology of the mammalian immune system. The products can be used for treating abnormal proliferation, regeneration, degeneration or atrophy. They can be used for treating e.g. cancerous conditions, degenerative conditions of the conditions transplantation rejection, graft versus boot disease, or inflammatory conditions. The products can also be used for detection, disgnossis and drug screening.
                                                                                                                                                                                                                                                                                                                                                                        ANY38992-96 and ANY38608 represent human monocyte genes, collectively designated KTE03. The genes are found in activated monocytes. The specification also describes other proteins encoded by activated monocytes, which are designated FPF03 and YE01. The genes function in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated activated monocyte cell gene(s) - used to develop products for treating e.g. cancer, depenerative conditions, buttoimmune responses, transplant rejection or inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-333325/29.
P-PSDB; AAW62777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adema GJ, G
Phillips JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9824906-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              differentiation; mammalian immune system; treatment; cancerous condition; degenerative condition; autoimmune response; transplantation rejection; grafe versus host disease; inflammatory condition; detection; diagnosis; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human monocyte gene designated YYB01.
                                                                                                                                                                                                                                                Sequence 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SCHE ) SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FDF03; activated monocyte:
                              81
                                                                                      seg 1/1
oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
                              ATGACCCCCATCCTCACGGTCCTGATCTCTCCGGGCTGAGCCTGGACCC
                                                      MctSerMetLeuValValPheLeuLeuTeuTrpGlyValThrTrpGlyPr 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type I transmembrane
                                                                                                                                                                        Rat Lo:
                                                                                      6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pages 71-73;
                                                                                                                                                                                                                                                BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zurawski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0041279.
96US-0032252.
96US-0762187.
96US-0033181.
                                                                                      AAV38992
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81..1400
                                                                                                                                                        80.50
1.238
53.719
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                                                                                      from: 1
                                                                                                                                                          Percent Identity: 32.231
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YE01; KTE03; control; development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ler LL, McClanahan TK,
Zurawski SM;
                                                                                                                                                                                                                                                Ç
                                                                                                                                                                                                                                              434 G; 328
                                                                                      6
                                                                                      1620
                                                                                                                                                                        Gaps:
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ID AAI51413 standard;
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                                                                                                                                                                                                                                                                    04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 CCTGGAGCTG
                                                                                                                                                                                                                   21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                           30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI51413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAI51413 standard; DNA; 311 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
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                                                                                                                                  WPI; 2001-488897/53.
                                                                                                                                                                                 (MOLE-)
                                                                                                                                                                                                           04 - OCT
                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                         WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #20099 used to measure gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 uLeuGluLeu 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 TGCTGTATCTATGGCAGCCACACTGCAGGCCTCTCAGAGAGCAGTGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
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CAGGACCCACGTGCAGGCAGGCAGGCCCTCCCCAAGCCCACCCTCTGGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGGGGAGCCTGGAGACGCAGGAGTACCATCTATATAGAGAAAAAGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGGCCAGTTCCCCATCCTATCCATCACCTGGGAACATGCAGGGCGGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ysHisGlnPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCACTCTGGATTACACGGATCCCACAGGAGCTT.....GTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCCAGGCTCTGTGATC...ACCCAAGGGAGTCCTGTGACCCTCAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
                                                                                                                                                           SG
                                                                                                                                                                                 MOLECULAR DYNAMICS INC
                                                                                                                                                         Hanzel
                                                                                                                                                                                                                                                                                                        2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                  2000US-0234687
                                                                                                                                                                                                                                            2000US-060B40B.
2000US-0632366.
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                                                                                                                                                                                                                     2000US-0236359
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                                                                                                                                                           Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                          in human placenta sample.
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The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

The present invention relates to single exon nucleic acid probes (SENP).

SEQ

ID No

20099;

654pp; English.

Human genome derived single exon nucleic acid probes useful for

gene expression in human placenta

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alignment_block:
US-09-471-276-831 x AAI51413/rev
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seq_documentation_block:
ID AAV15438 standard:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV15438
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                                    The present sequence represents a base sequence from the human chromosome 21, used in an example of the present invention. The present invention describes a method for detecting and isolating an active gene in which an uncommon restriction enzyme its prepared. The method comprises: (a) physically mapping a specified region of a chromosome and the base sequence upstream and downstream of the restriction enzyme site within the map, and (b) detecting and
                                                                                                                                                                                     Detection and isolation of active gene - by physically mapping specific region on chromosome and detecting and isolating gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
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                                                                                                                                                        Example 1; Page 13-14; 21pp; Japanese.
                                                                                                                                                                                                                                 WPI; 1998-254322/23
                                                                                                                                                                                                                                                                                         16-AUG-1996;
                                                                                                                                                                                                                                                                                                                     16-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                  03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                JP10057062-A
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxyreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene fragment CBR from chromosome 21q22.2 SEQ ID NO:14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV15438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CATGGTCTTGAAGCCTACGGAGAGGGAGACGCTGACCTCCCAGCTCAAGT 221
                                                                                                                                                                                                                                                             (RIKA ) RIKAGAKU KENKYUSHO
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                            isolating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGTGAGCAGGAACCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpGlyAlaGlnGluProValHisLeuAspSerProAlaIleLysHisGln 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheLeu....LeuThrGlyAspThrGlnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTCTTCTTGGGCCCCCTCACAGATGATGCGCTTGGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .GlyProProGlyAspSerArgLeuProAla.....ValGlnGluT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311
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                          the active gene
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                                                                                                                                                                                                                                                                                         96JP-0216406
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2.469
51.613
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Sequence 1001 BP; 210 A; 286 C;

328 G;

177 T; 0 other;

WPI; 2000-500381/45

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DR PA XXX
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US-09-471-276-831 x AAV15438/rev
                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID AAC04209 standard; cDNA; 622
                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC04209
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                            Dumas Milne Edwards J,
                                                                                                                                                                                                                                                  gene therapy; chromosome mapping; ss
                                                                                                                                                                                                                                                               Human; 5' EST; expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 yTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValLeuA 117
                                                           (GEST ) GENSET
                                                                                         26-FEB-1999;
                                                                                                                          21-FEB-2000; 2000EP-0200610
                                                                                                                                                         06-SEP-2000
                                                                                                                                                                                       EP1033401-A2
                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oVal.....HisLeuAspSerProAlaIleLysHisGlnPheLeuLeuT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGGCGTTATGGACCCCGCAGACGCCCAGGAGCCCCAGTGCATCGGTTCTTC 849
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                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                         9905-0122487
                                                                                                                                                                                                                                                                                                protein 5'
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1.435
45.000
                            Duclert A,
                                                                                                                                                                                                                                                                                                EST,
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                                                                                                                                                                                                                                                                                                  SEQ ID NO: 8284.
                            Giordano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                 protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001
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alignment_scores
                                                                                                                                                                                                                                                                                                              seq_documentation_block: ID AAZ90654 standard; DNA; 735
                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ90654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-471-276-831 x AAC04209/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align scg 1/1 to reverse of: AAC04209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNAs encoding secreted proteins to ORF has yet been conclusively identified within the present sequence. The 5 ISSTs were prepared from lotal human RNAs or polyx+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (dTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain (uil length CDNAs and genomic DNAs. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain (uil length CDNAs and genomic DNAs. 5' ESTs are decrived from mRNAs with intact 5' ends and can therefore be used to obtain upstream regulatory sequences and to design excrete the vectors.
                                           US6027929-A
                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID 8284; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic ocid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genemic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                    Nostoc sp.
                                                                                                                                NspI restriction endonuclease; NspIR;
                                                                                                                                                                           Nostoc NspI restriction endonuclease (NspIR) encoding DNA
                                                                                                                                                                                                                          13-JUN-2000
                                                                                                                                                                                                                                                                      AAZ90654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 622 BP; 149 A; 126 C; 159 G; 183 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 oValHisLeuAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 GlyAspSerArgLeuProAlaValGlnGluTrpGly...AlaGlnGluPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sSerLeuAlaLeuAspGly 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GinLeuSerLysLeuLeuGluLeuThrGlyProLysValLeu...AlaCy 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence is one of a large number of 5' ESTs derived from
                                                                                                                                                                                                                                                                                                                                                                                                                               CGCACTGACCGTCGATGGG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGTCTC.....CTGACATGGCCTCAGCTGATTACAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCAGCCTGGGAAACACAGTGAGACCTCGTCTCTACCTGCTCCGTGGCTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp*** 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACATACTCAGCTGCCTGTAATCCAACAGTTTGGAAGGCTGAGGCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                       (first entry)
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1.678
61.644
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                                                                                                                                   Nostoc;
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                                                                                                                                NspI methylase;
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                                                                                                                                Nsplm;
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX85010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAZ90654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-471-276-831 x AAZ90654
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                                                                                                                                                                                                                                                                                                    541 CGATGTATCAAAACTGGT
                                                                                                                                                                                                                                                                                                                                                        491
                                                                                                                                                                                                                                                                                                                                                                                                          441 CTTAACATCTATGAATGATAATGAAATCAAGCGAAAGTTTCAATTGTTGA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 GATCATAGATTTCCG...ATGGAAAGATGGGGAGCTAGTGAGCCTCCACA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a MspI restriction endonuclease (MspIR), obtained from Nostoc sp. The MspIR is recombinantly obtained using MspI methylase (MspIm) premodified E. coli K strain RRI (gammabES) The endonuclease and methylase are useful for creating recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               creating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY57323
                                                                                                                                                  Human secreted protein gene No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 735 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules. The present sequence represents a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 3; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated DNA encoding the NspI endonuclease and methylase, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NEWE ) NEW ENGLAND BIOLABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1998;
                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                   71 sLeuAspSer.....ProAlaIleLysHisGlnPhe...LeuLeuT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AspSerArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHi
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                                                                                                                                                                                                                                                                                                                                                                                hrGlyAspThrGlnGlyArgTyrArg......CysArg 94
                                                                                                                                                                                                                                                                                                                                                        AGAAAGATACCTCTGGCAATCACAATCTTTTAAAATCAAGAAGCTGTGAG 540
                                                                                                                                                                                                                                                                                                                            SerGlyLeuSerThrGly
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Ratio:
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                                                                                                                                                                             (first entry)
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2.097
64.286
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                                                                                                                                                                                                                                   DNA;
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Gaps:
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cognitive disorder; schizophrenia; prostate; obesity; osteochast; thymns; osteoporosis; erthritis; testis; lung; thyroiddlis; thyroid; digestum; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

Human: secreted protein; Kusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal ds; Inmune system; asthm; lymphocytic disease; brain, hepatic; lymphoma; inflammation; ischaemic slock; Alzheimer's disease; restronsis; AIDS;

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alignment_block:
US-09-471-276-831 x AAX85010
                                                                                                                                                                                                                       alignment_scores:
                                                                                                           Align seg 1/1
                                                                                                                                                                                 Percent
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77-NOV-1997
                                                                                                                                                                                                                                                                                                    This sequence represents a nucleic acid molecule which encodes a scerered human protein. The gene number is given in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to a human immunoglobulin FC portion (e.g., AAX84924) for increasing the stability of the fused protein as compared to the human protein only the father than the fused protein as compared to the human protein only the cald sequences. AAX84932-X85057, amino acid sequences AAX84937-X77933) which are useful for reverenting treating or amplibrating modical conditions each be diagnosed by determining the amount of the new polymore to be specific uses are described for each of the 125 polymore.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carter KC, EDILL.
The H, Lafleur DW,
                                                     433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 322-323; 507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human secreted proteins and coding sequences useful for treating disorders of the immune system and hyperprollferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB: AAY27644, AAY27787, AAY27788, AAY27789, AAY27790, AAY27791, AAY27792, AAY27793, AAY27794.
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                                                                                                                                                                                                                                                                  Sequence 1863 BP;
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483 AGCCTGCTGCAGACACAACCTCTCTGCAGCAGCGGGGGCTGGAGCTCAC 532
                          20 uAlaAlaIlePheTyrGluThrGln***SerLeu....TrpAlaGluS 35
                                                                                4 LeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyProValThrGl
                                                     ATGGCTGTGAAATTTCTCTGGTGGGGGATGACCTGGATCCCGAGCGGGAA
                                                                                                                                                                             Similarity:
                                                                                                                                                                                                                                                                                           AAX84933 for described uses).
                                                                                                                                                                                                          Quality:
                                                                                                                                                                                              Ratio:
                                                                                                           to: AAX85010
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97US-0066095.
97US-0066089.
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97US-0066090
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97US-0064987.
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DW, Moore PA,
                                                                                                                                                                               75.50
1.641
51.111
                                                                                                                                                                                                                                                                457 A; 462 C; 488 G; 450 T; 6 other
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                                                                                                           from: 1 to: 1863
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27.778
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                                             Align seg 1/1 to: AAX88978
                                                                              US-09-471-276-831 x AAX88978
                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                  The present invention describes new proteins for inhibiting dephosphorylase. The proteins can be combined with tyrosine phosphatase SHP-1, SHP-2 or inositol-5-phosphatase SHIP by phosphating tyrosine. The present invention also describes an immunoreceptor comprising one the above proteins, and DMA coding the above proteins. The new proteins can be used as an immunomodulatory agent. The present sequence encodes
                                                                                                                                                                                                                        Sequence 1906 BP;
                                                                                                                                                                                                                                                     a protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 21-22; 30pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                              New peptide - useful for inhibiting dephosphorylase
                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY24321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-422622/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHP-2; inositol-5-phosphate SHIP; phosphating tyrosine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dephosphorylase inhibiting protein; p91; tyrosine phosphatase SHP-1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX88978 standard; DNA; 1906 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      533 CAACACATCTGCCTACCTCACTATTGCTGGGGTGGAGAGCATCACTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYOK-) UNIV OKAYAMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoreceptor; immunomodulatory agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 AlaGlnGluProValHis 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 erGluHis***LeuLysThrLeu.....
oGlyProProGlyAspSerArgLeuProAlaValGln.GluTrpGly...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAGAGCTCCTGAGGCAGGCTCGTTATCGGCTGCGACACGGAGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dephosphorylase inhibiting p91-like protein #4 encoding
                                                                                                                                                           Quality:
                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97JP-0362285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97JP-0362285.
                                                                                                                          75.50
1.302
50.877
                                                                                                                                                                                                                        518 A; 546 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 700
                                                from:
                                                                                                                            Percent
                                                -
                                                                                                                                                                                                                        419 G; 423
                                                                                                               Identity: 28.947
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                                                                                                                                                           Length:
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seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAF18310
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                                                     Polynuclectide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAF5106 - AAF55848 Lung concer associated proteins and polynuclectide sequences, their acquists, and antagonists may have neuroprotective; cytootatic cardioactive; and antagonists may have neuroprotective; cytootatic cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 786-787; 1425pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
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(ROSE/) ROSEN C A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointostinal, pulmonary, cardiovascular, renal, and proiderstive disorders. The proteins may also be used in the treatment of vounds infectious diseases, polynucleotide sequences ANF845 - ANF8483 and peptide ANF8494 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
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1 AC012313 Homo sapiens chrome
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9b. htg ; AC010250

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                                                                                                                                               ATGTCCATGCTCGTGGTCTTTCTCTTGCTGTGGGGTGAGGCCTCCTGGGG 11594
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Ratio:
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**NOTE: This is a "working draft sequence. It currently consists of 2 contigs. Gaps between the contigs.

**are represented as runs of N. The order of the pieces.
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DOE Joint Genome Institute.
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181942: contig of 181942 bp in length 181943 182043: gpp of unknown length 182043 186451: contig of 409 bp in length.
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This sequence will be replaced
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Center Project Name: 835906
Center clone name: CTD-2619J13
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seq_documentation_block:
LOCUS AK027222
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                                                                                                                                                                                                                                                                                                                                                  Submitted (29-AUG-2000) to the DDBJ/EMBL/GenBank databases. Sumio Sugano, Institute of Redical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dal, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T
Shibahara, T., Tanaka, T. and Nakamura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
2 (bases 1 to 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawakami, T., Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsamura, K., Makajima, Y., Mizman, T., Merinaga, M., Tanigami, A., Fujii, Y., Ozaki, K., Hirao, M., Fujiara, T., Ozaki, K., Hirao, M., Tanaka, T., Ozaki, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, T., Izoyai, T., and Sugano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oligo capping: fis (full insert sequence).
Homo sapiens human lung cDNA to mRNA, clone_lib:LNG clone:LNG11861
                                                                                          University of Tokyo
                                                                                                                                                                                                                                                            NEDO human cDNA sequencing project supported by Ministry of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                               Agency).
                                                                                                                                                                                                                                                                                                 (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286;
Fax:81-3-5449-5416)
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Location/Qualiflers
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                                                                                                                                                                            REFERENCE
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Ohio Un:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1908)
Kopchick,J.J. and Tiong,J.
                                                                                                                                             Growth hormone-regulatable liver genes and
                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                       AX045627.1 GI:11344029
                                                                                                                                                                                                                                        nouse mouse.
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Location/Qualifiers
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                            /organism-"Mus musculus"
/db_xref-"taxon:10090"
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/tissue_type="human lung"
/note="cloning vector pwEl8SFL3"
/note="cloning bector pwEl8SFL3"
/note="cloning bector pwEl8SFL3"
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/db_xref="taxon:9606"
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               475 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 GTGGACCATGCTAAGCAATGCTGTGGAGGTGACAGGGGAAAGAGCCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 yTrp***GlnLeuSerLysLeuLeuGluLeuThrGlyProLysValLeuA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 GCTTTTCCCTGGGGGCCATTACAAGTAACAACAGTGGCATCTACCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         199 CGGGTGGTTCCTGAGTCAAGTCCGACTTGAGACACAGGTGCTGTCATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 GTTGATTTGCCG.....ACTAAGGTCTTCGAGCTGATCCAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 AGCCTCAGTCCCTGCTGGAACCCTGGGCAAACCTGACCCTGGTGTGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 lnPheLeuLeu.....ThrGlyAspThrGlnGlyArgTyrArgCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 luSerGluHis***LeuLysThrLeuGlyGln......CysAsp 46
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                                                                                                                                                            Gardmo.C., Persson.B. and Mode.A.
Cloning of a novel growth hormoner regulated rat complementary deoxyribonuclatic acid with hormology to the human alphalB-glycoprotein, characterizing a new protein family endogrinology 142 (6), 2695-2701 (2001)
                                                                                                                                                                                                                                                                                                                 Rattus norvegicus
Enkatryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                      AJ302031
AJ302031.1 GI:11877347
Alpha 1B-glycoprotein.
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                          Submitted (12-DEC-2000) Gardmo C., Department of Medical Nutrition, Karolinska Institutet, Novum F60, Huddinge, S-14186, SWEDEN
                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RATTUS norvegicus mRNA for putative alpha 1B-glycoprotein
                                                                                                 Gardmo,C
                                                                                                                                                                                                                                                                                                              Rattus.
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a Institutet, Novum F60, Location/Qualifiers
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                                      lyTrp***GlnLeuSerLysLeuLeuGluLeuThrGly.....
                                                                                                                        sArgSerGlyLeuSer...
                                                                                                                                                                     CGCTTTTCCCTGGGGGGCCATTACAAGTAACAACAGTGGCGTCTACCGCTG 316
                                                                                                                                                                                                           GlnPheLeuLeu.....ThrGlyAspThrGlnGlyArgTyrArgCy 93
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AGTGGACAATGCTAAGCAATGCTTTGGAGGTGACAGGGGAAAGAGCCCTTG 416
                                                                               CCGATGTGGCGTGGAACCCCCTGTTGACATTCAACTGCCAGCGCTGAGCA 366
                                                                                                                                                                                                                                                       ATGGCTGGTTCCTCAGTCAAGTCCGACTGGAGACACCGGTGTTGTCATAT
                                                                                                                                                                                                                                                                                             uTrpGlyAlaGlnGlu.ProValHisLeuAspSerProAlaIleLysHis 79
                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCTCAATCCTTGCTGGAACCCTGGGCAAACCTCACACTGGTCTGCGCA 179
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/dev_stage."adult"
30. .1571
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PUT OLDALSKWIMLSNALEYTGK ELI PP PAHADPYSNIT PGGLPYYL MCKVAMROU
TYLLKKEGYUGTYGK PUT HAND Y SECSYLTI HAGEDSEBESA IYTI KASA
TYLLKKEGYUGTYGK PUT HAND Y SECSYLTI HAGEDSEBESA IYTI KASA
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/product. Putative alpha 1B-glycoprotein
/protein_id-"CAC19029.1"
/db_xref-"G1:11877348"
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1.523
52.410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELVREGEKTPFWMASTTSTSAFLKLSFVGPQHTGNYSCRYTALSPFTFESGISDPVEV
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IYMEQAPPFSGSASSEPLELRINGPAPKPRLEALWKGKVPLGHEAIFQCHGHVPRVSM
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/translation.*MSSLTTVLLLMGTTLGPGNALMLNSGSEPELRAEPOSLLEPWAN
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/db_xref.."taxon:10116"
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                                                                 316 CAGGGGACCCTGGAGGCCCAGGAATACCGTCTGGTTAAAGAGGGGAAGCCC 365
                                                                                                                                                                                                                                       219 CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
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                                                                                                     roGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.....
                                                                                                                                                                                                                                                                              oValThrGluAlaAlaIlePheTyrGluThrGln***SerLeuTrpAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL
                                                                                                                                                 AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT 315
                                                                                                                                                                                        luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP 50
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1 (bases 1 to 956)
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SKATLMASPGSVISHGNSVTIRCGGTLEAQEVRLVENSPERMYTUSHSERNEYTUSH
SKATLMASPGSVISHGNSVTIRCGGTLEAQEVRLVENSPERMYTUSHSERNYTL
SKATLMASPGSVISHGNSVTISHGNSVTIRGGTGATAL
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SKATLMASPGSVENSVTIRGGTGATAL
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COCSRLREDRFILTEEGDHKLSWTLDSQLTPSGQFQALFPVGPVTPSHRMALRCYGSR
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/db_xref.."GI:11876400"
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/note- "unnamed protein product"
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/db_xref "taxon:9606"
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LOCUS AX046966
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                                      luSerGluHis***LeuLysThrLeuGlyGln..CysAspAlaAspValP 50
                                                                                                                                                                                       MetSerMetLeuValValPheLeuLeuLeuTrpGlyValThrTrpGlyPr
  AGCCAGGCTCTGTGATC...AGCCGGGGGAACTCTGTGACCATCCGGTGT
                                                                           CAGGACCCACGTGCAGGCAGGGAACCTCTCCAAAGCCACCCTCTGGGCTG
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1016)
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Sequence 29 from Patent WO0068383.
AX046966
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VVLGILIFQDWHSQRSPQAAAGR*
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IPSWTEHHAGRYRCYYYSPAGWSEPSDPLELVVTGFYNKPTLSALPSPVVTSGENVTL
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/db_xref="GI:11876396"
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LOCUS AF324830
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1 (bases is to 185)
Wende, H., Zigler A. and Volz A.
Genomic organization of the LUZ11 gene, a novel member of the
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Unpublished
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AF324830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (29-NOV-2000) Institut
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OCGSRLRFDRFILTEEGDHKLSWTLDSQLTPSGQFQALFPVGPVTPSHRWHLRCYGSR
LHILQVN3EPSDLLEIPYSGAAGNLSSGNKSDSGTASHIADYAVENLIRWGMAGLIL
VVLGILIFQDWHSQASEPQAAGR:
1 388 c 376 g 315 t
                                                                                                               /translation="MAPWSHPSAQLQPVGGDAVSPALMVLLCLGLSLGPRTHVQAGNLSKATLWAEPGSVISRGMSVTIRCQGTLEAQEVKLVKEGSPEPWDTQNPLEPKNKARFS
                                                                                                                                                                                                                                                             /note="immunoglobulin superfamily receptor; similar
sequence in GenBank Accession Number AF212842"
                                                                                                                                                             /protein_id="AAK52451.
/db_xref="G1:14028660"
                                                                                                                                                                                                                                                                                                                               /gene-"ILT11"
121. .1020
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/db_xref="taxon:9606"
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                                                                                                                                                                                                               /product="immunoglobulin-like transcript 11 protein"
                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                              /gene-"ILT11"
                                                                                                                                                                                                                                                                                                                                                                                /cell_type~"peripheral blood leukocytes"
1. .1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 GTGAGCCCTGCCCTCATGGTTCTGCTCTGCCTCGGGCTGAGTCTGGGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysLeuLe 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCCAGGCTCTGTGATC...AGCCGGGGGGAACTCTGTGACCATCCGGTGT 321
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                                                                                                                                                                                                    Submitted (04-MAR-1997) Medicine, Harvard Medical School and Brigham and Women's Hospital, 250 Longwood Avenue, Room 628, Boston, MA 02146, USA
                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                      Arm, J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                            Arm,J.P., Nwankwo,C. and Austen,K.F. Molecular identification of a novel family of human immunoglobulin superfamily members that possess immunoreceptor tyrosine-based inhibitory motifs and homology to the mouse gp49Bl inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Euteria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1603)
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                           /organism."Homo sapiens"
/db_xref "taxon:9606"
/chromosome."19"
/map "19413.4"
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55.833
/cell_type: "monocyte"
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Identity: 34.167
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mat_peptide
                                                                                                                                                                                                                            239 GCCCAGCACCCTGGGACAGACAGAACCCACTG......GAGCCCAAG 279
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                                                          90
                                                                                                                  280 AACAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCAGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                 49 ValProGlyProProGlyAspSerArgLeuProAla.ValGlnGlu.... 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 laGluSerGluHis***LeuLysThrLeuGlyGln...CysAspAlaAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SerMetLeuValValPhe....LeuLeuLeuTrpGlyValThrTrpGl
   ATACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTCACAGCCCAGTGACC
                                                   gTyrArgCysArgSerGlyLeuSerThrGlyTrp***GlnLeuSerLysL 107
                                                                                                                                                                                                                                                                           .....TrpGlyAlaGlnGluProValHisLeuAspSerProAla 76
                                                                                                                                                                                                                                                                                                                                              GTGTCAGGGGACCCTGGAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAA 238
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                                                                                                                                                                         IleLysHisGlnPhe.....LeuLeuThrGlyAspThrGlnGlyAr 90
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/produc:-monoyte inhibitory receptor precursor"
/protein_id-"AAB68655.1"
/protein_id-"AAB68655.1"
/bl_xref-"G1:2351799
/cl_xref-"G1:2351799
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1393. 1603
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1273 . . 1290
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886. .1389
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EDRQMDTEAAASEAPQDVTYAQLHSFTLRQKATEPPPSQEGASPAEPSVYATLAIH*
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Patent: WO 0068383-A 17 16-NOV-2000;
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Cosman,D.J., Anderso
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27 GCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTGAGTCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
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Hsu,M.-L.
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Mammalia; Butheria; Primates: Catarrhini; Hominidae; Homo
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LÜVSKKESLSVOPGET VAREETITI JOCUSTANEYULKIKGEBUDELOAAAOADROA
                                                                                              /product-"leucocyte immunoglobulin-like receptor-1"
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/db_xrefu-Gi:2267170"
                                                                                                                                                                 /codon_start*1
                                                                                                                                                                                       /note ."LIR-1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhiui; Hominidae; Homo.

Homo sapiens human AF009007.1 Homo sapiens immunoglobulin-like transcript

2c mRNA, complete cds.

03-DEC-1997

GI:2660705 2018 bp

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Samardids, J., Angman, L., Cella, M., and Lopez-Butct, M.
A common, inhibitory receptor for major histocompatibility complex
class I malecules on human lymphoid and myelomonocytic cells
J. Exp. Med. 186 (11), 1809-1818 (1997)
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PQSGLGRHVGVVIGILVAVVLLLLLLLLLLLHRRQGKHWTSSPAQLPMPRKKTSM
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LSQANTTLGEVSKSYGGGY KYGAHNLSSEMSAPSBUDILIAGGYDRVSLSVOPGP
TVASGENVTLLCQSQGMWQTFLLTKEGAADDWRLESTYQSQKYQAEFPWGPYTSAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPPILTVLICLGLISLGPRTHVQAGHLFKPTLMAEPGSVITQGSB
VTLRCQGQETQFYRLYEEKTAAM TRI PQELVKGGYPLGSQUAFQCFSLCKEG
DPAGRSESSDFLLWTGAST KFFLSAGPSFVMVSGGWYLQCSGVPGCFSLCKEG
EDEHPQCLNSQPHAEGSSRAIESVGPVSPSRRWYBCYAYDSNSPYBNILSDLLELL
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1.288
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/db_xref="GI:2660706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ILT2c; alternatively spliced form of ILT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="myelomonocytic; NK; /map="19q13.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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LOCUS AF009005
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2 (bases
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Smartidis, J., Angman, L., Cella, M., and Lopez-Bottet, M.
A common inhibitory receptor for major histocompatibility complex
class I molecules on human lymphoid and myelomonocytic cells
j., Byr., Med. 166 (11), 1809-1818 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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DTAGRSESSDPLELVVTGAYIKPTLSAQPSPVVNSGGNVILQCDSQVAFDGFSLCKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="immunoglobulin-like transcript
/protein_id="AAC51879.1"
/db_xref="GI-2560702"
                                    KATEPPPSQEGPSPAVPSIYATLAIH"
                                                                                    HSRPRREMASPPSPLSGEFLDTKDRQAEEDRQMDTEAAASEAPQDVTYAQLHSLTLRR
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/chromosome="19"
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alignment_scores:

Quality:

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Percent Identity:

Length:

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Ratio: Percent Similarity:

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysH1sGlnPhe.....LeuLeuThrGlyAspThrGlnGlyArgTyr 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
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                                                                                                                                                                          IMMUNEX
                                                                                                                                                                                                Patent:
                                                                                                                                                                                                             Family of immunoregulators designated receptors (lir)
                                                                                                                                                                                                                                                  1 (bases 1 to 2777)
Cosman, D.J., Anderson
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                human.
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3 from Patent W00068383
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                                                                                                                                                                          CORPORATION (US)
                                                                                                                                                                                             WO 0068383-A 3 16-NOV-2000;
  /protein_id~"CAC18927.1"
/db_xref~"GI:11876371"
                                    /note "unnamed protein product"
/codon_start-1
                                                                                            /organism."Homo sapiens"
/db_xref."taxon:9606"
                                                                              891
                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            2777 bp
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ACCESSION
                                  DEFINITION
                                                                         seq_documentation_block:
                                                                                                           seq_name: gb_pr:AF004230
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alignment_block:
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                                                                                                                                                                                                                                                                                                             107 uLeuGluLeuThr.....
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                                                      ...SerLeuAlaLeuAspGlyAlaSer 126
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TCACAGGTGGCATTTGATGGCTTCAGT 632
                                                                                                                              AGCCCAGCCCCGTGGTGAACTCAGGAGGGAATGTAATCCTCCAGTGTGAC
                                                                                                                                                                                                                                                       CCTGGAGCTGGTGACAGGAGCCTACATCAAACCCACCCTCTCAGCCC
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                                                                                                                                                                                        CGCTGTTACTATGGTAGCGACACTGCAGCCCGCTCAGAGAGCAGTGACCC 505
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UGBEPTDRGLOMRSSPAADAQEENLYAAVKHTQPEDGVEMDTRQSPHDEDPQAVTYAE
KKHSRPRREMASPASDLSGEFLDTKDRQAEEDRQMTTEAAASEAPQDVTTAQLHSLTTV
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GTYRCYGSQSSKPYLLTHPSDPLELVVSGPSGPSSPTTGPTSTSAGPEDQPLTPTGS
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DTAGRESESDELLLVTGAY I KFTLSAQPSFVWSGGWI I LQCDSQWAFDGFSLCKBL
EDERHOCLHSOPHAKGSEKA I ESVORPSFSREKWAF UCLY NDSKEY FEBSLEFDLLEILL
VLGVSKKFSLSVQPGF I YAF EETILTI LQCGSDAG YNRFVLYKDGERDFI LQLAGAQPQAG
VLGVSKKFSLSVQPGF I YAF EETILTI LQCGSDAG YNRFVLYKDGERDFI LQLAGAQPQAG
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Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 cl-7) mRNA, complete cds. AFO04230

AF004230

2897 bp

27-AUG-1997

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MEDLINE
REFERENCE
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AUTHORS
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US-09-471-276-831 x AF004230
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roGlyProProGlyAspSerArgLeuProAlaVal.GlnGlu.....
                                                                         AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT
                                                                                                                                                  luSerGluHis***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
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A new human gene complex encoding the killer cell inhibitory
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DTAGASESSED LELUVTGAN I KENTLAADPERVIKUSGGWILLOGGOVAPOGESICKEG
EDBHOGLI SKODHARGSBA I ESWGEVBESSERWAYEC KAYOSKEP ESKLESULKELL
BEBHOGLI SKODHARGSBA I ESWGEVBESSERWAYEC KAYOSKEP ESKLESULKELL
KLAVSKKYSLSKODDE TVANBEFITLOGGSROAV KREPU KYGGEBOETO LUAGADPOM
LSQANETILGEV SESKGGOYEC (TCAHKLSSENSARED LULLI ROQFYDAVELSKODDE)
VASCERNITILLOGOSROAVIOTE LUKGGANDDHALLESTYGORY KOAEPPWARPT SKAND
GYTRCYGSOSKRY DLUTHESD PLELLVASCERSCHESTYGORY KOAEPPWARPT SKANDOHRACKAW
GRETTORG GJORG SKANDOHRACKAWA TO KANDOHRACKAW
GRETTORG GJORG SKANDOHRACKAWA
GRETTORG G
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/db_xref="G1-2343109"
/translation="MTPTLTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVITQGSP
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171. .2126 ·
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/db_xref="taxon:9606"
/Chromosome="19"
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LOCUS AF072099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUN-1998) Dept
Tennis Court Road, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Torkar,M., Trowsdale,J. and Wilson,M.J Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Torkar,M., Norgate,2., Colonna,M., Trowsdale,J. and Wilson,M.J. Isotypic variation of novel immunoglobulin-like transcript/Killer cell inhibitory receptor loc1 in the leukocyte receptor complex Eur. J. Immunol. 28 (12), 3959-3967 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa: Chordata: Cranlata; Vertebrata; Eucaleostomi;
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
1 (bases 1 to 5354)
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/protein_id="AAC99761.1".
/protein_id="AAC99761.1".
/bl_xrei="G1:3776464"
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/translation="HttpfffallCLCLSLGPRTHMQAGPLPKPTLMAEDGSVISMONS
VTIWCQGTLEAREYRLDKEESPAPMDRQNPLEPKNKARESIPSMTEDYAGRYRCYYRS
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2107. 2157,2792. .2908,3217.
4612. .4770,4850. .4996)
/note="ILT3"
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4612 .4770,4850 .>5554)
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/db_xref="taxon:9606"
/chromosome="19"
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                                                                                                                 /product="immunoglobulin-like
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us-09-471-276-831 x AF072099
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LOCUS AF189768
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Liu, W.R.,
                                                                     Eukaryota; Mctazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                     Homo sapiens
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Ashworth, L.K. and Arm, J.P.
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join(3061. 3456.3933. 3968.4155. 4439.4587. 4886, 5200. 5250.5531. 5581.6216. 6332.6641. 6716.6800.7098. 7150.8036. 8194.8274. 8830)
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On Jun 29, 2000 this sequence version replaced gi:8576078
Draft Sequence Produced by DOE Joint Genome Institute
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Gaps:
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_htg:AL139117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
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LOCUS AL139117 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7484 GGAAGGTCTTGGGATCCAGCCTCTGATTTTCTTCCAGGGCCCCCTCCCCAA 7533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 AlaSer 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGTCCCAGCCCCAGGCTCTGCCCTCAGGAAGGGGGTCAGCTCTCAGGG 7870
Assembly programs XGA4; version 4.5
Assembly programs XGA4; version 4.5
Sequencing vector: M13: M77815: 100% of reads
Chemistry: Dye-terminator ANI: 61% of reads
Chemistry: Dye-primer-amersham: 2% of reads
Chemistry: Dye-primer-amersham: 2% of reads
Chemistry: Dye-primer N19 Dye; 0% of reads
Consensus quality: 14716 bases at least 040
Consensus quality: 148180 bases at least 040
Consensus quality: 148180 bases at least 020
Insert size: 14639; sum-of-contigs
Insert size: 14639; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAGCCCAGTGACCCCCTGGAGCTGGTGATGACAGGTGAGAGGACACTCA 7820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTATGCAGGGAGATACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTC 7770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp** 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGATAAAGAGGAAAGCCCAGCACCCTGGGACAGACAGAACCCACTG....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...CysAspAlaAspValProGlyProProGlyAspSerArgLeuProAla 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAG....CTGGGGGAAC 7579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n***SerLeuTrpAlaGluSerGluHis***LeuLysThrLeuGlyGln. 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...GlyProLysValLeuAlaCysSerLeu......AlaLeuAspGly 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euAspSerProAlaIleLysHisGlnPhe.....LeuLeuThrGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ValGlnGlu.....TrpGlyAlaGlnGluProValHisL 72
                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-APR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquirles: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 13, 2001 this sequence version replaced gi:9796322.
                                                                                                                                                                                                                                                                          Center project name: dJ52N12
                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: humguery@sanger.ac.uk
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Yertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bbases 1 to 148497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROGRESS ***, in ordered pieces. AL139117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 19 clone RP1-52N12, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                               Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                  Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL139117.8 GI:12189412
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BASE COUNT
ORIGIN
seq_documentation_block:
                                   seq_name: gb_pr:HSU82979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84701 TCTGTGACCATCTGGTGTCAGGGGACCCTGGAGGCTCGGGAGTACCGTCT
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                                                                                     84992 GCATCT 84997
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                                                                                                                                                                    GGGGTCCCAGCCCAGGCTCTGCCCTCAGGAAGGGGGGTCAGCTCTCAGGG 8499.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGGTCTTGGGATCCAGCCTCTGATTTTCTTCCAGGGCCCCTCCCCAA 84654
                                                                                                                              AlaSer 126
                                                                                                                                                                                                                                                                                                                                         GACTATGCAGGGAGATACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTC
                                                                                                                                                                                                                                                                                                                                                                         AspThrGlnGlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp** 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 euAspSerProAlaIleLysHisGlnPhe.....LeuLeuThrGly 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .ValGlnGlu.....TrpGlyAlaGlnGluProValHisL 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyValThrTrpGlyProValThrGluAlaAlaIlePheTyrGluThrGl
                                                                                                                                                                                                             ..GlyProLysValLeuAlaCysSerLeu......AlaLeuAspGly 124
                                                                                                                                                                                                                                                      ACAGCCCAGTGACCCCCTGGAGCTGGTGATGACAGGTGAGAGGACACTCA 84941
                                                                                                                                                                                                                                                                                               *GlnLeuSerLysLeuLeuGluLeuThr.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
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49.265
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| 33951 c 33464 g
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clone_end:SP6
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1. .148497
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/db_xref~"taxon:9606"
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Percent Identity: 33.824
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alignment_block:
US-09-471-276-831 x HSU82979
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Ouality:
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                                                                                                                                                      GCCCCTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAG.. 119
..CTGGGGGAACTCTGTGACCATCTGGTGTCAGGGGACCCTGGAGGCTCG
                                                                                                                                                                                                                                          eTyrGluThrGln***SerLeuTrpAlaGluSerGluHis***LeuLysT
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1 (Dases 1 to 1396)
Samaridis, J. and Colonna, M.

Cloning of novel immnoglobulin superfamily receptors expressed on human myeloid and lymphoid cells; structural evidence for new stimulatory and inhibitory pathways
Bur. J. Immunol. 27 (3), 660-665 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-DEC-1996) Basel Institute for Immunology, 487 Grenzacherstrasse, Basel CH-4005, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. 1
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Cella,M., Dohring,C., Samaridis,J., Dessing,M., Brockhaus,M.,
Lanzavecchia,A. and Colonna,M.
A novel inhibitory receptor (II/3) expressed on monocytes,
macrophages, and dendritic cells involved in antigen processing
J. Exp. Med. 185 (10), 1743-1751 (1997)
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Human immunoglobulin-like transcript-3 mRNA, complete cds.
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/db_xref."taxon:9606"
/chromosome."19"
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Align seg 1/1

to: AC008984 from: 1

to: 39829

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                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                               www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Mainut Creek, CA 94598, USA On Feb 17, 2000, this sequence version replaced gi:6910557. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-FEB-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
4_(bases i to 39829)
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DOE Joint Genome Institute and Stanford Human Genome Center
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Submitted (03-AUG-1999) Production Sequencing
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DOE Joint Genome Institute and Stanford Human Genome Center.
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AC008984
AC008984.5 GI:6984369
                                                                                                                                                                                                                                                                                                                             Quality: Phrap Quality >=40 99.6% of Sequence: Estimated Total Number of Errors is 0.1.
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9405 c 9541 g 10360
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/chromosome="19"
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                                                                                                          ACCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCA 21912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-APR-2001) Sanger Centre, Hinxton, Cambridgesh; CBIO 15A, UK. E-mail enquirites: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 24, 2001 this sequence version replaced gi:13624978.
* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 97137)
                                                                                             coverage: 8.38x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: SC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROGRESS ***, 6 unordered pieces
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19 clone RP3-598H20,
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FEATURES

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BASE COUNT
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16293 ACCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCA 16342
                                                                                                                                                                                                                                                                                   16152 CTGTGACCATCCGGTGTCAGGGGACCCTGGAGGCCCAGGAATACCGTCTG 16201
                                                                                                                                                                                                                                                                                                                                                                            16105 AGCCACCCTCTGGGCTGAGCCAGGCTCTGTGATC...AGCCGGGGGAACT 16151
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                                                                                                                                                                                    GTTAAAGAGGGAAGCCCAGAACCCTGGGACACACAGAACCCACTG.....
                          uAspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAspThrGln. 88
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Ratio:
                                                                                           .GAGCCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGC
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runs of N, but the exert sizes of the gaps are unknown
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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2884 2983 contig of 2885 bp in length
2884 25322 contig of 2335 bp in length
5323 5422: gap of 100 bp in length
5423 7.551: gap of 100 bp in length
7.552 37551: gap contig of 2182 bp in length
9753 9833: gap of 100 bp in length
9843 94641: contig of 84808 bp in length
98442 94741 gap; contig of 2396 bp in length
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/note="assembly_fragment:02197"
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9834. 94641
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55.556
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/db_xref:"taxon:9606"
/chromosome:"19"
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94742. .97137
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alignment_block:
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                                      1 MetSerMetLeuValValPheteuLeuLeuTrpGlyValThrTrpGlyPr 17
ATGACCCCCATCCTCACGGTCCTGATCTGTCTCGGGCTGAGTCTGGGCCC
                                                                                                                                                                                                                                                         Quality:
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Immunity 7 (2), 273-282 (1997)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LSQANETIJGPVSRSVGGQYRCYGAHRUSSENSAPSDFLDILIAGQYEDRSVLSVQPGP
TVASGENVTLLQOSQGMYGTELLTKEGAADDPHILBSTYOSGKXQAEPRIGFVTSAIIA
GTYRCYGSQSSKYPILTHPSOPIELIVSGPSGCPSSPTTGFTSTGSRGADPHIPTGSD
PQSGLGHHLGVVI GILVAVILLILLILLILLILHERGOKHMFTGOKKAUPGHAGAV
GPEPTDRGIJGMSSPAADAQEENIYAANXHTQPEDGVBMOTRSPHDEDPQAVTYAEVK
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643 c 534 g 360 t
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VTLRCGGGETQFYRLYEKKTAPMTTRIPGELVKKGGPLPSTTWBHAGKYRCTYGS
DTAGRSESSDFLELWTGATY IRFUSAQPSFWANSGGWYTLQCGSQWAFGFTLGKBG
EDEHPQCLNSQPHARGSSRAIFSVGFVSPSRRWWYKCYAYDSNSPYBMSLPSDLLELL
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56.198
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/db_xref-"GI:2267168"
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/db_xref."taxon:9606"
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LOCUS AF009006
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GTYRCYGSQSSKPYLLTHPSDPLELVVSAGPEDQPLTPTGSDPQSGLGRHLGVVIGIL
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                                                                                            Jammaridis, J. and Colonna, M. Samaridis, J. and Colonna, M. Samaridis, J. and Colonna, M. Cloning of novel immunoglobulin superfamily receptors luman myeloid and lymphoid cells: structural evidence stimulatory and inhibitory pathways pair. J. Kmnunol. 27 (3), 660-665 (1997)
Sammaridis.J. and Colonne.M.
Direct Submitted (16-DEC-1996) Basel Institute for Immunology,
                                                                                                                                                                                                                                                                                                                                                                                                         Human immunoglobulin-like transcript 2 U82279
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Adema G. Jan, Meyaard L., Gorman, D.M., McClanahan, T.K., and phillips J.H. Jr.
Ig superfamily 'disfr' receptors expressed in monocytes
Patent: US 6140076-A 21 31-007-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    luSerGluHls***LeuLysThrLeuGly..GlnCysAspAlaAspValP 50
    uLeuGluLeu 110
                                                                  CGCTGTTACTATGGTAGCGACACTGCAGGCCGCTCAGAGAGCAGTGACCC 647
                                                                                                                                                                                             AGGGCCAGTTCCCCATCCCATCCATCACCTGGGAACATGCAGGGCGGTAT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGGGGGGCCAGGAGCCCAGGAGTACCGTCTATATAGAGAAAAGAAAAC 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGGACCCACGTGCAGGCAGGCACCTCCCCAAGCCCACCCTCTGGGCTG
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                                                                                                                           ArgCysArgSerGlyLeuSerThr...GlyTrp***GlnLeuSerLysLe 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCAGGCTCTGTGATC...ACCCAGGGGAGTCCTGTGACCCTCAGGTGT 456
                                                                                                                                                                                                                                                                                                                                                                                       .....TrpGlyAlaGlnGluProValHisLeuAspSerProAlaIleL 78
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Cosman,D.J., Anderson,D.M. and Borges,
Family of immunoregulators designated
receptors (lir)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GTVRCYGSOSKFYLLTHPSDPLELTVSGPSGGFSSTTGFTSTGGEDQDFTPGGSD
POSGLGRHLGVVIGLUAVILLLLLLLLTLFILHHROGKHMTSTGGFDQALDFQHPAGAN
GPEPTDRGLQHRSSPAADAQEENLYAANKHTQPEDGVEMDTRSPHDEDPQAVTYAEVK
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/db_xref="taxon:9606"
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26140 ATCAGCTGGGGGAGCCCCGTGACCATCTGGTGTCAGGGGGAGCCTGGAGGC
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Ratio:
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Submitted (30 MAR-2001) DOE Joint Genome Institute, 2800 Mitchell

Drive, Walnut Creek, CA 94598, USA

On Mar 30, 2001 this sequence version replaced gi:7711454.

Draft Sequence Produced by DOE Joint Genome Institute

WWW.jgi.doe.gov
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3 (bases 1 to 84087)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Enkaryota; Metazoa; Chordata: Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence
Estimated Total Number of Errors is 0.2.
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human
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/db_xref="taxon:9606"
/chromosome="19"
/clone="CTD-2337J16"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1395)
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                                                        292
                                                                                                                     /product-immunoglobulin-like transcript 8"
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/note~"immunoglobulin superfamily member; ILT8"
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                                                                                                                                                                                                                                                                                                                                                                                                            /map="19q13.4"
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/db_xref "taxon:9606"
/chromosome "19"
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Catarrhini; Hominidae;
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US-09-471-276-831 x AF041262
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Ar322217
                                                     Submitted (18-NOV-2000) Neurobiology University, 2153 North Campus Drive, Location/Qualifiers 1, 1745
                                                                                                                                               2 (bases 1 to 1745)
Bernard, D.J. and Woodruff, T.K.
                                                                                                                                                                                                                    Inhibin Binding Protein in Rats: Alternative Transcripts and Regulation in the Piturkary across the Estrous Cycle Moi. Endocrinol. 15 (4), 654-667 (2001)
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Bernard, D.J. and Woodruff, T.K.
                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/organism· "Rattus norvegicus"
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                                                                                       and Physiology, Northwestern Evanston, IL 60208, USA
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LOCUS AF031554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
complete cds.
AF031554
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Colonna, M., Navarro, F., Bellon, T., Llano, M., Carcia, P.,
Samaridis, J., Angman, L., Cella, M., and Lopez-Botet, M.
A common inhibitory receptor for major histocompatibility complex
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2066)
                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   AF031554.1 GI:2665642
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/protein_id=*AnA40084.1"
/protein_id=*AnA40084.
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VERSION KEYWORDS

SOURCE ACCESSION DEFINITION

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REFERENCE

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J. Exp. Med. 186 (11), 1809-1818 (1997)
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.GlyArgTyrArgCysArgSerGlyLeuSerThrGlyTr 101
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/product="immunoglobulin-like transcript 5,
/producti_id="AAC51901.1"
/db_xref="Gi1565643"
/translation="MTPALTALLCLGLSLGPRTRYQAGPFPKPTLWAEPGSYISWGSP
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/chromosome="19"
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/clone="17.18"
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Gaps: 5
Percent Identity: 30.159
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Quality:
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21168090
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Bernard D.J. and Woodruff, T.K.
Bernard D.J. and Woodruff, T.K.
Tablibin Binding Protein in Rats: Alternative Transcripts and
Regulation in the Pituitary across the Estrous Cycle
Moll. Endocrinol. 15 (4), 654-667 (2001)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentla; Sclurognathi; Muridae; Murihae;
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LIMCOG PVHGVOYILHKEGEATSMOLIMDSYSNEGAFPIINISGASIGRYSCCYHRDIMNS
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QPIEQQRPSGYRADFWMPVVRDQDSGVYSCVYYLDSAPLVASNHSNSLEIWVTDKPPK
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                                                                                                                                                                                                                                                                                       Colonna, M., Navarro, F., Bellon, T., Liano, M., Garcia, P.,
Smartidis, J., Angman, L., Cella, M., and Lopez-Botte, M.
A common inhibitory receptor for major histocompatibility complex
class I molecules on human lymphoid and myelomonocytic cells
i. Exp., Med. 186 (11), 1809-1818 (1997)
                                                                                                                                                                Grenzacherstrasse, Basel CH-4005,
                                                                                                                                                                                    Direct Submission Submitted (20-JUN-1997) Basel Institute for Immunology,
                                                                                                                                                                                                                                Colonna, M
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1 (bases 1 to 2063)
Colonna, M., Navarro, F., Bellon, T., Llano, M., Garcia, P.,
Samaridis, J., Angman, L., Cella, M. and Lopez Botet, M.
                                                                                   Blomo sapiens
Blomo sapiens
Blomo sapiens
Blomo sapiens
Blomo sapiens
Blomo sapiens
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                      mRNA, complete cds.
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protein id="AAC51898.1"
/db_xref="GI:2662446"
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Percent Identity: 30.159
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                                       GAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACA 269
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from:

6

Percent Identity: 30.159

GAGCCCTGGGACAGAAATAACCCACTG.

227

200 54 SerGluHis***LeuLysThrLeu 42

102

34

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A common inhibitory receptor for major histocompatibility complex class I molecules on human lymphoid and myelomonocytic cells J. Exp. Med. 186 (11), 1809-1818 (1997) 98044746 2 (bases 1 to 2053)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
YATLAIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pproduct="immunoglobulin-like transcript 5 protein"
/protein_id="AAC5188.1"
/db_xreff="G1:2662456"
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VTIWCQGSLEAQEYQLDKEGSPEPWDRNNPLEPKNKARFSIPSMTQHHAGRYRCHYYS
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/chromosome="19"
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/db_xref="taxon:9606"
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alignment_block:
US-09-471-276-831 x AF009639
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Homo sapiens clone 31
mRNA, complete cds.
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98044246
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Sameridis, J., Anopman, L., Cella, M., and Lopez-Botat, M.,
A common inhibitory receptor for major histocompatibility complex
class I molecules on human lymphoid and myelomonocytic cells
class, McG. 166 (11), 169-818 (1997)
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Memmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2063)
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                                                                                                                             Ratio:
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  to: AF009639
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TYRCYGSRSSNPHLLSFPSEPLELMVSGHSGGSSLPPTGPPSTPGLGRYLEVLIGVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"immunoglobulin-like transcript 5 protein"
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/protein_id="AnC51894.1"
/db_xref="G1-566248"
/translation="MTPALTALICLGLSLGPRTRMQAGPEPKPTLMAEPGSVISWGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note: "immunoglobulin superfamily; inhibitory receptor"
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/clone:"31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref~"taxon:9606"
/cell_type~"myelomonocytic"
                                                                                                                                                                                                                                                                                                  LDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start~1
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                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/translation~"MTPALTALLCIGLSIGPRTRMQAGPFPKPTLWAEPGSVISWGSP
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                                                                                                               /codon_start~3
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/clone~"17.23"
                                                                                                                                                                                                                              /chromosome~"19"
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/db_xref-"taxon:9606"
/map·"19q13.4"
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SAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNMTLRCGSQKGYHHFVLMKEGE

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Colonna.M., Navarro.F., Bellon.T., Llano.M., Garcia.P.,
Samaridis.J., Angman.L., Cellan, and Lopez-Botet, M.
A common inhibitory receptor for major histocompatibility complex
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Homo sapiens clone 17.7
mRNA, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Grenzacherstrasse, Basel CH-4005,
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....GlyArgTyrArgCysArgSerGlyLeuSerThrGlyTr 101
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QEENLYAAVKDTQSEDRVELDSQQSFNDEDQAVTYAVKHSSSRRBAMSPRSSLSGE
ELDTKDRQVEEDKQMOTEAAASEASGDVTYAQLHSLTLARKATEPPPSQGGEPPAEFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VASGENVTLLCQSWWQFDTFLLTKEGAAHPPLRLRSMYGAHKYQAEFPMSPVTSAHAG
TYRCYGSRSSNPHLLSHPSEPLELVVSGHSGGSSLPPTGPPSTPGLGRYLEVLIGVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOLPRTLDSQQLHSGGPQALFPVGPVTPSHRMRFTCYYYYMYMYMSHSQDPLEL
SGVSRRPSLTLDGQQPVLAPGQSLTIDJCGSDVGYDBFVJKTSGBHDLQBPGQQDQAGLL
SQANFTLGPVSRSYGGQYRCTGAHNLSSEMSAPSDPLN1LMAGG1YDTVSLSAQPGPT
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/protein_id="AAC51890.1"
/db_xref="G1.562430"
/translation="MTPALTALLCLGLSLGERTEMOAGPFPKPTLMAEPGSVISWGSP
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/db_xref="taxon:9606"
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Samartidis, J., Anquan, L., Cella, M., and Lopez-Botket, M.
A common inhibitory receptor for major histocompatibility complex
class I molecules on human Impebrid and myelomonocytic cells
cl. Exp., Med. 166 (11), 1809-1818 (1997)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QFENLYAAVKDTQSEDRVELDSQQSPHDEDPQAVTYAPVKHSSPRREMASPPSSLSGE
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SQANFTLGPVSPSNGGYRCYGAHNLSSBWSAPSDFULLMAGGYTDYSLSADGETY
VASCBNVTLLCDSWGDDYFLLYSCAAHEPLALBSWGAHKYDAFEPKSPYFSAING
TYRCYGSRSSNPHILLSHPSEPLELVVSGHSGGSSLPPTGPPSTPGLGRYLEVL1GVSV
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SAGWSEPSDILE WMTGPYMFUTLSALPSVVASGGNARPS FPSMTQHHAKEGE
HOLPRTLDSQOLHSGGPQALFPVGPVTPSHRWRFTGYYYYTMYPWWWSHPSDPLETILP
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/protein_id:-AAC51896.1*
/bt.xrefe*G1.2662442*
/translation-*MTPALTALLCLGLSLGPRTRMOAGPFPKPTLMAEDGSVTSWGSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colonna M., Navario, F., Bellon, T., Llano, M., Garcia, P.,
Smarridis, J., Angman, L., Cella M., and Lopez-Bucte, M.,
A common inhibitory receptor for major histocompatibility complex
class indecentes on human jumphoidand myelomomocytic cells
J. Exp. Med. 186 (11), 1869-1818 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-JUN-1997) Basel Institute for Immunology, 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grenzacherstrasse, Basel CH-4005,
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1 (bases 1 to 2066)
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/product+*immunoglobulin-like transcript
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AF009636
Colonna, M., Navarro, F., Bellon, T., Llano, M., Garcia, P., Samaridis, J., Angman, L., Cella, M. and Lopez Botte, M. A common inhibitory receptor for major histocompatibility complex class I molecules on human lymphoid and myelomonocytic cells
                                                                                                                                                                                                                                                                          AF009636 2091 bp mRNA PRI 05-DEC-1997
Homo sapiens clone 17.8 immunoglobulin-like transcript 5 protein
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2091)
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alignment_block:
US-09-471-276-831 x AF009636
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/protein_id="AAC51891.1"
/db_xref="GI:2662432"
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/chromosome="19"
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Samartidis, J., Angman, L., Cella, M., and Lopez-Botte, M.,
A common inhibitory receptor for major histocompatibility complex
class I molecules on human lymphoid and myelomonocytic cells
J. Exp. Med. 166 (1), 1699-1818 (1997)
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/db_xrefo"taxon:9606"
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Ricko D.O. Bruce D., Mundt M., Doggett N., Munk C., Saunders E.,
Robinson, D., Jones M., Buckinghum J., Chasteen, L., Thompson, S.,
Robinson, D., Horest M., Buckinghum J., Chasteen, L., Longmire J.,
Robinson, D., Jones M., Buckinghum J., Chasteen, L., Longmire J.,
Robinson, D., Jones M., Temmer J., Melchek L., Longmire J.,
Robinson, D., Walter M., Charles M., Longmire J., Maltible M.,
White, S., Legy S., Tatun, O., Campbell, C., Revoctt, J., Maltible M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Mctazoa: Chordsta: Cranista: Vertebrata: Eutelostomi; Mammalia: Euthoria: Primatos: Catarrhini; Hominidae; Homo. 1 (bases 1 to 4755)

Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryunt, J., Tesmer, J., Maincke, L., Longnire, J., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltble, M., Misra, M., and Deaven, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Institute, Los Alamos National Laboratory, MS M888, Los Alamos, NM 87545, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-SEP-1998) Center for Human
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/clone."306E6"
                                                                                                                                                               /chromosome-"16"
/map:"16p13.3"
join(1. .350,1825.
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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ORIGIN
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AUTHORS
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                                                                                                                                   TITLE
                                                                                                                                                                                                                                                ORGANISM
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                                                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgLeuProAlaValGlnGluTrpGlyAlaGlnGluProValHisLeuAs 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThrGlyTrp***GlnLeuSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   euLeuThrGlyAspThrGlnGlyArgTyrArgCysArgSerGlyLeuSer 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boduslavity, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
                                                                                                                             Eukaryota; Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 68007) Nusbaum,C. and Lander,E. Homo. sapiens Chromosome 2, Clone RPII-684C2
                                                                                                                                                                                                                                                                                                             AC041031
AC041031.1 GI:7534234
                                                                                                                                                                                                                                                                                                                                                           SAMPLING
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                                                                                                                                                                                                                                             Homo sapiens
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/note="GRAIL 2 excellent exon,
h 1297 c 1466 g 1077 t
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52.336
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1 others
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Collymore.A., Cooke.P., DeArellano.K., Dewar,K., Diaz.J.S., Dodge.S., Domino.M., Doyle.M., Ferreira.P., FitzHigh.W., Gage.D., Galadgan,J., Gardyna.S., Goyetta.P., FitzHigh.W., Gage.D., Garand-Pierre.N., Grant.G., Hagos.B., Heaford.A., Horton.L., Howland,J.C., Lilev.I., Johnson, R., Jones.C., Yann.L., Karatas.A., Klein,J., LaNcoque.K., Lamazares.R., Landers.T., Leboczky,J., Levine,R., Litu.G., Liu.G., Locke.K., Macdonald.P., Marquis,N., Heciarthy.M., McEwan.P., McCurr.A., McCernan,K., McChernan,K., Pierre.N., Wirphy,T., Naylor,J., McChernan,C., T., O'Connell.P., O'Neil.D., Oliver,T.M., Ollver,J., Peterson,K., Pierre.N., Pisani,C., Pollvra,Y., Raymond,C., Riley,R., Ragoov,P., Rothman,D., Roy,A., Santos,R., Schuer,S., Schuer,S., Severy,P., Spencer,B., Schuer,S., Theodore.J., Tirrell,A., Travers,M., Trigillo,J., Vassiliev,H., Viel,R., W.A., Wilson,B., M., X., Wyman,D., Ye,W.J., Voung,G., Zainoun,J., Zimmer,A., and Zody,M.

JOURNAL SE

Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information

Center project Information Center project name: L9625 Center clone name: 684_C_2

MOTE: This record contains 77 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will

be preserved. 9616 6099 2508 2607: 760 859: gap of 100 bp 1626: contig of 767 bp in length 97 3496; gap of 100 bp 100 pp 100 bp
100 bp
100 bp
6879: contig of 781 bp
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0 7765: confi-8633: contig of 768 bp 8733: gap of 100 km 1726: 100 bp 7 705: contig of 786 bp 1 865: gap of 100 bn 8633: conti-100 bp 100 bp 100 bp 237; gap of 100 5998; com 2507: contig of 781 bp in length
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	length	'n	285	40593; co	981
	length	in	0 65	39711: c	994
	length	in	750 b	38846; co	888
	length	Ín		37996; co	37191 37997
	length	'n	772	37090: co	631
	length	in	00	36218:	543
	length	in	1,000	35338: c	U 10 4 4
	length	in	778	34433: 0	365
	length	'n	98	33555: co 655: gap o	276
	length	in	802 b	32666: co 766: gap o	186
	length	in	783 00 b	31764; co 1864; dap o	176
	length	Ė	775 00 b	30881: co	380
	length	'n	798 00 b	30006: co 0106: gap o	920
-	length	5	802 100 b	108: c	910
-	length	5	908	gap of	820
	Tendru	. :	100 bp	gap of	729
	langth	: :	100 4	gap of	636
	length	<u>.</u>	100 bp	gap of	5.5
	length	'n	100 b	gap of 520; conti	462
	length	ij	100 bp of 782 bp	844: gap of 24626: conti	384
	length	Ħ	800	23744: co	294
	length	in	788	22844: co	205
	length	ä	781	21956: co	117
	length	Ξ	790	21075: co	026
	length	'n	765	20185: co	941
	length	'n	805	19320: co	951
	length	'n	909	18415: co	760
	length	5	516	17506: co	565
	length	in.	270	16555: co	5 7 8 S
	length	Ín	of 783 bp	681: co	200
	length	ín	768	14798: co	200
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alignment_scores: Quality:	*		*	*	*:	• *				*		•	*	•	*	•	*		*	*	*	*	•	•	*	*	*		*	*	*		*	*
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91.00	61160: gap of	61060: contig	60262: gap of	60162; contig	59355: gap of	50255 COPTION	58353: contig	57562: gap of	57462: contig	56691; gap of	56591: contiq	55783: gap of	55683: contig	54893: gap of	54793: contig	54009: gap of	53909; contig	53139: gap of	53039: contig	52238: gap of	52138: contig	51339: gap of	51239: contig	50458: gap of	50358: contig	,	g	48671: gap of	48571; contig		9		46788; contig	
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alignment_block:

Us-09-471-276-831 x AC041031/rev ...

Length: 150
Gaps: 68
Gaps: 6

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15-DEC-2000

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KEYWORDS
SOURCE
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                                                            363 CCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCAG
                                                                                                                                                                                                                            272 TTAAAGAGGGAAGCCCAGAACCCTGGGACACACAGAACCCACTG.....
                                                                                                                                                                                   73 AspSerProAlaIleLysHisGlnPheLeuLeuThrGlyAspThrGln...
                                                                                                                                                                                                                                                                 61 alGlnGlu.....TrpGlyAlaClnGluProValHisLeu 72
                                                                                                                                                                                                                                                                                                                                                  45 CysAspAlaAspValProGlyProProGlyAspSerArgLeuProAla.V
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                                                                                                                                                                                                                                                                                                                TGTGACCATCCGGTGTCAGGGGACCCTGGAGGCCCAGGAATACCGTCTGG
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                 InLeuSerLysLeuLeuGluLeu 110
                                                                                                                                           ...GAGCCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
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Family of immunoregulators designated Leukocyte immunoglobulin-like receptors (lir)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Manmalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35 from Patent
AX046972
                                                                                    ....GlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***G 103
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/db_xref="taxon:9606"
73. .834
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LTEEGDHKLSWISDSCIPPSGOPALFPYTTSHRWILRCYGSRRHILLOVISEPSD
LLEIPVSGEATVFSSTIGGSQTGCGELYROGSPC"
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/db_xref="G1:11876402"
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1. .997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MAPWSHPSAQLQPVGGDAVSPALMVLLCLGNLSKATLWAEPGSV/
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Gaps: 4
Percent Identity: 37.333
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                                                                                                                                  103 InLeuSerLysLeuLeuGluLeu 110
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                                                                                                                                                                                      385 CCATGCAGGGAGATACCGCTGTTACTACTACAGCCCTGCAGGCTGGTCAG
                                                                                                                                                                                                                                                                                                                                                        294 TTAAAGAGGGAAGCCCAGAACCCTGGGACACACAGAACCCACTG.
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                                                                                                  AGCCCAGCGACCCCCTGGAGCTG 457
                                                                                                                                                                                                                         .....GlyArgTyrArgCysArgSerGlyLeuSerThrGlyTrp***G
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Mammalia; Eutherla: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1007)
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/protein_id="GAC18937.]"
/bl_xeri="G1:11876396"
/bl_xeri="G1:11876396"
/translation="MapwshesAOLOpVgGDAVsPALMVLLCLGNLSKATLMAEPGSV
ISGGMSVT1RCQGTLEAQDETALVWEGSEEPMDTONDELDFKMKARFS1EGDEFI
LGSGMSVT1RCQGTLEAQDETALVWEGSEEPMDTONDELDFKMKARFS1ESDEFI
LTEEGDHKLSWTLDSQLTPSGQFOALFPWGFVTPSHRWMLRCYGSRRHILQVWSEEPSD
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1. .1007
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576.849 Million cell updates/sec
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075022;
01-NOV-1998 (TREMBLrel. 08, Greated)
01-NOV-1998 (TREMBLrel. 08, Last sequence update)
01-NOV-1998 (TREMBLRel. 17, Last annotation update)
LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR-3.
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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01 MAR-2001 (TrEMHLrel. 16, Created)
01 MAR-2001 (TrEMHLrel. 16, Last sequence update)
01 JUN-2001 (TrEMHLrel. 17, Last annotation update)
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SMART; SM00409; IG; 3.
SMART; SM00410; IG_like; 1.
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    Eukaryota; Metazoa;
                                 HOMO Sapiens (Human)
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STRAIN-SPRAGUE DAWLEY; TISSUE-LIVER;
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Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SEQUENCE
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SMARF; SM00409; IG; 1.
SMART; SM00410; IG; like; 2.
PROSITE; PS00120; LIPASE SER;
SEQUENCE 631 AA; 69226 MW;
                                                                                                                                                                                                                                                                                  InterPro; IPR003599;
InterPro; IPR003600;
InterPro; IPR003006;
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01-JUN-2001 (TLEMBLIFEL 17, LAST ANNOTATION update)
MONOCYTE INHIBITORY RECEPTOR PRECURSOR.
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NCBL_TaxID-9606;
[1]
                                                                                                                                                                 PROSITE; PS00120;
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SMART; SM00410; IG_11ke;
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HSSP; P43626; INKR.
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Arm J.P., Nwankwo C.,
Submitted (MAR-1997)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF025533; AAB87667.1; HSSP; P43626; INKR.
                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: TO IMMUNOGLOBULIN AND DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: TO IMMUNOGLOBULIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VISWGSPYTIWCQGSLEAQEYQLDKEGSPEPLDRNNPLEPKNKARFSIPSMTQHHAGRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VOEWG------AQE------PVHLD-----SPAIKHQFLLTGDTQ----GRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAE-------PG----S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHYYSSAGWSEPSDPLEL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                       631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                       AA,
                                                                                                                                                                 LIPASE_SER;
                                                                   23
631
69385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
Primates;
                                                                                                                                                                                                                                                           Ig_llke.
Ig_MHC.
Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.7%;
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   13.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Austen K.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 90.5; b
Pred. No. 0.09
10; Mismatches
   Score 87.5;
                                                                                          POTENTIAL.
MONOCYTE INHIBITORY RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNKNOWN_1.
E77E1ED8D42F9C25 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                       61CF1967B08D79FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kubin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         631
                                                                                                                                                                                                                                                                                                                                                                                                                             MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAJOR HISTOCOMPATIBILITY COMPLEX
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   В
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Length 631;
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RESULT
075021
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Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 38; Conserv
                    UI-NOV-1998 (TrEMBLrel. 08, Created)
01-WOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
LEUCOCYTE IMMUNOCLOBULIN-LIKE RECEPTOR-5.
LIR-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                015468 PRELIMINARY;
015468;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro: IPR003600; Ig_11ke.
InterPro: IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMARF; SM00410; IG_11ke; 2.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM W.A.
AUSTEIN K.F.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases,
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MONOCYTE INHIBITORY RECEPTOR
                                                                                                                                                                          075021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P43626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U91925; AAB68665.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                           109
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                                                                                                                                                                                                                                                                                                                EL 110
   sapiens (Human)
                                                                                                                                                                                                                                                                                            F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDA------DVPG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHYYSSAGWSEPSDPLEL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRSGLSTGWXQLSKLLEL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLDRNNPLEPKNKARFSIPSMTEHHAGRYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VQEWG-----AQE-----PVHLD----SPAIKHQFLLTGDTQ---GRYR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAE-----
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                                                                                                                                                                                                                                                                                                                                                                                             P-----
                                                                                                                                                                                                                                                                                                                                                                                                                                     PPGDSRLPAVQEWGAQEPVHLDSPAIKHQF----LLTGDTQGRYRCRSGLSTGWXQLSKLL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLCLGLSLGPRTHMQAGPLPKPTLWAEPGSVISWGNSVTIWCQGTLEAREYRLDKEESPA 67
                                                                                                                                                                                                                                                                                               115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                          WDRQNPL---EPKNKARFSIPSMTEDYAGRYRCYYRSPVGWSQPSDPL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 N
49297 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.8%;
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Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 0.21;
ll; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84.5; DB Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MONOCYTE INHIBITORY RECEPTOR 76D1E24A82EA1399 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                          448 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------ PG-----S 37
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Best Local
                                                                                                                        Matches
                                                                                                                                               Best Local Similarity
                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      075023;
075023;
01-NOV-1998
01-NOV-1998
01-JUN-2001
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Pfam: PF00047; ig; 2.
SMART; SM00410; IG_like; 2.
448 AA; 49325 MW;
                                                                                                                                                                                                                                      Pfam; PF00047; ig; 3.
SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 2
SEQUENCE 590 AA; 64125
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF025534; AAB87668.1; HSSP; P43626; 1NKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
LEUCCCYTE IMMUNOGLOBULIN-LIKE RECEPTOR-8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF025532; AAB87666.1; HSSP; P43626; 1NKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003600;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.,
J. Imaunol. 0:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003600; InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO IMMUNOGLOBULIN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunol. 0:0-0(1997)
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                                                                         1 MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLK----TL---GQCDA-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLCLGLSLGPRTHMQAGPLPKPTLWAEPGSVISWGNSVTIWCQGTLEAREYRLDKEESPA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLWGVTWGPVTEAAIFYETQXSLWAE-----SEHXLKTLGQCDA------DVPG 51
                          MTLTLSVLICLGLSVGPRTCVQAGTLPKPTLWAEPASVIARGKPVTLWCQGPLETEEYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003600; Ig_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hsu M.-L., Fanger N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -WDRQNPL---EPKNKARFSIPSMTEDYAGRYRCYYRSPVGWSQPSDPL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                    Ig.
Ig_like.
Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.8%;
                                                                                                                                            12.3%;
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                                                                                                                                                                                                                         .; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84.5; DB Pred. No. 0.31;
                                                                                                                 Pred. No. 0.8
5; Mismatches
                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                             8E7AB249F12E44CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76D1E0B7AD3A1399 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kubin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X
                                                                                                                                         DB
0.89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cosman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Indels
                                                                                                                                                                   4;
                                                                                                                                                                                                                                             CRC64
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                                                                                                                                                                   Length 590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                        Indels
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                                                                                                                        27;
                                                                                                                     Gaps
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47

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RESULT
O79089
ID 9089
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O7
D7 01
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                           Q79089;
Q79089;
01-NOV-1996
01-NOV-1996
01-JUN-2001
SEQUENCE FROM N.A.
STRALN-PATTENT A30;
MEDLINE-94303241; PubMed-8030283;
Wieland U., Hartmann J., Suhr H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PREM: FAVOUR SMART; SM00409; IG; 2.
SMART; SM00410; IG_11ke; 1.
SMART; SM00410; AA; 71018 MW;
                                                                                                                                                                                                                                Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-UN-2001 (TREMBLrel. 17, Last annotation update)
LSUCOCYTE INMUNOCLOBULIN-LIKE RECEPTOR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukeryota: Metazoa; Chordata; Croniata; Vortobrata; Euteleostomi;
Kommalla; Euteria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           075025
                                                                                                                                                                                                NCBI_TaxID-11676;
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InterPro; IPR003599;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF009221; AAB63522.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hsu M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosman D., Fanger N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      075025;
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DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSDPLELVVTGAYIKPTLSAQPSPVVNSGGNVILQCDSQVAFDGFS 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQE-----WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVPGPPGDSRLPAVQEWGAQEPVHLDSPATKHQFLLTGDTQGRYRCRSGLSTGWXQLSKL 107
                                                                                                                                                                                                                                                                                                                                                      6 (TrEMBLrel. 01, Created)
6 (TrEMBLrel. 01, Last sequence update)
1 (TrEMBLrel. 17, Last annotation update)
INFECTIVITY FACTOR).
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24.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93AF8F021A22949D CRC64;
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Salzberger B., Eggers H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPKVLAC -- SLALDGAS 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
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Best Local
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Best Local Similarity
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015070;
01-JAN-1998
01-JAN-1998
01-JUN-2001
KIAA0364.
                                                                                                                                                                                                                                                                                                  Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Momura N., Ohara O.;
*Pradiction of the coding sequences of unidentified human genes. VII The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                     Pfam: PF00047; 1g; 12.
SMART; SM00408; IGC2; 1.
SMART; SM00410; IG_like; 7.
SEQUENCE 1327 AA; 147971
                                                                                                                                                                                                                                                            code for large proteins in vitro.*;
DNA RES. 4:141-150(1997).
-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000475; Viral_infect.
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFECT.
PRODOM; PD000063; Viral_infect; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "In vivo genetic variability of the HIV-1 vif gene.";
Virology 203:43-51(1994).
EMBL: Z30601; CAA83078.1:
                                                                                                                                                                                       interPro;
                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                            InterPro; IPR003598; Ig_c2
                                                                                                                                                                                                                             HSSP; P43626; 1NKR
                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97349984; PubMed 9205841;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIAA0364
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                                                                                      Local Similarity
75
                      23
                                                23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV
                                                                                                                                                                                                                                                     DOMAIN.
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                                                IFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQEPVHLDS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIVWQVDRMRIRTWKSLVKHHIYISRKATGWFYRHHYESTHPRVSSEVHIPLGDARLVIT
------PAIKH----QFL---LTGDTQGRYRCRSGLSTGWXQLSKLLELTGP
                         ILMDPQPELWIESNY----
                                                                                                                                                                                                                                      AB002362; BAA20819.1;
                                                                          30;
                                                                                                                                                                                   IPR003600; Ig_like
IPR003006; Ig_MHC.
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 AA;
                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                           (Human).
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Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22676 MW;
                                                                                    11.5%;
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                                                                                                                                      147971 MW;
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                        ----POAPWEN----ITLW-CRSPSRISSKFLLLKDK
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Pred. No.
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Last annotation update)
                                                                                    Score 76; D
Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                          Mismatches
                                                                                                                                      736C689FEC94D2E1 CKC64;
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                                                                                                DB 4;
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                                                                                               Length 1327;
                                                                          Indels
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                                                                          38;
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                                                                      Gaps
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Best Local Similarity
Matches 22; Conser
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Q9ZHP2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           055002
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01-JUN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
PAIRED-IG-LIKE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SapI restriction-modification systems Mol. Gen. Genet. 260:226-231(1998). EMBL; AF056036; AAC97191.1; -
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Xu S.-Y., Xiao J.-P., Ettwiller L.,
Dalton M., Robinson D.P., Petronzio
Ware J., Slatko B., Benner J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Cyanobacteria;
NCBI_TaxID=82765;
                                                                                                                                                                                                                                              Yamashita Y., Pukuta D., Tsuji A.,
Nishikawa Y., Ohyama Y., Ohmori H.
J. Biochem. 123:0-0(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nostoc sp. ATCC 29411
                        SMART; SM00409; IG; 3.
SMART; SM00410; IG_like; 2.
NON_TER 635 635
                                                                                                                                                                                       EMBL; AF041036; AAB96928.1; HSSP; P43626; 1NKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN P91C) (FRAGMENT).
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           SEQUENCE
                                                                                      Pfam; PF00047; ig; 5.
                                                                                                                                                                   MGD; MGI:1276541; Pirall.
                                                                                                                                                                                                                                                                                                                               STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10090;
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                                                                                                         InterPro;
                                                                                                                            [nterPro;
                                                                                                                                             interPro;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 DSRLPAVQEWGAQEPVHLDS---PAIKHQF-LLTGDTQGRYR------CRSGLSTG 100
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                                                                                                   IPR003599; Ig.
IPR003600; Ig_like.
IPR003006; Ig_MHC.
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(TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 AA;
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635
; 70558 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
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17,
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                                                                                                                                                                                                                                                                                                           Tsuji A., Nagabukuro A.,
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Pred. No. 1.6;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
(KILLER CELL INHIBITORY
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                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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           8A6CA830D1BDB3D9 CRC64;
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in Escherichia coli.*;
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                                                                                                                                                                                                                                                                                           Takai
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Query Match

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Q9Q719;
01-MAY-2000
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Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.
Nishikawa T., Nagai K., Sugano S., Takahashi Pujii A., Hara H.,
Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
Arita M., Nahekura T., Ishii S., Kawai Y., Saito K., Yamanoto J.,
Wakamatsu A., Nakamura Y., Nagihari K., Masuho Y., Oshima A.;
"NEDOO human cDNA sequencing project.";
                                                                                                                                                                                                                                                                                                                                   Ol-OCT-2000 (TEEMBLEE! 15, Created)
Ol-OCT-2000 (TEEMBLEE! 15, Last sequence update)
Ol-OCT-2000 (TEEMBLEE! 15, Last annotation update)
CDNA FLJ10565 FIS, CLONE NT2RP2002954.
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Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFECT.
ProDom; PD000063; Viral_infect; 1.
SEQUENCE 192 AA; 22589 MW; E90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Janssens W., Laukkanen T., Salminen M.O., Carr J.K., Van der Anwera G., Heyndrickx L., Van der Groen G., McCu "HLV-1 subtype H near-full genome reference strains and subtype-H-containing inter-subtype recombinants."; Submitted (EEP-1999) to the BMBL/GenBank/DDBJ databases. BMBL, AF190127; AAF18396.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae;
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01-JUN-2001
                                                                                                                                             SEQUENCE FROM N.A.
Isogai T., Ota T., Hayashi K.,
                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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Primates; Catarrhini;
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Pred. No.
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                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
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098/03; O1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLRel. 17, Last sentation update)
4 PPOTRETICAL 50.7 KDA PROTEIN.
                      Submitted (NOV-2000) to the EMBL/GenBank/DDBJ EMBL; BC000132; AAH00132.1;
                                                                                                          Homo sepions (Human).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
Mammalla: Eutherla: Primates: Catarrhini: Hominidae: Homo.
                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 71.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FFB-2000) to the EMBL/GenBank/DDBJ databases EMBL; AK001427; BAA91685.1; -.
 SEQUENCE
            Hypothetical
                                                Strausberg R.;
                                                             TISSUE CHORIOCARCINOMA;
                                                                                                                                                                                                     О9вмм3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC001750; AAH01750.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                   NCBI_TaxID .9606;
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647 AA; 71717, MW;
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                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ,
                                                                                                                                                                                                                                                                                                                                                                                                                                              50706 MW;
                                                                                                                                                                                                                                                                                                                                                                                           11.3%;
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                                                                                                                                                                                                                                                                                                                                                                                         Score 75;
Pred. No.
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                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              4929E4CEADCF50A7 CRC64;
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 9F45C88511311460 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       No.
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84
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1.6;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 458;
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                                      databases
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                                                                                                                                                                                                                                                                                                                               -GSQESRHLLSPQLVQYQ 55
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RROCCOS GETTT
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Q9P209
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Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OSP209
OSP209
OPP209;
01-0CT-2000 (TrEMBLrel. 15, C. 01-0CT-2000 (TrEMBLrel. 15, L. 01-UJN-2001 (TrEMBLrel. 17, L. NIANISIS) PROTEIN (FRAGMENT).
                                                                                                  070434 PRELIMINARY;
070434;
01-AUG-1998 (TTEMBLTel. 07, 0
01-AUG-1998 (TTEMBLTel. 07, 1
01-JUN-2001 (TTEMBLTel. 17, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nagase 7., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human
genes.XVII.The complete sequences of 100 new cDNA clones from brain
which code for large proteins in vitro.";
DNA Res. 7:143-150(2000).
EMBL; AB040952; BAA95043.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sepiens (Human).
Eukaryota; Metazoo; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                Eukaryota;
                                                                              PIRA11
                      NCBI_TaxID-10090;
                                                             Mus musculus (Mouse).
                                                                                         KILLER ACTIVATORY
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00446; LRRcap; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-20277482; PubMed 10819331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIAA1519
                                     Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00560; LRR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001611; LRR.
InterPro; IPR003603; LRRcap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                        81 FLLTGDT--QGRYRCRSGL----STGWXQL 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                             --- CGDSGKQGRETRRSSCRGCCLEKMPWSQL 274
                                                                                                                                                                                                                                                                                  ADDEAVLNLIAECEWDLGRPPGSTSFSQKGREADSR-----GSQESRHLLSPQLVQYQ 245
                                                                                                                                                                                                                                                                                                          AESEHXLKTLGQCDADVPGPPG------DSRLPAVQEWGAQEPVHLDSP-AIKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- CGDSGKQGRETRRSSCRGCCLEKMPWSQL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDEAVLNLIAECEWDLGRPPGSTSFSQKGREADSR-----GSQESRHLLSPQLVQYQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AESEHXLKTLGOCDADVPGPPG-------DSRLPAVQEWGAQEPVHLDSP-AIKHQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLLTGDT -
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                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                     648 AA; 71801 MW;
                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -QGRYRCRSGL----STGWXQL 104
                                                                                       BLrel. 07, Last sequence update)
BLrel. 17, Last annotation update)
RECEPTOR-LIKE PROTEIN P91D (FRAGMENT)
                                     Rodentia;
                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.3%;
                                                                                                                                                                                                                                                                                                                                                 31.38;
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                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                 Score 75;
Pred. No.
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Pred. No.
                                     Sciurognathi;
                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     44AC3750072B661E CRC64;
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                                       Muridae;
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SEQUENCE FROM N.A.

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ACCOCCARRANCE COCCARRANCE COCC
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055001
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Query Match
Best Local S
Matches 32
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Best Local Similarity 28.6
Matches 32; Conservative
                                                                                                                  InterPro: IPB003509: Ig
InterPro: IPB003500: Ig_lHc.
InterPro: IPB003006: Ig_HC.
Pram: PP00047: Ig; Is
SMART: SM00409: IG_lKer: 2.
SEAURY: SM0410: IG_lKer: 2.
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01-JUN-2001 (TrEMBLrel.
PAIRED-IG-LIKE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O55001;
01-JUN-1998 (TrEMBLrel.
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Nishikawa Y. Ohyama Y. Ohmori H. Ono M., Takai T.
"Genomic structures and chromosomal location of p91, a nov
regulatory receptor family."
J. Blochem. 123:356-368(1998).
                                                                                                                                                                                                                                                                                                                                                                             Yamashita Y., Fukuta D., Tsuji A.,
Nishikawa Y., Ohyama Y., Ohmori H.,
J. Biochem. 123:0-0(1998).
-!- SIMILARITY: TO IMMUNOGLOBULIN A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIRA10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN P91B).
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MGD; MGI:1276541; Pirall.
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                                                                                                                                                                                                                                                                                                            EMBL; AF041035; AAB96927.1; HSSP; P43626; INKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                     MGD; MGI:1276542; Piral0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-129/SV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
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                                                                                                                                                                                                                                                                                                                                                         DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSQKTQSTQTLQQPGNKGKFFIPSVTQQHAGQYRCYCYSSAGWSQPSDTLEL
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
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                          11.3%;
28.6%;
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11;
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Last annotation update)
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Pred. No. 6
                          Score 74.5;
Pred. No. 6
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                                                                                                                     5311DFE6D291BF11 CRC64;
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   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    AND MAJOR HISTOCOMPATIBILITY COMPLEX
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, Ono M., Takai
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                                                DB 11;
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   48;
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T.;
                                             Length 680;
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RESULT
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                             075018
075018;
01-NOV-1998
01-NOV-1998
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09WPD4;
01-NOV-1999
01-NOV-1999
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS: PROD349; VIRIONINFECT.
PRODOM; PD000063; VIRAL_infect; 1.
SEQUENCE 192 AA; 22805 MW; CEB7D94BB76F6280 CHC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long-term asymptomatic individuals.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ
EMBL; AF143108; AAD37875.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9WPD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vigne R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hassaine G., Agostini I., Candotti
Agut H., Autran B., Barthalay Y., T
                       EMBL; AF025529; AAB87663.1; -. HSSP; P43626; 1NKR.
                                                                      -!- SIMILARITY:
DOMAIN.
                                                                                                                  Borges L., Hsu M.-L., F
J. Immunol. 0:0-0(1997)
                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                            LEUCOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00559; Vif;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000475; Viral_infect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Characterization of human immunodeficiency virus type 1 vir gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VIOBOO3A1L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-11676;
                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFLLLWGVTWGPVTEA----AIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV
                                                                                                                                                                                                                                                                                                                                     98 (TrEMBLrel. 08, Created)
98 (TrEMBLrel. 08, Last sequence update)
01 (TrEMBLrel. 17, Last anostation update)
IMMUNOGLOBULIN-LIKE RECEPTOR-6B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                 IMMUNOGLOBULIN
                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.2%;
                                                                                                                                         Fanger N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; DB :
Pred. No. 1.8;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                         Kubin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
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                                                                                                                                             Cosman
                                                                                                 HISTOCOMPATIBILITY COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
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IPR003600; Ig_like

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RESOLT 10 5054T 10 50
RESULT 22
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Best Local S
Matches 34
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01-WOV-1998 (TrEMBLrel. 08, Created)
01-WOV-1998 (TrEMBLrel. 08, Last sequence update)
01-WOV-2001 (TrEMBLrel. 17, Last annotation update)
LEUCOCYTE IMMUNOCLOBULIN-LIKE RECEPTOR-1.
Homo sapiens (Human).
Q9LVK0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           викатуоta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla: Eutherla; Primates; Catarrhini; Hominidae; Homo.
NGI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 4.
SMART; SM00409; IG; 2.
SMART; SM00410; IG_11ke; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro: IPR003599;
InterPro: IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P43626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsu M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cosman D.,
                                                                                                                                              103
                                                                                                     109
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                                                                                                                                                                                                                                                                                                                                                         Local Similarity 26.0 cs 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21
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                                                                                                                                              QUSKLLEL 110
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                                                                                                     ESSDPLEL
                                                                                                                                                                                      GOETQEYRLYREKKTAPWITRIPQEL---VKKGQFPIPSITWEHAGRYRCYYGSDTAGRS
                                                                                                                                                                                                                            VQE-----WGAQEPVHLDSPAIKHQF---LLTGDTQGRYRCRSGLST-GWX 102
                                                                                                                                                                                                                                                                           MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVI----
                                                                                                                                                                                                                                                                                                                MSMLVVFLLLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               650 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                               70816 MW;
                                                                                                                                                                                                                                                                                                                                                                             11.2%;
26.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borges L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QEIVK------KGQFPIPSITWEHTGRYRCFYGSHTAG
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Pred.
                                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 4; Length 650 Pred. No. 6.8;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               D1321C0982B44BCA CRC64;
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  187
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A
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                                                                                                                                                                                                                                                                                                                                                         50;
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clones, 7:131-135(2000).
DNA Res. 7:131-135(2000).
EMBL; AB019229; BAB02330.1;
EMBL; AB019229; BAB02330.1
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01-0CT-2000
01-0CT-2000
InterPro; IPR000475; Viral_infect
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; Viral_infect; 1
SEQUENCE 192 AA; 22513 MW; 07
                                                                                                                                          "In vivo genetic variability of the Virology 203:43-51(1994).
EMBL; 230684; CAAB3164.1; -
                                                                                                                                                                                                                                    Wieland U., Hartmann J., Kuehn J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN COLUMBIA;
Sato S., Nakamura Y.
Submitted (OCT-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta; Eukaryota; Tracheophyta;
Spermatophyta: Magnoltophyta: eudocvjtedons; core eudicots; Rosidae;
eurosids II. Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                        MEDI.INE-94303241; PubMed-8030283;
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-PATIENT A17;
                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; Retroid
NCBI_TaxID-11676;
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features of the region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 20277480; PubMed 10819329;
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(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 15, Last annotation
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to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                        Salzberger B.,
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       CRC64;
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                                                                                                                                                                                                                                                            H.J.,
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                           Sova P., van Ranst M., Gupta P., Balachandran R., Chao W., Itescu 9 McKinley G., Volkky B.J.; "Conservation of an intact human immunodeficiency virus type 1 vif gene in vitro and in vivo.; "J. virol. 69.257-2564(1995).

EMBL: 042260; AAA83809.1; "EMBL: 042260; AAA8809.1; "EMBL: 042260; AAA8809.1
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073438.9 PRELIMINARY: PRT: 104 DAA.
073438.0 PRELIMINARY: PRT: 104 DAA.
073408.0 PRELIMINARY: PRT: 104 DAA.
073438.0 PRT: 104 D
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MEDLINE-99077292: PubMed-9862476:
Xu S.-Y., Xiao J.-P., Ettwiller L., H
Dalton M., Robinson D.P., Petronzio T
Ware J., Slatko B., Benner J.;
"Cloning and expression of the Apall,"
                                                                        InterPro: IPR000475; Viral_infect
Pfam; PF00559; Vif; 1.
ProDom; PD000063; Viral_infect; 1
SEQUENCE 104 AA; 12534 MW; 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nostoc sp. ATCC 29106.
Bacteria: Cyanobacteria:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1
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Gen. Genet. 260:226-231(1998). 
, AF056037; AAC97193.1; -. 
SE: 1388: NspHI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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21; Conservative
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10, Last sequence update)
16, Last annotation update)
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5; Mismatches
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Pred. No. 3
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                                                                             2249B6ACA3C67412 CRC64;
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in Escherichia coli.*;
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Q73413;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
SEQUENCE FROM N.A.
MEDLINE-95191036; PubMed-7884906;
SOWA P., Van Ranst M., Gupta P.,
Workinley G., Volsky D.J.;
"Conservation of an infract human
gene in vitro and in vivo.";
                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                             Viruses; Retroid
NCBI_TaxID=11676;
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5 (TrEMBLrel. 01, 05 (TrEMBLrel. 01, 01, 01) (TrEMBLrel. 17, 01)

Last sequence update)
Last annotation update)

Lentivirus

immunodeficiency virus type 1 vif Balachandran R., Chao W., Itescu Created)

PRELIMINARY;

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Q73410
Q73410;
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Q1-NOV-1996
Q1-NOV-1996
Q1-JJN-2QQ1
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gene in vitro and in vivo.";
J. Virol. 69:2557-2564(1995).
EMBL: U41179: AAA83771.1; -
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SEQUENCE 192 AA; 22655 MW; 4B1
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McKinley G., Volsky D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95191036; PubMed=7884906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; Retroid viruses; NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1
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68 TYWG----
                                                                                                                                                           Local Similarity
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                                62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
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                                                                      8 MIVWQVDRMRIRTWKSLVKHHMYISKKAKEWSYRHHYESTHPKISSEVQIPLGDARLVIT
                                                                                                      8 LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
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(TrEMBLrel. 17, Last annotation update)
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Pred. No.
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Q91QD9;
01-OCT-2000
01-OCT-2000
01-JUN-2001
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01-NOV-1996
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gene in vitro and in vico";
J. Virol, 69.2557-2564(1995).
EMBL, U42261, AAM88BJO 11:0.
InterPro: IPRODATS; Viral_infect.
Piam; PRODS9; VIFIONINFECT.
PRINTS; PRODS9; VIFIONINFECT.
PRINTS; PRODS9; VIFIONINFECT.
PRINTS; PRODS9; VIFIONINFECT.
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Int.crPro; IPR000475; Viral_infect.
Pfam; PF00559; Vit; 1
PRIMTS: PR00349; VIRIONINFECT.
PRODOS: PD00063; VIRI_infect: 1
SEQUENCE 192 AA; 22670 MW; CB2
Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sova P., van Ranst M., Gupta P., Balachandran R., McKinley G., Volsky D.J.;
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Viruses; Retroid viruses; Retroviridae;
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                                                                       Last sequence update)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 192;
                                                                                                                                                                         ₹
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chao W., Itescu S.,
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RESULT Q9VN92

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SOR BERT REAR SON
В
                                                     Query Match
Best Local S
Matches 23
                                                                                                                 InterPro; PRO00475; Viral Infect.
Pfem: PF00559; Vif: 1.
PRINTS; PR00349; VIRIONINFECT.
Probom: P0000063; Viral_Infect: 1.
SEQUENCE 192 AA; 22692 MW; 59E
                                                                                                                                                                                        Arch. Virol. 145:1021-1027(
EMBL; AB034495; BAA93952.1;
                                                                                                                                                                                                                             "Comparison of proviral accessory genes
                                                                                                                                                                                                                                                            Yamada T.,
                                                                                                                                                                                                                                                                         MEDLINE 20338596; PubMed-10881687
                                                                                                                                                                                                                                                                                     STRAIN PATIENT 16;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCB1_TaxID·11676;
[1]
                                                                                                                                                                                                                    infection. ";
                                                     Local Similarity
hes 23; Conserv
 œ
                          8 LLLLWGV-----TWGPVTEAATFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
MIVWQVHRMRIRTWKSLVKHHIHISKKAKEWAYRHHYESTNPRISSEVHIPLGDAKLVIA 67
                                                                                                                                                                                                                                                          Iwamoto A.:
                                                     Conservative
                                                                                                                                                                                                     145:1021-1027(2000).
                                                                10.9%;
                                                   Score 72; DB :
Pred. No. 3;
14; Mismatches
                                                                                                                       59EAB6422515AB9C CRC64
                                                                             DB 12; Length 192;
                                                                                                                                                                                                                                 immunodeficiency virus type 1
                                                                                                                                                                                                                                               between long-term
                                                     41;
                                                       Indels
                                                     24;
                                                     Gaps
                                                     Ψ
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68 TYWC----
                                                                                                                                                                        62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGWXQ
PRELIMINARY;
                                                                                                                       -----LHTGER--NWHLGQGVSIEWRQ 91
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Q9VN92; CG12163 PROTEIN. CG12163. Ol-MAY-2000 (TrEMBLIGE). 13, Created)
Ol-MAY-2000 (TrEMBLIGE). 13, Last sequence update)
Ol-JUN-2001 (TrEMBLIGE). 17, Last annotation update) SEQUENCE FROM N.A. Ephydroidea; Dro NCBI_TaxID-7227; Pterygota; Neoptera; Drosophila Eukaryota; melanogaster (Fruit fly) Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Drosophilidae; Drosophila Endopterygota; Diptera; Brachycera; Muscomorpha;

RA Addiss M.D., Celniker S.E., Nott R.A., Evens C.A., Goovpe J.D.,
RA Mannatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA Saltton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Saltton R.C., Rogers Y.-H.C., Elazej R.G., Champe M., Pfeiffer B.D.,
RA Handan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Welson C.R., Miklos G.L.G.,
RA Harlis M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakteroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bahadari D., Bolshakov S.,
RA Barkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Bussan D.A., Butler H., Cadleu E., Conter A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA Chen D., Bous D., Beller R., Deng T., Bays A.D., Dew I., Dietz S.M.,
RA Chodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischman M.,
RA Hostin N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Hostin N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum X.A.,
RA Hostin N.L., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Katchum X.A., MEDLINE-20196006; PubMed-10731132;

Jalali M., Kalish F., Karpen G.H., Ke Z., Kennison J.Â., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Krvitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., ×. A.,

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Welson D.R., Nelson K.A. Nixon K., Nasskern D.R., Pacleb J.H.,
AN Palazzolo M., Pittman G.S., Pen S., Pollard J., Putl V., Reses M.G.,
A Pellert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
AN Shue B.C., Siden K.Hamos I., Simpson M., Schoeler F., Shen H.,
AN Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
AN Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbod J.,
AN Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbod J.,
AN Williams S.M., Woodsge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
AN Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao X., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao X., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao X., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao X., Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
R HSSP, P25779, AAM, SCHOLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
              MEDLINE-20477377: PubMed-10984043:
Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
Hickey M.J., Brinkman F.S.L., Hafnagle W.O., Rowalik D.J., Lagrou M.
Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
Brody L.L., Coulter S.N., Folger K.R., Kab A., Larbig K., Limm R.M.,
Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
Reizer J., Saler M.H., Hancock R.E. & Lovy S., Olson M.V.;
Complete genome sequence of Pseudomonas aeruginosa PAOI, an
opportunistic pathogen."
Nature 406:259-594(200).
                                                                                                                                                                                                                                                                                                                                                       Q9HUR4;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                    PROBABLE ALDEHYDE DEHYDROGENASE. annotation update)
PA4899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00705; PAPAIN.
ProDom; PD031531; Sarcocystatin;
SMART; SM00043; CY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0037303; CG12163.
InterPro; IPR000010; Cystatin.
InterPro; IPR00068; Peptidase_C1.
InterPro; IPR00344; Sarcocystatin.
InterPro; IPR003149; Finolprot_act_site.
Pfam; FP00112; Peptidase_C1; 1.
PRINTE: PR00175; Phany
                                                                                                                                                                                                STRAIN-PAO1
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HUR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                                    NCBI_TaxID-287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 VHLDSPAIKHQ------FLLTGDTQGRYRCRSGLSTGWXQLSKLLELTGPKVLAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 WGVT-WGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQEP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V----TQVKNQGSCGSCWAFSVTGNIEGLYAVKTG-----ELKEFSEQELLDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGITEFADMTSSE--YKERTGLWQRDE--AKATGGSAAVVPAYHGE--LPKEFDWRQKDA 266
AE004903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00640; THIOL_PROTEASE_ASN;
PS00139; THIOL_PROTEASE_CYS;
PS00639; THIOL_PROTEASE_HIS;
PS00639; THIOL_PROTEASE_HIS;
PS00639; Thiol protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G.,
                                                                                                                                                                                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milshina N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53545 MW; 130DE83869498EF1 CRC64;
                                                                                                                                                                                                                                                                                    gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
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                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                              489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H.O.,
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RESULT
Q73435
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Q73412
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   SSEPPPP
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Best Local S
Matches 21
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Best Local Similarity
Matches 32; Conserv
                                                     O73435
O73435
O73435:

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Q73412;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
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PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
Complete proteome.
489 AA; 52697 MM: DEFRAREFF7779700
                                               VIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000475; Viral_infect
Pfam; PF00559; Vif; 1.
PRINTS; PR00349; VIRIONINFFCT.
Probom; PD000063; Viral_infect; 1
SEQUENCE 192 AA; 22707 MW; 57/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Conservation of an intact human immunodeficiency virus type 1 vif
gene in vitro and in vivo."
J. virol. 69:257-2564(1995).
EMBL; U41181; AAA83773.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIRUS
Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; Retroid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                   TYWG---
                                                                                                                                                                                                                                                                                                                                            QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW
                                                                                                                                                                                                                                                                                                                                                                                         MIVWQVDRMRIRTWKSLVRHHMYVSKKAKEWSYRHHYESTHPKISSEVQIPLGDARLVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFPARVHGRIVESDVPGKESRVYRSAIGVVGVISPWNFPLHLT-QRSIAPALALGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --PAIKHQFLLTGDTQGR----YRCRSGLSTGWXQLSKLLELTGPKVLACSLALDGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPSARAAVLYKAVEVFDRRHEEIVDWIIR-----ESGSTRLKAEIEWGAARAITLESA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQEPVHLDS- 74
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G., Volsky D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                             ------LHTGERE--WHLGQGVSIEW
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17,
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                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                     Created)
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Pred. No.
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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   Lentivirus
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Best Local S
Matches 23
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046780;
046780;
01-JUN-1998
01-JUN-1998
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Q99BT8;
Q1-JUN-2001
Q1-JUN-2001
Q1-JUN-2001
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Pfam; PF00559; V1f; 1.
PRINTS; PR00349; VIRIONINFFCT.
ProDom; PD000063; VIral_infect; 1
ProDom; PD000063; VIral_infect; 1
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McKinley G., Volsky D.J.;
Consorvation of an intact human immunodeficiency virus type 1 vif
gene in vitro and in vivo.;
J. Vicol. 69.2557-256 (1995).
EMBL; U42237; AAA88806.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-TV001-2;
Scriba T.J., Treurnicht F.K.,
Janse van Rensburg E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization and phylogenetic analysis subtype C accessory genes.";
AIDS Res Hum. Retroviruses 0:0-0(2001).
EMBL: AF325742; AAK09096.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; Retroid viruses; Retroviridae; Lentivirus NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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les 22; Conser
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                                                                                                                                                                                                                                                                                        LIVWQVDRMKIRTWNSLVKHHMYISRRASGWSYKHHFESRHPKVSSEVHIPLGDARLVIK 67
                                                                                                                                                                                                                                                                                                                                      LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYWG-----LNTGERD--WHLGQGVSIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLLWGV-----TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIVWQVDRMRIRTWKSLVKHHIYISRKTKGWVYRHHYESTNPKTSSEVHIPLGDARLVVT
(TrEMBLrel.
                                                                                                                                                                                               73
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                                                                     PRELIMINARY;
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90,
                                                                                                                                                                                                                                                                                                                                                                                                           . 88;
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                                                                                                                                                                                                                                                                                                                                                                                    12;
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Pred. No. 3.9;
12; Mismatches
                       Created)
Last sequence update)
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Pred. No.
                                                                     PRT;
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SEQUENCE FROM N.A. NCBI_TaxID~6239; Rhabditidae; Peloderinae;

STRAIN-BRISTOL N2; MEDLINE-94150718; PubMed-7906398;

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Button J., Connell M., Copsey T., Copper J., Coulson A.
Crarton M., Dear S., Bu Z., Durbin R., Favello A., Fillon M.,
Gardner A., Green P., Hewkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Lakrellia Phomes
Lightning J., Lloyd C., Kirsten J., Wortlmore B., Colliphan M.,
Parsons J., Percy C., Riken L., Roopra A., Saunders D., Shownkeen Brasons J., Percy C., Riken L., Roopra M., Sauther S., Staden N., Sulston J.,
Thierry-Nies J., Thomas K., Vaudin M., Vaughan K., Shiston R.,

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RESULT 045087 ID 04

045087 PRELIMINARY: 045087; 01-JUN-1998 (TrEMBLrel. 0 01-JUN-1998 (TrEMBLrel. 0 01-JUN-1990) (TrEMBLrel. 1 C17H12.1 PROTEIN.

06, 06,

PRT;

643

Last sequence up Created)

update)

Caenorhabditis elegans

Eukaryota; Metazoa;

Nematoda; Chromadorea; rinae; Caenorhabditis.

Rhabditida; Rhabditoidea;

C17H12

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102

XQLSKLLELTGPKVLACSLALDG

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83

YNOSEAGSHTLOWVLGCDVGLDG

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                                                            Query Match
Best Local Similarity
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                            SUBMILTED (NOV-1997) to the EMBL/GenBank/DDBJ dAtabases.
-- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIC
-- SUBMINIT: DAMER OF SHILARITY, SHOULD ABOUT CHAIN (BETA-2-
MICROGLOBULIN) (BY SHILARITY).
                                                                                                                                                                                                Pfam; PF00047; ig: 1. Pfam; PF00129; MHC_I; 1.
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Submitted (NOV-1997) t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                  Glycoprotein; MHC;
                                                                                                                                                              PROSITE; PS00290; IG_MHC; 1
                                                                                                                                                                        ProDom; PD000050; MHC_I; 1.
SMART; SM00407; IGcl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BL;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9913
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
                         46
 35
                                                                                                                                                                                                                                                                                                MICROGLOBULIN) (BY SIMILARITY SIMILARITY: TO IMMUNOGLOBULIN
                                                                                                                                                                                                                                                                                        DOMAIN
DSDAPNPRMEPRAP----WMEQEGPEYWEA-----MTRDAKKAQQRLRTGLNTIRGF 82
                        DADVPGPPGDSRLPAVQEWGAQE-PVHLDSPAIKHQFLLTGDT-QGRYRCRSGLST--GW 101
                                                                                                                                                                                                                      IPR003597; Ig_c1.
IPR003006; Ig_MHC
IPR001039; MHC_I.
                                                                                                             288
288 AA;
                                                 Conservative
                                                                                                                                              Transmembrane
                                                                                                             32994 MW;
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                                                 13;
                                                          Score 71;
Pred. No.
                                                                                                            833F22F170ECAB58 CRC64;
                                                 Mismatches
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                                                 28;
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                                                 Indels
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Submitted (FEB-1998) to the
EMBL, AF645642; AAC02580.1;
InterPro; IPR001680; WD40.
Pfam; PF004000, WD40; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TREMBLIREL 01, 01-NOV-1996 (TREMBLIREL 01, 01-JUN-2001 (TREMBLIREL 17, VIRUS INFECTIVITY FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q73436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geisel C.;
Submitted (FEB-1998)
                                                                                                                                                                                                                                                                                                    InterPro; IPR000475; Viral_infect. pfam; PF00559; Vif; 1. Probom; PF0000063; Viral_infect; 1. SEQUENCE 147 AA; 17456 MW; AE0
                                                                                                                                                                                                                                                                                                                                                                                                                              gene in vitro and in vivo.";
J. Virol. 69:2557-2564(1995).
EMBL; U42258; AAA83807.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immunodeficiency virus type 1
Viruses; Retroid viruses; Retroviri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; WD repeat
SEQUENCE 643 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50294; WD_REPEATS_REGION; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00320; GPROTEINBRPT SMART; SM00320; WD40; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95191036; PubMed-7884906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLDVAWSPV-HPAVF----ASIDADGNIFVWNLNE---DVEGPV--ARLRA----GAEG 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLWGVTWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAVQEWGAQ- 67
                                                                                                LLLWGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPVHLD----SPAIKHQFLLTGDTQGR---YRCRSGL----STGWXQLSKLL 108
                                     M1VWQVDRMRIRTWKSLVKHHIYISRKTKGWCYRHHYESTNPKTSSEVHIPLGDARLIVT
                                                                                                                                                                                        Similarity
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                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                -TWGPVTEAAIFYETQXSLWAESEHXLKTLGQCDADVPGPPGDSRLPAV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72048 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
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Last annotation updat
                                                                                                                                                      Score 70; DB
Pred. No. 3.7;
L4; Mismatches
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                                                                                                                                                                                                                                                                                                             AEOFC620FB3F9DE6 CRC64
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Best Local :
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Q9DPZ9;
01-MAR-2001
01-MAR-2001
01-JUN-2001
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*Conservation of an intact human immunodeficiency virus type 1 vif gene in vitro and in vivo.*

J. Virol. 69:2557-2564(1995).

EMBL: U42256. AAA83805.1:

InterPro. ITR000475; Viral infect.

Ffam. PF00559; Vif; 1.

Ffam. PF0059; Vif; 1.

PFNINTS: PR00349; VIRIONINFECT.

PRINTS: PR00349; VIRIONINFECT.

PRODM: DF000653; Viral infect: 1.

SEQUENCE 192 AA: 22484 MW; 65C50FE6B6D73FEC CRC64;
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Q73434;
Q1-NOV-1996
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Ndung'u T. Renjifo B. Novitsky V.A. McLane
Submitted (JUL-2000) to the DMBL/GenBank/DDBJ
BMBL, AF290039, AAG34021.1; - THEFFOT, IPR000475; VIFA _infect.
Figur, PF00559; VIF. 1.
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                                                                                                                                                                                                                                                                                                        Ndung'u T.,
Essex M.;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=20569522; Pu Ndung'u T., Renjifo
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type
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01-JUN-2001
                                                                                                                                                                                                                 Virology
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          "Molecular cloning and biological characterization
l subtype C from Botswana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 QEWGAQEPVHLDSPAIKHQFLLTGDTQGRYRCRSGLSTGW 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                  PubMed=11118362;
fo B., Novitsky V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Retroviridae; Lentivirus
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                                                                                            M.F., Esse
databases
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01-MAY-1999
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01-JUN-2001
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VIF PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rodenburg C.M., Ll. Y., Trosk S.A., Chen Y., Decker J., I
Allen S., Shaw G.M., Hahn B.H. Gao F.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL, AP28623; AAK30956.];
SEQUENCE 192 AA: 22625 MW; EOF8C15FE8211645 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses: Retroid
NCBI_TaxID-11676;
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STRAIN-94IN476;
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Viruses; Retroid viruses; Retroviridae;
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Length Indels

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EMBL: AF040946; ANB9700B.1; J
EMBL: AF04094B ANB9700B.1; J
EMBL: AF04094B ANB9700B.1; J
EMBL: AF040950 ANB9700B.1; J
EMBL: AF040950 ANB9700B.1; J
EMBL: AF040951 ANB9700B.1; J
EMBL: AF040952 ANB9700B.1; J
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054999;
01-JUN-1998
                                                                                                                                                                                                                                                      EMBL;
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Matsuda Y., Nishikawa Y.,
J. Biochem. 123:0-0(1998)
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01-JUN-2001 (TrEMBLE-E 17, Last annotation update)
PAIRED-IG-LIKE RECEPTOR B (KILLER CELL INHIBITORY RECEPTOR-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davison A.J., Sauerbier W., Dolan A., Addison C., McKinnell R.G.;
"Genomic studies of the fucke tumor herpesytrus (RaHV-1).";
Submitted (MOV-1998) to the EMBL,/GenBank/DDBJ databases.

EMBL, AF110004: AAD12285.1;
SEQUENCE 728 AA: 81366 MN: 78F7921CA573743D CRC64:
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COS54_22.
Ranid herpesvirus 1 (Lucke tumor herpesvirus).
Viruses; dsDNA_viruses, no RNA stage; Herpesviridae
                                                            Pfam: PF00047; ig: 5. SMART; SM004409; IG: 1. SMART; SM000410: IG: 1ike; 2. SMART; SM00410: IG: 1ike; 2. SEQUENCE 841 AA; 93225 MW;
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;

    -!- SINILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

                                                                                                                                                                                                                                                                                                                              STRAIN-129/SV;
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                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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Rodentia;
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Sciurognathi; Muridae;
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Best Local S
Matches 21
Query Match
Best Local Similarity
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01-AUG-1998
01-AUG-1998
01-JUN-2001
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01-AUG-1998
01-AUG-1998
01-JUN-2001
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Submitted (JAM-1998) to the BMBL/GenBank/DDBJ databases.
EMBL: AF042102: AAD02210.1;
LinterPro: IPR000475; Viral_infect.
PRODOS: Viral_infect.
PRODOS: Viral_infect.
PRINTS: PR00349; VIRTONINFECT.
PRODOM: PR000063: Viral_infect; 1.
SEQUENCE 192 AA: 22500 MA: 22A97D251BC1ED40 CRC64;
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                                                                                         InterPro; IPR000475; Viral_infect
Pfam; PF00559; Vif; 1.
PRINTS; P800349; VIRIONINFECT.
ProDom; P8000063; Viral_infect; 1
SEQUENCE 192 AA; 22599 MW; 0D0
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF049494; AAC68843.1; -
                                                                                                                                                                                                                                                              STRAIN-HIV-1JC;
Mwaengo D.M., Novembre F.J.;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Viruses; Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
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Pred. No.
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                       Length 192;
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071971;
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01-AUG-1998
01-AUG-2001
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EMBL, AR069495; AAC688521; -
InterPro, IPRO00475; VIral_infect.
Plam, PP0059; VIf: 1
PRINTS; PR00349; VIRIONINEFCT.
PRODOM: PD00065; VIRIA_Infect; 1
SEQUENCE 102 AA; 22398 MM; AAE7908042ABC99
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
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Mwaengo D.M., Novembre F.J.;
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LHTGERE--WHLGHGVSIEWRKRS
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Pred. No. 6.4;
18; Mismatches
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Last annotation update)
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